```
  Query Match             1.2%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 74;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        463 AGCAGCCTGCAGGGGGAGGA 482
              ||||| |||||||| |||||
Db         1 AGCAGGCTGCAGGGAGAGGA 20


RESULT 14
AX404468/c
LOCUS       AX404468                 21 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 294 from Patent WO0224747.
ACCESSION   AX404468
VERSION     AX404468.1  GI:21437749
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U. and Hoffmeyer,S.
  TITLE     Polymorphisms in human genes of cardiovascular regulators and their
            use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 0224747-A 294 28-MAR-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="artificial sequence"
BASE COUNT        1 a      11 c      3 g      6 t

  Query Match             1.2%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 74;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        463 AGCAGCCTGCAGGGGGAGGA 482
              ||||| |||||||| |||||
Db         21 AGCAGGCTGCAGGGAGAGGA 2


RESULT 15
I26171
LOCUS       I26171                   21 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 22 from patent US 5556786.
ACCESSION   I26171
VERSION     I26171.1  GI:1606041
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kere,J., Schlessinger,D. and de la Chapelle,A.
  TITLE     Anhidrotic ectodermal dysplasia gene and method of detecting same
  JOURNAL   Patent: US 5556786-A 22 17-SEP-1996;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
BASE COUNT        6 a      5 c      4 g      6 t

  Query Match             1.2%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 74;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         78 TGAATAATAGCAGTTCTACC 97
              |||||||||||| |||| ||
Db          2 TGAATAATAGCACTTCTGCC 21


RESULT 16
I86414
LOCUS       I86414                   21 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 22 from patent US 5700926.
ACCESSION   I86414
VERSION     I86414.1  GI:3206132
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kere,J., Schlessinger,D., de la Chapelle,A. and Srivastava,A.Kumar.
  TITLE     Molecular cloning of the anhidrotic ectodermal dysplasia gene
  JOURNAL   Patent: US 5700926-A 22 23-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
BASE COUNT        6 a      5 c      4 g      6 t

  Query Match             1.2%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 74;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         78 TGAATAATAGCAGTTCTACC 97
              |||||||||||| |||| ||
Db          2 TGAATAATAGCACTTCTGCC 21


RESULT 17
AR162099
LOCUS       AR162099                 18 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 29 from patent US 6258558.
ACCESSION   AR162099
VERSION     AR162099.1  GI:16229168
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Szostak,J.W., Roberts,R.W. and Liu,R.
  TITLE     Method for selection of proteins using RNA-protein fusions
  JOURNAL   Patent: US 6258558-A 29 10-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        3 a      2 c      7 g      6 t

  Query Match             1.2%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 65;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        679 GTGGTATTTGGGAGCCAG 696
              |||||||||| |||||||
Db          1 GTGGTATTTGTGAGCCAG 18


RESULT 18
AR166624
LOCUS       AR166624                 18 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 29 from patent US 6281344.
ACCESSION   AR166624
VERSION     AR166624.1  GI:16242025
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Szostak,J.W., Roberts,R.W. and Liu,R.
  TITLE     Nucleic acid-protein fusion molecules and libraries
  JOURNAL   Patent: US 6281344-A 29 28-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        3 a      2 c      7 g      6 t
```

```
  Query Match             1.2%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 65;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        679 GTGGTATTTGGGAGCCAG 696
              ||||||||||| |||||||
Db          1 GTGGTATTTGTGAGCCAG 18


RESULT 19
AR279832
LOCUS       AR279832                 18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 29 from patent US 6518018.
ACCESSION   AR279832
VERSION     AR279832.1  GI:29714977
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Szostak,J.W. and Roberts,R.W.
  TITLE     RNA-antibody fusions and their selection
  JOURNAL   Patent: US 6518018-A 29 11-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        3 a      2 c      7 g      6 t

  Query Match             1.2%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 65;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        679 GTGGTATTTGGGAGCCAG 696
              ||||||||||| |||||||
Db          1 GTGGTATTTGTGAGCCAG 18


RESULT 20
AX039833
LOCUS       AX039833                 18 bp    DNA     linear   PAT 18-NOV-2000
DEFINITION  Sequence 222 from Patent WO0063441.
ACCESSION   AX039833
VERSION     AX039833.1  GI:11229862
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Herrnstadt,C. and Davis,R.E.
  TITLE     Single nucleotide polymorphisms in mitochondrial genes that segreg
            ate with alzheimer's disease
  JOURNAL   Patent: WO 0063441-A 222 26-OCT-2000;
            MITOKOR (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="PCR primer"
BASE COUNT        7 a      7 c      3 g      1 t

  Query Match             1.2%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 65;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         23 AAACCAAACCCAGCTACG 40
              |||||| ||||||||||||
Db          1 AAACCAGACCCAGCTACG 18


RESULT 21
AR224969/c
LOCUS       AR224969                 21 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 76 from patent US 6441149.
ACCESSION   AR224969
VERSION     AR224969.1  GI:23334086
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Herrnstadt,C., Ghosh,S.S., Clevenger,W., Fahy,E.D. and Davis,R.E.
  TITLE     Diagnostic method based on quantification of extramitochondrial DNA
  JOURNAL   Patent: US 6441149-A 76 27-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
BASE COUNT        5 a      2 c      8 g      6 t

  Query Match             1.2%;  Score 16.2;  DB 1;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 96;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 GCATACTCCTCAATTACCCAC 71
              |||||||| ||||| | ||||
Db         21 GCATACTCTTCAATCAGCCAC 1


RESULT 22
AX039751/c
LOCUS       AX039751                 21 bp    DNA     linear   PAT 18-NOV-2000
DEFINITION  Sequence 140 from Patent WO0063441.
ACCESSION   AX039751
VERSION     AX039751.1  GI:11229780
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Herrnstadt,C. and Davis,R.E.
  TITLE     Single nucleotide polymorphisms in mitochondrial genes that segreg
            ate with alzheimer's disease
  JOURNAL   Patent: WO 0063441-A 140 26-OCT-2000;
            MITOKOR (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="PCR primer"
BASE COUNT        5 a      2 c      8 g      6 t

  Query Match             1.2%;  Score 16.2;  DB 1;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 96;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 GCATACTCCTCAATTACCCAC 71
              |||||||| ||||| | ||||
Db         21 GCATACTCTTCAATCAGCCAC 1


RESULT 23
AX404674
LOCUS       AX404674                 22 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 48 from Patent WO0224745.
ACCESSION   AX404674
VERSION     AX404674.1  GI:21437955
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Abken,H. and Schinkoethe,T.
  TITLE     Method for detecting tumor cells
  JOURNAL   Patent: WO 0224745-A 48 28-MAR-2002;
            Abken, Hinrich (DE)
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FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Sonde"
BASE COUNT        8 a      0 c      2 g     12 t

  Query Match             1.2%;  Score 16.2;  DB 1;  Length 22;
  Best Local Similarity   85.7%;  Pred. No. 1.1e+02;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1145 TTTTTTCTTTTTGGAAGTAAA 1165
              |||||| |||||||||  |||
Db          1 TTTTTTTTTTTTGGAAAAAAA 21


RESULT 24
AR261288/c
LOCUS       AR261288                23 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 5 from patent US 6322780.
ACCESSION   AR261288
VERSION     AR261288.1  GI:28072198
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Lee,L.F., Nazerian,K., Witter,R.L., Wu,P., Yanagida,N. and
            Yoshida,S.
  TITLE     Marek's disease virus vaccines for protection against Marek's
            disease
  JOURNAL   Patent: US 6322780-A 5 27-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
BASE COUNT        4 a     10 c      6 g      3 t

  Query Match             1.2%;  Score 16.2;  DB 1;  Length 23;
  Best Local Similarity   85.7%;  Pred. No. 1.1e+02;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        519 CAACCTGCCGGAGGAGCAGCT 539
              |||| |||||| || ||||||
Db         21 CAACTTGCCGGGGGGGCAGCT 1


RESULT 25
AX272819/c
LOCUS       AX272819                17 bp    mRNA    linear   PAT 29-OCT-2001
DEFINITION  Sequence 388 from Patent WO0162911.
ACCESSION   AX272819
VERSION     AX272819.1  GI:16545556
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
            Ellis,J.H.
  TITLE     Method and reagent for the inhibition of grid
  JOURNAL   Patent: WO 0162911-A 388 30-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      8 c      4 g      0 t

  Query Match             1.2%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 69;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        299 CTGCTGTGGGGGCTGC 314
              ||||||||||||||||
Db         17 CTGCTGTGGGGGCTGC 2


RESULT 26
AX272820/c
LOCUS       AX272820                17 bp    mRNA    linear   PAT 29-OCT-2001
DEFINITION  Sequence 389 from Patent WO0162911.
ACCESSION   AX272820
VERSION     AX272820.1  GI:16545557
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
            Ellis,J.H.
  TITLE     Method and reagent for the inhibition of grid
  JOURNAL   Patent: WO 0162911-A 389 30-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      9 c      4 g      0 t

  Query Match             1.2%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 69;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        299 CTGCTGTGGGGGCTGC 314
              ||||||||||||||||
Db         16 CTGCTGTGGGGGCTGC 1


RESULT 27
AR195424/c
LOCUS       AR195424                20 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2 from patent US 6350868.
ACCESSION   AR195424
VERSION     AR195424.1  GI:20244861
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Weston,B.W. and Hiller,K.M.
  TITLE     Antisense human fucosyltransferase sequences and methods of use
            thereof
  JOURNAL   Patent: US 6350868-A 2 26-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT       11 a      3 c      3 g      3 t

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1322 CTTTTGTAGATCTTGTGTT 1340
              |||||||||||||  |||
Db         19 CTTTTGTAGATCTTCAGTT 1


RESULT 28
AR208816/c
LOCUS       AR208816                20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 25 from patent US 6383809.
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```
ACCESSION   AR208816
VERSION     AR208816.1  GI:21510069
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank. and Cowsert,L.M.
  TITLE     Antisense inhibition of cytohesin-1 expression
  JOURNAL   Patent: US 6383809-A 25 07-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        3 a      6 c      8 g      3 t

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        521 ACCTGCCGGAGGAGCAGCT 539
              |||||||||||||||  ||
Db         20 ACCTGCCGGAGGAGCTCCT 2


RESULT 29
AR306782
LOCUS       AR306782                 20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 19 from patent US 6548734.
ACCESSION   AR306782
VERSION     AR306782.1  GI:31697107
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Glimcher,L.H. and Ranger,A.M.
  TITLE     Methods relating to modulation of cartilage cell growth and/or
            differentiation by modulation of NFATp activity
  JOURNAL   Patent: US 6548734-A 19 15-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        6 a      3 c      7 g      4 t

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        934 CTGGAGAAGAGGTGTGAGC 952
              ||||||||||| | |||||
Db          1 CTGGAGAAGAGCTATGAGC 19


RESULT 30
AX000290
LOCUS       AX000290                 20 bp    DNA     linear   PAT 10-MAR-2000
DEFINITION  Sequence 6 from Patent EP0897990.
ACCESSION   AX000290
VERSION     AX000290.1  GI:7240716
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Jaeger,S. and Sobek,H.
  TITLE     Reduction of cross contamination within nucleic acid amplifications
  JOURNAL   Patent: EP 0897990-A 6 24-FEB-1999;
            BOEHRINGER MANNHEIM GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        8 a      3 c      6 g      3 t

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGCAG 292
              ||||| |||||||| ||||
Db          1 ATCAATGAGGAAGCTGCAG 19


RESULT 31
AX003992
LOCUS       AX003992                 20 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 52 from Patent WO9923249.
ACCESSION   AX003992
VERSION     AX003992.1  GI:9927652
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
  TITLE     Specific and sensitive method for detecting nucleic acids
  JOURNAL   Patent: WO 9923249-A 52 14-MAY-1999;
            KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);
            ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="SK102"
BASE COUNT        8 a      3 c      6 g      3 t

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGCAG 292
              ||||| |||||||| ||||
Db          1 ATCAATGAGGAAGCTGCAG 19


RESULT 32
AX006768
LOCUS       AX006768                 20 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 17 from Patent WO0003013.
ACCESSION   AX006768
VERSION     AX006768.1  GI:9994810
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leegwater,A.C., Van der Vliet,H.N., Chamuleau,R.A. and Groenink,M.
  TITLE     Gene and protein involved in liver regeneration
  JOURNAL   Patent: WO 0003013-A 17 20-JAN-2000;
            LEEGWATER ADAM CORNELIS JOZEF (NL); VLIET HENDRIK NIELS V D (NL);
            AMSTERDAM MOLECULAR THERAPEUTI (NL); CHAMULEAU ROBERT ANTOINE FRANC
            (NL); GROENINK MARTIJN (NL)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="primer R1570RAP"
BASE COUNT        5 a      5 c      6 g      4 t

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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```
Qy        551 TGGCAGGCATGCACACACT 569
              ||||||| ||| |||||||
Db          1 TGGCAGGGATGTACACACT 19


RESULT 33
AX147015
LOCUS       AX147015                  20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 9 from Patent WO0137291.
ACCESSION   AX147015
VERSION     AX147015.1  GI:14346286
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weindel,K., Riedling,M. and Geiger,A.
  TITLE     Magnetic glass particles, method for their preparation and uses
            thereof
  JOURNAL   Patent: WO 0137291-A 9 25-MAY-2001;
            Roche Diagnostics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide probe (HIV)"
     modified_base   1
                     /note="Ruthenium3+-(tris-bipyridyl)-derivatisation"
                     /mod_base=OTHER
BASE COUNT        8 a      3 c      6 g      3 t

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGCAG 292
              ||||| |||||||| ||||
Db          1 ATCAATGAGGAAGCTGCAG 19


RESULT 34
AX350454/c
LOCUS       AX350454                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 79 from Patent WO0181578.
ACCESSION   AX350454
VERSION     AX350454.1  GI:18616060
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Vernet,C.A., Fernandes,E.R., Gerlach,V., Shimkets,R.A.,
            Malyankar,U.M., Boldog,F.L., Zerhusen,B.D., Spytek,K.A.,
            Majumder,K., Tchernev,V.T., Padigaru,M., Patturajan,M.,
            Burgess,C.E., Gangolli,E.A., Smithson,G., Rastelli,L.,
            Macdougall,J.R., Taupier,R.J., Grosse,W.M. and Alsobrook,J.P.
  TITLE     Novel proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 0181578-A 79 01-NOV-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Ag743 Forward Primer"
BASE COUNT        5 a      2 c      7 g      6 t

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        641 TCTGCATCCCCCAAGACCT 659
              ||||||||| ||||||| |
Db         19 TCTGCATCCACCAAGACAT 1


RESULT 35
AX428913
LOCUS       AX428913                  20 bp    DNA     linear   PAT 21-JUN-2002
DEFINITION  Sequence 9 from Patent EP1201752.
ACCESSION   AX428913
VERSION     AX428913.1  GI:21540303
KEYWORDS    .
SOURCE      Human immunodeficiency virus
  ORGANISM  Human immunodeficiency virus
            Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
            lentivirus group.
REFERENCE   1
  AUTHORS   Schmuck,R., Staepels,J., Meier,T., Wehnes,U. and Russmann,E.
  TITLE     Methods for the analysis of non-proteinaceous components using a
            protease from a bacillus strain
  JOURNAL   Patent: EP 1201752-A 9 02-MAY-2002;
            Roche Diagnostics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Human immunodeficiency virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:12721"
     modified_base   1
                     /note="Ruthenium3+-(tris-bipyridyl)-derivatisation"
                     /mod_base=OTHER
BASE COUNT        8 a      3 c      6 g      3 t

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGCAG 292
              ||||| |||||||| ||||
Db          1 ATCAATGAGGAAGCTGCAG 19


RESULT 36
AX428986
LOCUS       AX428986                  20 bp    DNA     linear   PAT 21-JUN-2002
DEFINITION  Sequence 9 from Patent EP1201753.
ACCESSION   AX428986
VERSION     AX428986.1  GI:21540357
KEYWORDS    .
SOURCE      Human immunodeficiency virus
  ORGANISM  Human immunodeficiency virus
            Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
            lentivirus group.
REFERENCE   1
  AUTHORS   Russmann,E., Schmuck,R., Meier,T., Staepels,J. and Wehnes,U.
  TITLE     Methods for the analysis of non-proteinaceous components using a
            protease from a bacillus strain
  JOURNAL   Patent: EP 1201753-A 9 02-MAY-2002;
            Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Human immunodeficiency virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:12721"
     modified_base   1
                     /note="Ruthenium3+-(tris-bipyridyl)-derivatisation"
                     /mod_base=OTHER
BASE COUNT        8 a      3 c      6 g      3 t

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGCAG 292
              ||||| |||||||| ||||
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```
Db          1 ATCAATGAGGAAGCTGCAG 19


RESULT 37
E32198
LOCUS       E32198                    20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Relief in cross contamination in nucleic acid amplification.
ACCESSION   E32198
VERSION     E32198.1  GI:13026683
KEYWORDS    JP 1999113599-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Harveruhauzen,G., Juergel,S. and Zobek,H.
  TITLE     Relief in cross contamination in nucleic acid amplification
  JOURNAL   Patent: JP 1999113599-A 6 27-APR-1999;
            BOEHRINGER MANNHEIM GMBH
COMMENT     OS   Artificial Sequence
            PN   JP 1999113599-A/6
            PD   27-APR-1999
            PF   14-AUG-1998 JP 1998229725
            PR   20-AUG-1997 DE 197 36 062:9
            PI   HARVERUHAUZEN GERUTO,JUERGEL STEPHAN,ZOBEK HALALT PC
            C12Q1/68,C12N9/99,C12N15/09,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   misc_feature    1.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
BASE COUNT        8 a      3 c      6 g      3 t

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGCAG 292
              ||||| |||||||| ||||
Db          1 ATCAATGAGGAAGCTGCAG 19


RESULT 38
AR298795/c
LOCUS       AR298795                  21 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 10530 from patent US 6537751.
ACCESSION   AR298795
VERSION     AR298795.1  GI:31686079
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 10530 25-MAR-2003;
FEATURES              Location/Qualifiers
     source           1. .21
                      /organism="unknown"
BASE COUNT       12 a      4 c      3 g      2 t

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1107 TGTAGTTTTCTGTTTAATT 1125
              |||||| ||||||||| ||
Db         20 TGTAGTGTTCTGTTTATTT 2


RESULT 39
AX033004/c
LOCUS       AX033004                  21 bp    DNA     linear   PAT 21-SEP-2000
DEFINITION  Sequence 11 from Patent WO0044786.
ACCESSION   AX033004
VERSION     AX033004.1  GI:10279907
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Jentsch,T.J.
  TITLE     Novel potassium channels and genes encoding these potassium
            channels
  JOURNAL   Patent: WO 0044786-A 11 03-AUG-2000;
            NEUROSEARCH AS (DK)
FEATURES              Location/Qualifiers
     source           1. .21
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
                      /note="PCR primer"
BASE COUNT        3 a      7 c      5 g      6 t

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        120 CGTCCACACGGGACAGGGA 138
              | |||||||||||| |||||
Db         20 CTTCCACACGGGAAAGGGA 2


RESULT 40
AX404465
LOCUS       AX404465                  21 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 291 from Patent WO0224747.
ACCESSION   AX404465
VERSION     AX404465.1  GI:21437746
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U. and Hoffmeyer,S.
  TITLE     Polymorphisms in human genes of cardiovascular regulators and their
            use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 0224747-A 291 28-MAR-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES              Location/Qualifiers
     source           1. .21
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
                      /note="artificial sequence-n=g or a"
BASE COUNT        5 a      3 c     11 g      1 t      1 others

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        463 AGCAGCCTGCAGGGGGAGGA 482
              ||||| |||| ||| |||||
Db          1 AGCAGGCTGCNGGGAGAGGA 20


RESULT 41
AX404466/c
LOCUS       AX404466                  21 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 292 from Patent WO0224747.
ACCESSION   AX404466
VERSION     AX404466.1  GI:21437747
KEYWORDS    .
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SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U. and Hoffmeyer,S.
  TITLE     Polymorphisms in human genes of cardiovascular regulators and their
            use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 0224747-A 292 28-MAR-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="artificial sequence-n=c or t"
BASE COUNT        1 a      11 c       3 g       5 t       1 others

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         463 AGCAGCCTGCAGGGGGAGGA 482
               ||||| |||| ||| |||||
Db          21 AGCAGGCTGCNGGGAGAGGA 2


RESULT 42
BD057122
LOCUS       BD057122                 21 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Identification of inhibitors of protein tyrosine kinase 2.
ACCESSION   BD057122
VERSION     BD057122.1  GI:22602728
KEYWORDS    JP 2001512309-A/4.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Duong,L.T. and Rodan,G.A.
  TITLE     Identification of inhibitors of protein tyrosine kinase 2
  JOURNAL   Patent: JP 2001512309-A 4 21-AUG-2001;
            MERCK & CO INC
COMMENT     PN   JP 2001512309-A/4
            PD   21-AUG-2001
            PF   09-FEB-1998 JP 1998535071
            PR   11-FEB-1997 US    60/037560
            PI   LE T DUONG,GIDEON A RODAN
            PC   C12Q1/48,A61K38/00,A61K45/00,A61P19/10,A61P29/00,A61P43/00, PC
              C12N15/09//
            PC   C12N9/12,C12N15/00,A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      7 c       4 g       5 t

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 1.1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         604 CTGAAGCCTGACACCTTCA 622
               ||||||| ||||||| |||
Db           2 CTGAAGCTTGACACCCTCA 20


RESULT 43
AX698525
LOCUS       AX698525                 22 bp    DNA     linear   PAT 02-APR-2003
DEFINITION  Sequence 14 from Patent WO03010335.
ACCESSION   AX698525
VERSION     AX698525.1  GI:29499353
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirel,D.B., Erlich,H.A., Bugawan,T.L., Noble,J.A. and Valdez,A.M.
  TITLE     Il-4 receptor sequence variation associated with type 1 diabetes
  JOURNAL   Patent: WO 03010335-A 14 06-FEB-2003;
            Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="probe used to identify IL4R polymorphisms"
BASE COUNT        5 a      4 c       8 g       5 t

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 22;
  Best Local Similarity   89.5%;  Pred. No. 1.2e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         435 GTTCAGAAAGTTGCTGAAG 453
               | |||||  ||||||||||
Db           3 GCTCAGAGAGTTGCTGAAG 21


RESULT 44
AX698554
LOCUS       AX698554                 22 bp    DNA     linear   PAT 02-APR-2003
DEFINITION  Sequence 43 from Patent WO03010335.
ACCESSION   AX698554
VERSION     AX698554.1  GI:29499382
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirel,D.B., Erlich,H.A., Bugawan,T.L., Noble,J.A. and Valdez,A.M.
  TITLE     Il-4 receptor sequence variation associated with type 1 diabetes
  JOURNAL   Patent: WO 03010335-A 43 06-FEB-2003;
            Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="hybridization probe"
BASE COUNT        5 a      4 c       8 g       5 t

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 22;
  Best Local Similarity   89.5%;  Pred. No. 1.2e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         435 GTTCAGAAAGTTGCTGAAG 453
               | |||||  ||||||||||
Db           3 GCTCAGAGAGTTGCTGAAG 21


RESULT 45
AX726065/c
LOCUS       AX726065                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3752 from Patent WO03025176.
ACCESSION   AX726065
VERSION     AX726065.1  GI:30505408
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
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  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 3752 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
BASE COUNT        2 a      4 c      6 g      5 t

  Query Match             1.1%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 90;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        626 ACCAGCTCCAGGAGCTC 642
              ||||||||||||||| ||
Db         17 ACCAGCTCCAGGAGATC 1


RESULT 46
AX316182
LOCUS       AX316182                  18 bp    DNA     linear   PAT 14-DEC-2001
DEFINITION  Sequence 4 from Patent WO0190353.
ACCESSION   AX316182
VERSION     AX316182.1  GI:17899361
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hildebrandt,T., van Muijen,G. and Weidle,U.
  TITLE     A process for determing the tumoricidal potential of a sample by
            the use of a nucleic acid which is downregulated in human tumor
            cells
  JOURNAL   Patent: WO 0190353-A 4 29-NOV-2001;
            F.HOFFMANN-LA ROCHE AG (CH)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="primer 312f6"
BASE COUNT        1 a      11 c      3 g      3 t

  Query Match             1.1%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        141 CCCGCTCGGCTCCGCTC 157
              ||||||| |||||||||
Db          2 CCCGCTCCGCTCCGCTC 18


RESULT 47
AR299716/c
LOCUS       AR299716                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 11451 from patent US 6537751.
ACCESSION   AR299716
VERSION     AR299716.1  GI:31687000
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 11451 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        6 a      4 c      7 g      3 t

  Query Match             1.1%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 1.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        225 TCCTCAGCCTCAGGCAT 241
              |||||| ||||||||||
Db         17 TCCTCATCCTCAGGCAT 1


RESULT 48
E09814
LOCUS       E09814                    20 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  Oligonucleotide for detecting Mycobacterium tuberculosis.
ACCESSION   E09814
VERSION     E09814.1  GI:22026443
KEYWORDS    JP 1995213288-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Segawa,M., Takarada,Y. and Shibata,H.
  TITLE     OLIGONUCLEOTIDE FOR DETECTING MYCOBATERIUM TUBERCLULOSIS AND USE
  JOURNAL   Patent: JP 1995213288-A 2 15-AUG-1995;
            TOYOBO CO LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1995213288-A/2
            PD   15-AUG-1995
            PF   04-FEB-1994 JP 1994012724
            PI   SEGAWA MASAYA, TAKARADA YUTAKA, SHIBATA HIDEJI PC
            C12N15/09,C12Q1/68,G01N33/58,(C12N15/09,C12R1:32),(C12Q1/68, PC
            C12R1:32);
            CC   strandedness: Both;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        3 a      4 c      6 g      7 t

  Query Match             1.1%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 1.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        497 TGCAGCGTCTTGGGGTC 513
              ||||||||||||| ||||
Db          2 TGCAGCGTCTTGAGGTC 18


RESULT 49
AX742758/c
LOCUS       AX742758                  22 bp    DNA     linear   PAT 12-MAY-2003
DEFINITION  Sequence 561 from Patent EP1302550.
ACCESSION   AX742758
VERSION     AX742758.1  GI:30576747
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lin,C.Y., Lin,R.W., You,C.M., Huang,H.H., Lee,B.H., Lee,H.H.,
            Lin,Y.J., Fan,C.C., Hsu,H.C., Shih,C.W., Yeh,C.H., Kao,Y.F.,
            Pan,C.L. and Chan,P.
  TITLE     Method and detector for identifying subtypes of human papilloma
            viruses
  JOURNAL   Patent: EP 1302550-A 561 16-APR-2003;
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          King Car Food Industrial Co., Ltd. (TW)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide for Identifying HPV CP8061"
BASE COUNT        7 a      8 c      3 g      4 t

  Query Match             1.1%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        469 CTGCAGGGGGAGGACTG 485
              ||||||| |||||||||
Db         20 CTGCAGGAGGAGGACTG 4


RESULT 50
AR038674/c
LOCUS       AR038674                 20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 8 from patent US 5807678.
ACCESSION   AR038674
VERSION     AR038674.1  GI:5958037
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Miller,W.L., Lin,D. and Strauss,J.F. III.
  TITLE     Identification of gene mutations associated with congenital lipoid
            adrenal hyperplasia
  JOURNAL   Patent: US 5807678-A 8 15-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      7 c      6 g      3 t

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        548 TGCTGGCAGGCATGCACACA 567
              ||||||| ||||||  ||||
Db         20 TGCTGGCTGGCATGGCCACA 1


RESULT 51
AR072286/c
LOCUS       AR072286                 20 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 89 from patent US 5948611.
ACCESSION   AR072286
VERSION     AR072286.1  GI:9999050
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Prockop,D.J., Ala-Kokko,L., Williams,C.J., Ritvaniemi,P.,
            Baldwin,C., Hopkinson,I. and Ahmad,N.Nina.
  TITLE     Primers and methods for detecting mutations in the procollagen II
            gene (COL2A1) that indicate a genetic predisposition for a
            COL2A1-associated disease
  JOURNAL   Patent: US 5948611-A 89 07-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        1 a      8 c      4 g      7 t

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        282 GGAAGCAGCAGCAATGTCTG 301
              |||||||||||||| || | |
Db         20 GGAAGCAGCAGCAGTGACAG 1


RESULT 52
AR225067
LOCUS       AR225067                 20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 33 from patent US 6441156.
ACCESSION   AR225067
VERSION     AR225067.1  GI:23334202
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Lerman,M.I., Latif,F., Wei,M.-H., Duh,F.-M., Minna,J.D., Sekido,Y.
            and Gao,B.
  TITLE     Calcium channel compositions and methods of use thereof
  JOURNAL   Patent: US 6441156-A 33 27-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      4 c      8 g      4 t

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        335 CTGGTGATAGTCACAGTGGC 354
              |||||||| |||||||  ||
Db          1 CTGGTGATGGTCACAGGAGC 20


RESULT 53
AR225077
LOCUS       AR225077                 20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 43 from patent US 6441156.
ACCESSION   AR225077
VERSION     AR225077.1  GI:23334212
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Lerman,M.I., Latif,F., Wei,M.-H., Duh,F.-M., Minna,J.D., Sekido,Y.
            and Gao,B.
  TITLE     Calcium channel compositions and methods of use thereof
  JOURNAL   Patent: US 6441156-A 43 27-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      4 c      8 g      4 t

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        335 CTGGTGATAGTCACAGTGGC 354
              |||||||| |||||||  ||
Db          1 CTGGTGATGGTCACAGGAGC 20


RESULT 54
AR265987
LOCUS       AR265987                 20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 168 from patent US 6492170.
ACCESSION   AR265987
VERSION     AR265987.1  GI:29694833
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

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REFERENCE   1  (bases 1 to 20)
  AUTHORS   Watt,A.T.
  TITLE     Antisense modulation of caspase 9 expression
  JOURNAL   Patent: US 6492170-A 168 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        5 a      8 c      3 g      4 t

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        567 ACTGCTCCAGCAGGCCCTCC 586
              ||||||||||  | ||| |||
Db          1 ACTGCTCCAGAATGCCATCC 20


RESULT 55
AR311045/c
LOCUS       AR311045                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 1582 from patent US 6559294.
ACCESSION   AR311045
VERSION     AR311045.1  GI:31704471
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 1582 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        2 a      5 c      5 g      8 t

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGCAGC 293
              ||||||   ||||||||||||
Db         20 ATCAAATGCGAAGCAGCAGC 1


RESULT 56
AR313415/c
LOCUS       AR313415                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 3952 from patent US 6559294.
ACCESSION   AR313415
VERSION     AR313415.1  GI:31706841
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 3952 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      4 c      5 g      7 t

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         17 TGGATTAAACCAAACCCAGC 36
              ||||||| |||| ||| |||
Db         20 TGGATTATACCAGACCAAGC 1


RESULT 57
AX611049
LOCUS       AX611049                  20 bp    DNA     linear   PAT 17-FEB-2003
DEFINITION  Sequence 2074 from Patent WO02072882.
ACCESSION   AX611049
VERSION     AX611049.1  GI:28406478
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cullen,P. and Seedorf,U.
  TITLE     Coronary chip
  JOURNAL   Patent: WO 02072882-A 2074 19-SEP-2002;
            OGHAM GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      8 c      7 g      3 t

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        532 GAGCAGCTGGGTGCCCTGCT 551
              |||||  ||||  ||||||||
Db          1 GAGCACCTGGCGGCCCTGCT 20


RESULT 58
I26397/c
LOCUS       I26397                    20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 89 from patent US 5558988.
ACCESSION   I26397
VERSION     I26397.1  GI:1606267
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Prockop,D.J., Ala-Kokko,L. and Ritvaniemi,P.
  TITLE     Primers and methods for detecting mutations in the procollagen II
            gene that indicate a genetic predisposition for osteoarthritis
  JOURNAL   Patent: US 5558988-A 89 24-SEP-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        1 a      8 c      4 g      7 t

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        282 GGAAGCAGCAGCAATGTCTG 301
              ||||||||||||| || | |
Db         20 GGAAGCAGCAGCAGTGACAG 1


RESULT 59
AR011122/c
LOCUS       AR011122                  21 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 30 from patent US 5762905.
ACCESSION   AR011122
VERSION     AR011122.1  GI:3969112
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Burton,D.R., Barbas,C.F. III, Chanock,R.M., Murphy,B.R. and
            Crowe,J.E. Jr.
  TITLE     Human neutralizing monoclonal antibodies to respiratory syncytial
            virus
  JOURNAL   Patent: US 5762905-A 30 09-JUN-1998;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
BASE COUNT        4 a      7 c      7 g      3 t

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        262 CTGGGCTGGCTGATCAAAGA 281
              .|||||||| ||| |||| ||
Db         21 CTGGGCTGCCTGGTCAACGA 2


RESULT 60
AR038293/c
LOCUS       AR038293                 21 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 49 from patent US 5804440.
ACCESSION   AR038293
VERSION     AR038293.1  GI:5957010
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Burton,D.R., Barbas,C.F. and Lerner,R.A.
  TITLE     Human neutralizing monoclonal antibodies to human immunodeficiency
            virus
  JOURNAL   Patent: US 5804440-A 49 08-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
BASE COUNT        4 a      7 c      7 g      3 t

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        262 CTGGGCTGGCTGATCAAAGA 281
              |||||||| ||| |||| ||
Db         21 CTGGGCTGCCTGGTCAACGA 2


RESULT 61
AR301192/c
LOCUS       AR301192                 21 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 21 from patent US 6538114.
ACCESSION   AR301192
VERSION     AR301192.1  GI:31688946
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Persson,M.A.A. and Allander,T.E.
  TITLE     Human monoclonal antibodies specific for hepatitis C virus (HCV) E2
            antigen
  JOURNAL   Patent: US 6538114-A 21 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
BASE COUNT        4 a      7 c      7 g      3 t

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        262 CTGGGCTGGCTGATCAAAGA 281
              |||||||| ||| |||| ||
Db         21 CTGGGCTGCCTGGTCAACGA 2


RESULT 62
AX088756
LOCUS       AX088756                 21 bp    DNA     linear   PAT 17-MAR-2001
DEFINITION  Sequence 82 from Patent WO0114416.
ACCESSION   AX088756
VERSION     AX088756.1  GI:13397552
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Neeper,M.P., Mcclements,W.L., Jansen,K.U., Schultz,L.D., Chen,L.
            and Wang,X.M.
  TITLE     Synthetic human papillomavirus genes
  JOURNAL   Patent: WO 0114416-A 82 01-MAR-2001;
            Merck & Co., Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Codon-Optimized HPV16 E2 fragment"
BASE COUNT        2 a      7 c      6 g      6 t

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        813 GCCGAGCGTCCTGATGCAGC 832
              |||| || || |||||||||
Db          1 GCCGTGCTTCTTGATGCAGC 20


RESULT 63
AX404463
LOCUS       AX404463                 21 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 289 from Patent WO0224747.
ACCESSION   AX404463
VERSION     AX404463.1  GI:21437744
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U. and Hoffmeyer,S.
  TITLE     Polymorphisms in human genes of cardiovascular regulators and their
            use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 0224747-A 289 28-MAR-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="artificial sequence"
BASE COUNT        5 a      3 c     12 g      1 t

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        463 AGCAGCCTGCAGGGGGAGGA 482
              ||||| |||| ||| |||||
Db          1 AGCAGGCTGCGGGGAGAGGA 20


RESULT 64
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AX404464/c
LOCUS       AX404464                  21 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 290 from Patent WO0224747.
ACCESSION   AX404464
VERSION     AX404464.1  GI:21437745
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U. and Hoffmeyer,S.
  TITLE     Polymorphisms in human genes of cardiovascular regulators and their
            use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 0224747-A 290 28-MAR-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="artificial sequence"
BASE COUNT        1 a      12 c       3 g       5 t

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        463 AGCAGCCTGCAGGGGGAGGA 482
              ||||| |||| ||| |||||
Db         21 AGCAGGCTGCGGGGAGAGGA 2


RESULT 65
I58582/c
LOCUS       I58582                    21 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 49 from patent US 5652138.
ACCESSION   I58582
VERSION     I58582.1  GI:2477820
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Burton,D.R., Barbas,C.F. and Lerner,R.A.
  TITLE     Human neutralizing monoclonal antibodies to human immunodeficiency
            virus
  JOURNAL   Patent: US 5652138-A 49 29-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
BASE COUNT        4 a       7 c       7 g       3 t

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        262 CTGGGCTGGCTGATCAAAGA 281
              |||||||| ||| |||| ||
Db         21 CTGGGCTGCCTGGTCAACGA 2


RESULT 66
AR180659
LOCUS       AR180659                  15 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 727 from patent US 6333152.
ACCESSION   AR180659
VERSION     AR180659.1  GI:20222692
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
  TITLE     Gene expression profiles in normal and cancer cells
  JOURNAL   Patent: US 6333152-A 727 25-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
BASE COUNT        2 a       3 c       3 g       7 t

  Query Match             1.1%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 84;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        745 CATGTTGCTGACTTT 759
              |||||||||||||||
Db          1 CATGTTGCTGACTTT 15


RESULT 67
AX272818/c
LOCUS       AX272818                  17 bp    mRNA    linear   PAT 29-OCT-2001
DEFINITION  Sequence 387 from Patent WO0162911.
ACCESSION   AX272818
VERSION     AX272818.1  GI:16545555
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
            Ellis,J.H.
  TITLE     Method and reagent for the inhibition of grid
  JOURNAL   Patent: WO 0162911-A 387 30-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a       9 c       3 g       0 t

  Query Match             1.1%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        300 TGCTGTGGGGGCTGC 314
              |||||||||||||||
Db         17 TGCTGTGGGGGCTGC 3


RESULT 68
AX272821/c
LOCUS       AX272821                  17 bp    mRNA    linear   PAT 29-OCT-2001
DEFINITION  Sequence 390 from Patent WO0162911.
ACCESSION   AX272821
VERSION     AX272821.1  GI:16545558
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
            Ellis,J.H.
  TITLE     Method and reagent for the inhibition of grid
  JOURNAL   Patent: WO 0162911-A 390 30-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a       9 c       4 g       0 t
```

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  Query Match             1.1%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        299 CTGCTGTGGGGGCTG 313
              |||||||||||||||
Db         15 CTGCTGTGGGGGCTG 1


RESULT 69
AX398234/c
LOCUS       AX398234                  17 bp    DNA     linear   PAT 27-MAY-2002
DEFINITION  Sequence 9 from Patent WO0220609.
ACCESSION   AX398234
VERSION     AX398234.1  GI:21261041
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bates,S.A., Gloger,I.S. and Read,S.G.
  TITLE     New use
  JOURNAL   Patent: WO 0220609-A 9 14-MAR-2002;
            SMITHKLINE BEECHAM PLC (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="primer"
BASE COUNT        3 a      7 c      5 g      2 t

  Query Match             1.1%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        536 AGCTGGGTGCCCTGC 550
              |||||||||||||||
Db         15 AGCTGGGTGCCCTGC 1


RESULT 70
AX687586
LOCUS       AX687586                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 318 from Patent EP1281758.
ACCESSION   AX687586
VERSION     AX687586.1  GI:29410282
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 318 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      5 c      7 g      3 t

  Query Match             1.1%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        630 GCTCCAGGAGCTCTG 644
              |||||||||||||||
Db          3 GCTCCAGGAGCTCTG 17


RESULT 71
AX687587
LOCUS       AX687587                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 319 from Patent EP1281758.
ACCESSION   AX687587
VERSION     AX687587.1  GI:29410283
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 319 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      5 c      6 g      4 t

  Query Match             1.1%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        630 GCTCCAGGAGCTCTG 644
              |||||||||||||||
Db          2 GCTCCAGGAGCTCTG 16


RESULT 72
AX687588
LOCUS       AX687588                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 320 from Patent EP1281758.
ACCESSION   AX687588
VERSION     AX687588.1  GI:29410284
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 320 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      6 c      5 g      4 t

  Query Match             1.1%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        630 GCTCCAGGAGCTCTG 644
              |||||||||||||||
Db          1 GCTCCAGGAGCTCTG 15


RESULT 73
AX690594
LOCUS       AX690594                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 3326 from Patent EP1281758.
ACCESSION   AX690594
VERSION     AX690594.1  GI:29413475
```

```
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 3326 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      6 c      5 g      3 t

  Query Match             1.1%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        631 CTCCAGGAGCTCTGC 645
              |||||||||||||||
Db          3 CTCCAGGAGCTCTGC 17


RESULT 74
AX690595
LOCUS       AX690595                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 3327 from Patent EP1281758.
ACCESSION   AX690595
VERSION     AX690595.1  GI:29413476
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 3327 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      7 c      4 g      3 t

  Query Match             1.1%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        631 CTCCAGGAGCTCTGC 645
              |||||||||||||||
Db          2 CTCCAGGAGCTCTGC 16


RESULT 75
AX690596
LOCUS       AX690596                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 3328 from Patent EP1281758.
ACCESSION   AX690596
VERSION     AX690596.1  GI:29413477
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 3328 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      7 c      4 g      3 t

  Query Match             1.1%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        631 CTCCAGGAGCTCTGC 645
              |||||||||||||||
Db          1 CTCCAGGAGCTCTGC 15


RESULT 76
AX100701/c
LOCUS       AX100701                  18 bp    DNA     linear   PAT 10-APR-2001
DEFINITION  Sequence 104 from Patent WO0121647.
ACCESSION   AX100701
VERSION     AX100701.1  GI:13619649
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Yen,F., Erickson,M.R., Fruebis,J. and Bihain,B.
  TITLE     Methods of screening for compounds that modulate the lsr-leptin
            interaction and their use in the prevention and treatment of
            obesity-related diseases
  JOURNAL   Patent: WO 0121647-A 104 29-MAR-2001;
            GENSET (FR)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide zinc finger LSR sequences"
BASE COUNT        0 a      2 c     14 g      2 t

  Query Match             1.1%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        186 CCCCGCCGCCCACCC 200
              |||||||||||||||
Db         18 CCCCGCCGCCCACCC 4


RESULT 77
AX095780
LOCUS       AX095780                  21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 958 from Patent WO0118250.
ACCESSION   AX095780
VERSION     AX095780.1  GI:13512007
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 958 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
```

```
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      7 c      7 g      1 t      1 others

  Query Match             1.1%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        513 CAGCGCCAACCTGCCGG 529
              ||||||||||:||| ||
Db          1 CAGCGCCAACYTGCAGG 17


RESULT 78
AR134114/c
LOCUS       AR134114                  18 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 2539 from patent US 6194150.
ACCESSION   AR134114
VERSION     AR134114.1  GI:14123019
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
  TITLE     Nucleic acid based inhibition of CD40
  JOURNAL   Patent: US 6194150-A 2539 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        1 a      4 c      4 g      9 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        277 AAAGAGGAAGCAGCAGCA 294
              |||||  |||  ||||||||
Db         18 AAAGACGAATCAGCAGCA 1


RESULT 79
AX718775/c
LOCUS       AX718775                  18 bp    DNA     linear   PAT 15-APR-2003
DEFINITION  Sequence 339 from Patent WO02103043.
ACCESSION   AX718775
VERSION     AX718775.1  GI:29891342
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Beimfohr,C. and Snaidr,J.
  TITLE     Method for the specific fast detection of bacteria which is harmful
            to beer
  JOURNAL   Patent: WO 02103043-A 339 27-DEC-2002;
            Vermicon AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonukleotid"
BASE COUNT        3 a      4 c      5 g      6 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         94 TACCGTACAACCCCGGAG 111
              |||||||  ||||  |||||
Db         18 TACCGTATAACCACGGAG 1


RESULT 80
AR016651
LOCUS       AR016651                  19 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 14 from patent US 5776762.
ACCESSION   AR016651
VERSION     AR016651.1  GI:3972928
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   North,M., Nishina,P., Noben-Trauth,K. and Naggert,J.
  TITLE     Obesity associated genes
  JOURNAL   Patent: US 5776762-A 14 07-JUL-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        6 a      5 c      6 g      2 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        822 CCTGATGCAGCTGAAGCT 839
              |||||  |||||  ||||||
Db          2 CCTGAGGCAGCAGAAGCT 19


RESULT 81
AR110274
LOCUS       AR110274                  19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 26 from patent US 6114502.
ACCESSION   AR110274
VERSION     AR110274.1  GI:12826550
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   North,M., Nishina,P., Naggert,J. and Noben-Trauth,K.
  TITLE     Gene family associated with neurosensory defects
  JOURNAL   Patent: US 6114502-A 26 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        6 a      5 c      6 g      2 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        822 CCTGATGCAGCTGAAGCT 839
              |||||  |||||  ||||||
Db          2 CCTGAGGCAGCAGAAGCT 19


RESULT 82
AX082062/c
LOCUS       AX082062                  19 bp    DNA     linear   PAT 27-FEB-2001
DEFINITION  Sequence 306 from Patent WO0109183.
ACCESSION   AX082062
VERSION     AX082062.1  GI:13170870
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U., Hoffmeyer,S., Eichelbaum,M. and Roots,I.
  TITLE     Polymorphisms in the human mdr-1 gene and their use in diagnostic
            and therapeutic applications
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  JOURNAL   Patent: WO 0109183-A 306 08-FEB-2001;
            EPIDAUROS AG Biotechnologie Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic"
BASE COUNT        2 a      5 c      9 g      3 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        577 CAGGCCCTCCGTCTGCCC 594
              |||| || ||||||||||
Db         19 CAGGGCCACCGTCTGCCC 2


RESULT 83
AX082064
LOCUS       AX082064                 19 bp    DNA     linear   PAT 27-FEB-2001
DEFINITION  Sequence 308 from Patent WO0109183.
ACCESSION   AX082064
VERSION     AX082064.1  GI:13170872
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U., Hoffmeyer,S., Eichelbaum,M. and Roots,I.
  TITLE     Polymorphisms in the human mdr-1 gene and their use in diagnostic
            and therapeutic applications
  JOURNAL   Patent: WO 0109183-A 308 08-FEB-2001;
            EPIDAUROS AG Biotechnologie Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic"
BASE COUNT        3 a      9 c      5 g      2 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        577 CAGGCCCTCCGTCTGCCC 594
              |||| || ||||||||||
Db          1 CAGGGCCACCGTCTGCCC 18


RESULT 84
AX131129
LOCUS       AX131129                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 2347 from Patent WO0130362.
ACCESSION   AX131129
VERSION     AX131129.1  GI:14137434
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
.           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 2347 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /note="Cyclin F ribozyme binding site"
BASE COUNT        3 a      6 c      6 g      4 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        877 GCCAAGTTCCAGGAGCTG 894
              ||||  ||||||||||||
Db          2 GCCAGCTTCCAGGAGCTG 19


RESULT 85
AR024053/c
LOCUS       AR024053                 20 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 3 from patent US 5795778.
ACCESSION   AR024053
VERSION     AR024053.1  GI:3977347
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Draper,K.G.
  TITLE     Method and reagent for inhibiting herpes simplex virus replication
  JOURNAL   Patent: US 5795778-A 3 18-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        1 a      8 c      6 g      5 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        130 GGACAGGGACGCCCGCTC 147
              |||||||||| ||| ||
Db         19 GGACAGGGACGGCCGATC 2


RESULT 86
AR117552/c
LOCUS       AR117552                 20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 42 from patent US 6140124.
ACCESSION   AR117552
VERSION     AR117552.1  GI:14098458
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Gaarde,W.A., Nero,P.S. and McKay,R.
  TITLE     Antisense modulation of P38 mitogen activated protein kinase
            expression
  JOURNAL   Patent: US 6140124-A 42 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        5 a      6 c      5 g      4 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1287 TACAGTTGCTCAGCCTGG 1304
              || || ||||||||||||
Db         19 TAGAGCTGCTCAGCCTGG 2


RESULT 87
AR220146
LOCUS       AR220146                 20 bp    DNA     linear   PAT 26-SEP-2002
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DEFINITION  Sequence 11 from patent US 6423543.
ACCESSION   AR220146
VERSION     AR220146.1  GI:23324589
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Marcotte,P.A. and Cowsert,L.M.
  TITLE     Antisense modulation of hepsin expression
  JOURNAL   Patent: US 6423543-A 11 23-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        3 a      6 c      10 g      1 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        721 CAGCAGCAGGGGGCCTGG 738
              ||||||| || |||||||
Db          2 CAGCAGCGGGCGGCCTGG 19


RESULT 88
AR224273/c
LOCUS       AR224273                  20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 3 from patent US 6440719.
ACCESSION   AR224273
VERSION     AR224273.1  GI:23333050
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Draper,K.G.
  TITLE     Method and reagent for inhibiting herpes simplex virus replication
  JOURNAL   Patent: US 6440719-A 3 27-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        1 a      8 c      6 g      5 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        130 GGACAGGGACGCCCGCTC 147
              |||||||||||| ||| ||
Db         19 GGACAGGGACGGCCGATC 2


RESULT 89
AR228837/c
LOCUS       AR228837                  20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 42 from patent US 6448079.
ACCESSION   AR228837
VERSION     AR228837.1  GI:27267976
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Gaarde,W.A., Nero,P. and McKay,R.
  TITLE     Antisense modulation of p38 mitogen activated protein kinase
            expression
  JOURNAL   Patent: US 6448079-A 42 10-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        5 a      6 c      5 g      4 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1287 TACAGTTGCTCAGCCTGG 1304
              || || ||||||||||||
Db         19 TAGAGCTGCTCAGCCTGG 2


RESULT 90
AX026947/c
LOCUS       AX026947                  20 bp    DNA     linear   PAT 16-SEP-2000
DEFINITION  Sequence 2 from Patent WO0039334.
ACCESSION   AX026947
VERSION     AX026947.1  GI:10187996
KEYWORDS    .
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1
  AUTHORS   Breviario,D. and Giani,S.
  TITLE     Process for the evaluation and the monitoring of genetic
            variability of vegetable species
  JOURNAL   Patent: WO 0039334-A 2 06-JUL-2000;
            BREVIARIO DIEGO (IT) ; GIANI SILVIA (IT) ; CONSIGLIO NAZIONALE
            RICERCHE (IT)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4530"
BASE COUNT        6 a      4 c      6 g      4 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        743 CGCATGTTGCTGACTTTC 760
              |||||| ||||||| |||
Db         20 CGCATGATGCTGACATTC 3


RESULT 91
AX092696/c
LOCUS       AX092696                  20 bp    DNA     linear   PAT 21-MAR-2001
DEFINITION  Sequence 108 from Patent WO0115676.
ACCESSION   AX092696
VERSION     AX092696.1  GI:13444753
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M.
  TITLE     Compositions and methods for modulating hdl cholesterol and
            triglyceride levels
  JOURNAL   Patent: WO 0115676-A 108 08-MAR-2001;
            University of British Columbia (CA) ; Xenon Genetics Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      7 c      6 g      2 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        991 TTCAGATCCGGCTTGGAC 1008
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                ||||| ||||| ||||||
Db         20 TTCAGGTCCGGGTTGGAC 3


RESULT 92
AX250355/c
LOCUS       AX250355                  20 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 23 from Patent WO0168682.
ACCESSION   AX250355
VERSION     AX250355.1  GI:15984122
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Reinl,S.J. and Turpen,T.H.
  TITLE     Self antigen vaccines for treating b cell lymphomas and other
            cancers
  JOURNAL   Patent: WO 0168682-A 23 20-SEP-2001;
            Large Scale Biology Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
                     /note="primer"
BASE COUNT        4 a      8 c      6 g      2 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        261 CCTGGGCTGGCTGATCAA 278
              ||||||||| ||| ||||
Db         19 CCTGGGCTGCCTGGTCAA 2


RESULT 93
AX286800/c
LOCUS       AX286800                  20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 35 from Patent WO0178796.
ACCESSION   AX286800
VERSION     AX286800.1  GI:17048833
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Millar,R.M., Lowe,S. and Conklin,D.Z.
  TITLE     Type II gonadotropin-releasing hormone receptor and polynucleotides
            encoding therefor
  JOURNAL   Patent: WO 0178796-A 35 25-OCT-2001;
            MEDICAL RESEARCH COUNCIL (GB)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic primer (antisense) : Human (Homo sapiens)
                     Type II GnRH recepto"
BASE COUNT        3 a      9 c      4 g      4 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        483 CTGCCGAGACGGTGTGCA 500
              ||||||||| |||| |||
Db         18 CTGCCGAGAAGGTGGGCA 1


RESULT 94
AX293643/c
LOCUS       AX293643                  20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 5405 from Patent WO0179548.
ACCESSION   AX293643
VERSION     AX293643.1  GI:17055326
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 5405 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"
BASE COUNT        5 a      7 c      6 g      2 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        161 GCTGATCCTCAAGGTCTC 178
              |||| |||||||||||  |
Db         20 GCTGGTCCTCAAGGTCGC 3


RESULT 95
AX554330/c
LOCUS       AX554330                  20 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 17 from Patent WO0244403.
ACCESSION   AX554330
VERSION     AX554330.1  GI:25898146
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   White,J.H.
  TITLE     Markers for testing analogs of vitamin d and therapeutical uses
  JOURNAL   Patent: WO 0244403-A 17 06-JUN-2002;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="primer"
BASE COUNT        4 a      8 c      3 g      5 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1014 CCTGAGATGGTGCCAAAG 1031
              ||||||||||| ||| |
Db         20 CCTGAGATGGTGACAAGG 3


RESULT 96
AX711019/c
LOCUS       AX711019                  20 bp    RNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 319 from Patent EP1288296.
ACCESSION   AX711019
VERSION     AX711019.1  GI:29787400
KEYWORDS    .
SOURCE      Herpes simplex virus unknown type
  ORGANISM  Herpes simplex virus unknown type
            Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
```

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            Alphaherpesvirinae; Simplexvirus.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 319 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Herpes simplex virus unknown type"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:126283"
BASE COUNT        1 a      8 c      6 g      5 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        130 GGACAGGGACGCCCGCTC 147
              ||||||||||| ||| ||
Db         19 GGACAGGGACGGCCGATC 2


RESULT 97
BD001157/c
LOCUS       BD001157                  20 bp    RNA     linear   PAT 31-JAN-2002
DEFINITION  Method and reagent for inhibiting viral replication.
ACCESSION   BD001157
VERSION     BD001157.1  GI:18625716
KEYWORDS    JP 2000342285-A/317.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
            Holesek,J.J. and Mamone,A.J.
  TITLE     Method and reagent for inhibiting viral replication
  JOURNAL   Patent: JP 2000342285-A 317 12-DEC-2000;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000342285-A/317
            PD   12-DEC-2000
            PF   01-MAY-2000 JP 2000132616
            PR   11-MAY-1992 US    07/882689,14-MAY-1992 US    07/882712 PR
            14-MAY-1992 US    07/882713,14-MAY-1992 US    07/882714 PR
            14-MAY-1992 US    07/882823,14-MAY-1992 US    07/882824 PR
            14-MAY-1992 US    07/882886,14-MAY-1992 US    07/882888 PR
            14-MAY-1992 US    07/882889,14-MAY-1992 US    07/882921 PR
            14-MAY-1992 US    07/882922,14-MAY-1992 US    07/883823 PR
            14-MAY-1992 US    07/883849,14-MAY-1992 US    07/884073 PR
            14-MAY-1992 US    07/884074,14-MAY-1992 US    07/884333 PR
            14-MAY-1992 US    07/884422,14-MAY-1992 US    07/884431 PR
            14-MAY-1992 US    07/884436,14-MAY-1992 US    07/884521 PR
            31-JUL-1992 US    07/923738,26-AUG-1992 US    07/935854 PR
            26-AUG-1992 US    07/936086,18-SEP-1992 US    07/948359 PR
            15-OCT-1992 US    07/963322,07-DEC-1992 US    07/987129 PR
            07-DEC-1992 US    07/987130,07-DEC-1992 US    07/987133 PI
            KENNETH G DRAPER,LEC W DADYKTZ,JAMES A MACSWIGEN, PI   DENNIS G
            MAYSEJAK,
            PI   JAMES J HOLESEK,ANTHONY J MAMONE
            PC   C12N15/09,C12N5/10,C12N7/00,C12N9/22//(C12N5/10,C12R1:91), PC
             C12N15/00,
            PC   C12N5/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32630"
BASE COUNT        1 a      8 c      6 g      5 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        130 GGACAGGGACGCCCGCTC 147
              ||||||||||| ||| ||
Db         19 GGACAGGGACGGCCGATC 2


RESULT 98
BD001586/c
LOCUS       BD001586                  20 bp    RNA     linear   PAT 31-JAN-2002
DEFINITION  Method and reagent for inhibiting viral replication.
ACCESSION   BD001586
VERSION     BD001586.1  GI:18626145
KEYWORDS    JP 2000342286-A/317.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
            Holesek,J.J. and Mamone,A.J.
  TITLE     Method and reagent for inhibiting viral replication
  JOURNAL   Patent: JP 2000342286-A 317 12-DEC-2000;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000342286-A/317
            PD   12-DEC-2000
            PF   01-MAY-2000 JP 2000132651
            PR   11-MAY-1992 US    07/882689,14-MAY-1992 US    07/882712 PR
            14-MAY-1992 US    07/882713,14-MAY-1992 US    07/882714 PR
            14-MAY-1992 US    07/882823,14-MAY-1992 US    07/882824 PR
            14-MAY-1992 US    07/882886,14-MAY-1992 US    07/882888 PR
            14-MAY-1992 US    07/882889,14-MAY-1992 US    07/882921 PR
            14-MAY-1992 US    07/882922,14-MAY-1992 US    07/883823 PR
            14-MAY-1992 US    07/883849,14-MAY-1992 US    07/884073 PR
            14-MAY-1992 US    07/884074,14-MAY-1992 US    07/884333 PR
            14-MAY-1992 US    07/884422,14-MAY-1992 US    07/884431 PR
            14-MAY-1992 US    07/884436,14-MAY-1992 US    07/884521 PR
            31-JUL-1992 US    07/923738,26-AUG-1992 US    07/935854 PR
            26-AUG-1992 US    07/936086,18-SEP-1992 US    07/948359 PR
            15-OCT-1992 US    07/963322,07-DEC-1992 US    07/987129 PR
            07-DEC-1992 US    07/987130,07-DEC-1992 US    07/987133 PI
            KENNETH G DRAPER,LEC W DADYKTZ,JAMES A MACSWIGEN, PI   DENNIS G
            MAYSEJAK,
            PI   JAMES J HOLESEK,ANTHONY J MAMONE
            PC   C12N15/09,C12N5/10,C12N7/00//A61K38/43,A61K39/125,A61K39/13,
            PC   A61K39/135,
            PC   A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
            PC   A61P1/16,
            PC   A61P31/14,A61P31/16,A61P31/18,A61P31/22,A61P35/02,C12Q1/68, PC
              (C12N15/09,C12R1:93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00, PC
             C12R1:93)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32630"
BASE COUNT        1 a      8 c      6 g      5 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        130 GGACAGGGACGCCCGCTC 147
              ||||||||||| ||| ||
Db         19 GGACAGGGACGGCCGATC 2
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RESULT 99
E37618/c
LOCUS       E37618                    20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method for detecting abnormality in human mitochondrial DNA.
ACCESSION   E37618
VERSION     E37618.1  GI:18626742
KEYWORDS    JP 2000175689-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kinoshita,S. and Hirai,T.
  TITLE     Method for detecting abnormality in human mitochondrial DNA
  JOURNAL   Patent: JP 2000175689-A 8 27-JUN-2000;
            OTSUKA PHARMACEUT CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000175689-A/8
            PD   27-JUN-2000
            PF   17-DEC-1998 JP 1998359276
            PR
            PI   SHIGETOSHI KINOSHITA,TETSUYA HIRAI
            PC   C12N15/09,C12Q1/68//(C12N15/09,C12R1:91),C12N15/00,(C12N15/00,
            PC   C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        5 a      3 c      6 g      6 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.6e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         47 CTTAGCATACTCCTCAAT 64
              || || ||||||||||||
Db         20 CTCAGGATACTCCTCAAT 3


RESULT 100
AX167170/c
LOCUS       AX167170                  21 bp    DNA     linear   PAT 03-JUL-2001
DEFINITION  Sequence 25 from Patent WO0142304.
ACCESSION   AX167170
VERSION     AX167170.1  GI:14596639
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Saris,C.M., Giles,J., Mu,S.X., Xia,M., Bass,M.B. and Craveiro,R.
  TITLE     Interleukin-1 receptor antagonist-related molecules and uses
            thereof
  JOURNAL   Patent: WO 0142304-A 25 14-JUN-2001;
            Amgen Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide 2351-48"
BASE COUNT        2 a      6 c      7 g      6 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        597 CACCAGCCTGAAGCCTGA 614
              || |||||| ||||||||
Db         21 CAGCAGCCTCAAGCCTGA 4


RESULT 101
AX259235
LOCUS       AX259235                  21 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 33 from Patent WO0173087.
ACCESSION   AX259235
VERSION     AX259235.1  GI:16508481
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hohn,T., Stavolone,L., de Haan,P.T., Ligon,H.T. and Kononova,M.
  TITLE     Cestrum yellow leaf curling virus promoters
  JOURNAL   Patent: WO 0173087-A 33 04-OCT-2001;
            Syngenta Participations AG (CH)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
BASE COUNT        3 a      3 c      6 g      9 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        674 CCAGCGTGGTATTTGGGA 691
              ||| |||||||||||| |
Db          1 CCATCGTGGTATTTGGTA 18


RESULT 102
AX259236/c
LOCUS       AX259236                  21 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 34 from Patent WO0173087.
ACCESSION   AX259236
VERSION     AX259236.1  GI:16508482
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hohn,T., Stavolone,L., de Haan,P.T., Ligon,H.T. and Kononova,M.
  TITLE     Cestrum yellow leaf curling virus promoters
  JOURNAL   Patent: WO 0173087-A 34 04-OCT-2001;
            Syngenta Participations AG (CH)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
BASE COUNT        9 a      6 c      3 g      3 t

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        674 CCAGCGTGGTATTTGGGA 691
              ||| |||||||||||| |
Db         21 CCATCGTGGTATTTGGTA 4


RESULT 103
AX356851
LOCUS       AX356851                  21 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 9 from Patent WO0206490.
ACCESSION   AX356851
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VERSION     AX356851.1  GI:18674099
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dudler,R., Schaffrath,U. and Lawton,K.A.
  TITLE     Lipoxygenase genes, promoters, transit peptides and proteins
            thereof
  JOURNAL   Patent: WO 0206490-A 9 24-JAN-2002;
            Syngenta Participations AG (CH) ; Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
BASE COUNT        2 a      1 c      1 g     16 t      1 others

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1139 ATGCCTTTTTTTCTTTTT 1156
              |||| |||||||| |||||
Db          2 ATGCTTTTTTTTTTTTTT 19


RESULT 104
AR305555/c
LOCUS       AR305555                  17 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 27 from patent US 6545162.
ACCESSION   AR305555
VERSION     AR305555.1  GI:31694964
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Dervan,P.B. and Baird,E.E.
  TITLE     Method for the synthesis of pyrrole and imidazole carboxamides on a
            solid support
  JOURNAL   Patent: US 6545162-A 27 08-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT       11 a      2 c      4 g      0 t

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.4e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1142 CCTTTTTTTCTTTTG 1157
              ||||||| ||||||||
Db         17 CCTTTTTGTCTTTTG 2


RESULT 105
AX725121/c
LOCUS       AX725121                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 2808 from Patent WO03025176.
ACCESSION   AX725121
VERSION     AX725121.1  GI:30504464
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 2808 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
BASE COUNT        3 a      4 c      6 g      4 t

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.4e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        627 CCAGCTCCAGGAGCTC 642
              |||||||||||||| ||
Db         16 CCAGCTCCAGGAGATC 1


RESULT 106
AX735260
LOCUS       AX735260                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 850 from Patent WO03025177.
ACCESSION   AX735260
VERSION     AX735260.1  GI:30514537
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 850 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      1 c      5 g      9 t

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.4e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1330 GATCTTGTGTTTCAGG 1345
              |||||||||||| |||
Db          1 GATCTTGTGTTTTAGG 16


RESULT 107
AR171472/c
LOCUS       AR171472                  18 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 113 from patent US 6297041.
ACCESSION   AR171472
VERSION     AR171472.1  GI:17910422
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: US 6297041-A 113 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        3 a      6 c      3 g      6 t

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.6e+02;
```

```
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1017 GAGATGGTGCCAAAGT 1032
              ||||||| ||||||||
Db         18 GAGATGGAGCCAAAGT 3


RESULT 108
AR171643/c
LOCUS       AR171643                 18 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 113 from patent US 6297051.
ACCESSION   AR171643
VERSION     AR171643.1  GI:17910593
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: US 6297051-A 113 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        3 a      6 c      3 g      6 t

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1017 GAGATGGTGCCAAAGT 1032
              ||||||| ||||||||
Db         18 GAGATGGAGCCAAAGT 3


RESULT 109
AX427085/c
LOCUS       AX427085                 18 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 49 from Patent WO0196604.
ACCESSION   AX427085
VERSION     AX427085.1  GI:21530468
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bee,G., Kohne,D.E., Korb,L., Peterson,T. and Yguerabide,J.
  TITLE     Assay for genetic polymorphisms using scattered light detectable
            labels
  JOURNAL   Patent: WO 0196604-A 49 20-DEC-2001;
            Genicon Sciences Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Exemplary probe for CYP2D6 allele detection"
BASE COUNT        3 a      3 c      9 g      3 t

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        562 CACACACTGCTCCAGC 577
              ||| ||||||||||||
Db         16 CACCCACTGCTCCAGC 1


RESULT 110
BD104495
LOCUS       BD104495                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD104495
VERSION     BD104495.1  GI:22650069
KEYWORDS    WO 0192572-A/599.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 599 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/599
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        3 a      2 c      6 g      7 t

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1182 TCTATAGGTGAGTGTT 1197
              ||||| ||||||||||
Db          3 TCTATGGGTGAGTGTT 18


RESULT 111
AX082063/c
LOCUS       AX082063                 19 bp    DNA     linear   PAT 27-FEB-2001
DEFINITION  Sequence 307 from Patent WO0109183.
ACCESSION   AX082063
VERSION     AX082063.1  GI:13170871
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U., Hoffmeyer,S., Eichelbaum,M. and Roots,I.
  TITLE     Polymorphisms in the human mdr-1 gene and their use in diagnostic
            and therapeutic applications
  JOURNAL   Patent: WO 0109183-A 307 08-FEB-2001;
            EPIDAUROS AG Biotechnologie Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="r=g or a"
BASE COUNT        2 a      5 c      8 g      3 t      1 others

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        577 CAGGCCCTCCGTCTGCCC 594
              |||| || |:||||||||
Db         19 CAGGGCCACYGTCTGCCC 2
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RESULT 112
AX082065
LOCUS       AX082065                 19 bp    DNA     linear   PAT 27-FEB-2001
DEFINITION  Sequence 309 from Patent WO0109183.
ACCESSION   AX082065
VERSION     AX082065.1  GI:13170873
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U., Hoffmeyer,S., Eichelbaum,M. and Roots,I.
  TITLE     Polymorphisms in the human mdr-1 gene and their use in diagnostic
            and therapeutic applications
  JOURNAL   Patent: WO 0109183-A 309 08-FEB-2001;
            EPIDAUROS AG Biotechnologie Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="y=c or t"
BASE COUNT        3 a      8 c      5 g      2 t      1 others

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        577 CAGGCCCTCCGTCTGCCC 594
              |||| || |:|||||||||
Db          1 CAGGGCCACYGTCTGCCC 18


RESULT 113
AX427086/c
LOCUS       AX427086                 19 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 50 from Patent WO0196604.
ACCESSION   AX427086
VERSION     AX427086.1  GI:21530469
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bee,G., Kohne,D.E., Korb,L., Peterson,T. and Yguerabide,J.
  TITLE     Assay for genetic polymorphisms using scattered light detectable
            labels
  JOURNAL   Patent: WO 0196604-A 50 20-DEC-2001;
            Genicon Sciences Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Exemplary probe for CYP2D6 allele detection"
BASE COUNT        4 a      3 c      9 g      3 t

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        562 CACACACTGCTCCAGC 577
              ||| ||||||||||||
Db         16 CACCCACTGCTCCAGC 1


RESULT 114
AX706670/c
LOCUS       AX706670                 19 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 367 from Patent WO03013534.
ACCESSION   AX706670
VERSION     AX706670.1  GI:29563093
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Heinrich,G. and Kerb,R.
  TITLE     Methods for the treatment of cancer with irinotecan based on CYP3A5
  JOURNAL   Patent: WO 03013534-A 367 20-FEB-2003;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     misc_feature    10
                     /note="r=a or g"
BASE COUNT        2 a      5 c      8 g      3 t      1 others

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        577 CAGGCCCTCCGTCTGCCC 594
              |||| || |:|||||||||
Db         19 CAGGGCCACYGTCTGCCC 2


RESULT 115
AX706671
LOCUS       AX706671                 19 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 368 from Patent WO03013534.
ACCESSION   AX706671
VERSION     AX706671.1  GI:29563094
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Heinrich,G. and Kerb,R.
  TITLE     Methods for the treatment of cancer with irinotecan based on CYP3A5
  JOURNAL   Patent: WO 03013534-A 368 20-FEB-2003;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     misc_feature    10
                     /note="y=c or t"
BASE COUNT        3 a      8 c      5 g      2 t      1 others

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        577 CAGGCCCTCCGTCTGCCC 594
              |||| || |:|||||||||
Db          1 CAGGGCCACYGTCTGCCC 18


RESULT 116
AX707600/c
LOCUS       AX707600                 19 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 367 from Patent WO03013536.
ACCESSION   AX707600
VERSION     AX707600.1  GI:29563773
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Heinrich,G. and Kerb,R.
  TITLE     Methods for treatment of cancer using irinotecan based on UGT1A1
  JOURNAL   Patent: WO 03013536-A 367 20-FEB-2003;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     misc_feature    10
                     /note="r=a or g"
BASE COUNT        2 a      5 c      8 g      3 t      1 others

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        577 CAGGCCCTCCGTCTGCCC 594
              |||| || |:||||||||
Db         19 CAGGGCCACYGTCTGCCC 2


RESULT 117
AX707601
LOCUS       AX707601                  19 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 368 from Patent WO03013536.
ACCESSION   AX707601
VERSION     AX707601.1  GI:29563774
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Heinrich,G. and Kerb,R.
  TITLE     Methods for treatment of cancer using irinotecan based on UGT1A1
  JOURNAL   Patent: WO 03013536-A 368 20-FEB-2003;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     misc_feature    10
                     /note="y=c or t"
BASE COUNT        3 a      8 c      5 g      2 t      1 others

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        577 CAGGCCCTCCGTCTGCCC 594
              |||| || |:||||||||
Db          1 CAGGGCCACYGTCTGCCC 18


RESULT 118
A17234
LOCUS       A17234                    20 bp    DNA     linear   PAT 31-MAR-1994
DEFINITION  Oligonucleotide 20-mer BB9513 (SEQ ID NO: 134).
ACCESSION   A17234
VERSION     A17234.1  GI:513003
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   .
  TITLE     STEM CELL INHIBITING PROTEINS
  JOURNAL   Patent: WO 9313206-A 134 08-JUL-1993;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        4 a      6 c      4 g      6 t

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        840 TTCAGATGGGTCAGCA 855
              |||||||| |||||||
Db          4 TTCAGATGCGTCAGCA 19


RESULT 119
AR027617
LOCUS       AR027617                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 134 from patent US 5856301.
ACCESSION   AR027617
VERSION     AR027617.1  GI:5938437
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Craig,S., Hunter,M.George., Edwards,R.Mark., Czaplewski,L.George.
            and Gilbert,R.James.
  TITLE     Stem cell inhibiting proteins
  JOURNAL   Patent: US 5856301-A 134 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      6 c      4 g      6 t

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        840 TTCAGATGGGTCAGCA 855
              |||||||| |||||||
Db          4 TTCAGATGCGTCAGCA 19


RESULT 120
AR130886
LOCUS       AR130886                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 2 from patent US 6190882.
ACCESSION   AR130886
VERSION     AR130886.1  GI:14119211
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Lee,C.-C., Albrecht,U., Eichele,G. and Sun,Z.Sheng.
  TITLE     Mammalian circadian rhythm-like gene
  JOURNAL   Patent: US 6190882-A 2 20-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        5 a      7 c      5 g      3 t

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        624 GGACCAGCTCCAGGAG 639
              |||||| |||||||||
Db          1 GGACCATCTCCAGGAG 16


RESULT 121
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AR142677/c
LOCUS       AR142677                 20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 7 from patent US 6203988.
ACCESSION   AR142677
VERSION     AR142677.1  GI:15103963
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kambara,H. and Uematsu,C.
  TITLE     DNA fragment preparation method for gene expression profiling
  JOURNAL   Patent: US 6203988-A 7 20-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT       15 a      3 c      0 g      2 t

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTGGA 1159
              ||||||| ||||||||
Db         18 TTTTTTTTTTTTGGA 3


RESULT 122
AR230980
LOCUS       AR230980                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 240 from patent US 6451602.
ACCESSION   AR230980
VERSION     AR230980.1  GI:27271767
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Popoff,I. and Cowsert,L.M.
  TITLE     Antisense modulation of PARP expression
  JOURNAL   Patent: US 6451602-A 240 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      7 c      4 g      5 t

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1289 CAGTTGCTCAGCCTGG 1304
              ||||| ||||||||||
Db          2 CAGTTACTCAGCCTGG 17


RESULT 123
AX027830/c
LOCUS       AX027830                 20 bp    DNA     linear   PAT 16-SEP-2000
DEFINITION  Sequence 7 from Patent WO0034492.
ACCESSION   AX027830
VERSION     AX027830.1  GI:10188674
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Robine,S., Louvard,D., Pinto,D. and Jaisser,F.
  TITLE     Regulatory sequences of the mouse villin gene - use in transgenesis
  JOURNAL   Patent: WO 0034492-A 7 15-JUN-2000;
            ROBINE SYLVIE (FR) ; INST CURIE (FR) ; LOUVARD DANIEL (FR) ; PINTO
            DANIEL (FR) ; CENTRE NAT RECH SCIENT (FR) ; JAISSER FREDERIC (FR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
BASE COUNT        4 a      5 c      5 g      6 t

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1288 ACAGTTGCTCAGCCTG 1303
              |||||||| |||||||
Db         19 ACAGTTGCGCAGCCTG 4


RESULT 124
BD138122/c
LOCUS       BD138122                 20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Antisense modulation of human MDM2 expression.
ACCESSION   BD138122
VERSION     BD138122.1  GI:23233067
KEYWORDS    JP 2002508944-A/48.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.
  TITLE     Antisense modulation of human MDM2 expression
  JOURNAL   Patent: JP 2002508944-A 48 26-MAR-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Unidentified
            PN   JP 2002508944-A/48
            PD   26-MAR-2002
            PF   26-MAR-1999 JP 2000538025
            PR   26-MAR-1998 US    09/048810
            PI   LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

            PI   COWSERT
            PC   C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
            PC   C12Q1/68,
            PC   C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Antisense modulation of human MDM2 expression FH   Key
                 Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      7 c      8 g      3 t

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        788 CCAGTGCCCTGGCTCG 803
              |||||||||||||| ||
Db         20 CCAGTGCCCTGGCCCG 5


RESULT 125
E28096/c
LOCUS       E28096                   20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for analyzing DNA fragment.
ACCESSION   E28096
VERSION     E28096.1  GI:13018321
KEYWORDS    JP 1999196874-A/7.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
```

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REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hideki,K. and Senshu,U.
  TITLE     Method for analyzing DNA fragment
  JOURNAL   Patent: JP 1999196874-A 7 27-JUL-1999;
            HITACHI LTD
COMMENT     OS   Unidentified
            PN   JP 1999196874-A/7
            PD   27-JUL-1999
            PF   14-JAN-1998 JP 1998005399
            PR
            PI   HIDEKI KAMIBARA,SENSHU UEMATSU
            PC   C12N15/09,C12Q1/68,G01N27/447,C12N15/00,G01N27/26 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT       15 a      3 c      0 g      2 t

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTGGA 1159
              ||||||| ||||||||
Db         18 TTTTTTTTTTTTTGGA 3


RESULT 126
E58956
LOCUS       E58956                    20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for complementary assay of protein binding enzyme.
ACCESSION   E58956
VERSION     E58956.1  GI:13019382
KEYWORDS    JP 2000023684-A/11.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Daniel,R.H.
  TITLE     Method for complementary assay of protein binding enzyme
  JOURNAL   Patent: JP 2000023684-A 11 25-JAN-2000;
            BOEHRINGER MANNHEIM CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2000023684-A/11
            PD   25-JAN-2000
            PF   07-JUN-1999 JP 1999159606
            PR   22-SEP-1989 US       410996
            PI   DANIEL R HENDERSON
            PC   C12N15/09,C12N1/21,C12N9/38,G01N33/535,G01N33/542//(C12N1/21,
            PC   C12R1:19),
            PC   C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT       6 a      6 c      5 g      3 t

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1288 ACAGTTGCTCAGCCTG 1303
              ||||||| |||||||
Db          3 ACAGTTGCGCAGCCTG 18


RESULT 127
I78497/c
LOCUS       I78497                    20 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 8 from patent US 5693756.
ACCESSION   I78497
VERSION     I78497.1  GI:3014651
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Li,X.-J., Blackshaw,S. and Snyder,S.H.
  TITLE     Amiloride-sensitive sodium channel and method of identifying
            substances which stimulate or block salty taste perception
  JOURNAL   Patent: US 5693756-A 8 02-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT       3 a      5 c      7 g      5 t

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        629 AGCTCCAGGAGCTCTG 644
              ||| ||||||||||||
Db         16 AGCCCCAGGAGCTCTG 1


RESULT 128
I79512
LOCUS       I79512                    20 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 3 from patent US 5707809.
ACCESSION   I79512
VERSION     I79512.1  GI:3207802
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Halverson,J. and Dvorak,J.
  TITLE     Avian sex identification probes
  JOURNAL   Patent: US 5707809-A 3 13-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT       6 a      3 c      7 g      4 t

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        670 TTGGCCAGCGTGGTAT 685
              | ||||||||||||||
Db          3 TAGGCCAGCGTGGTAT 18


RESULT 129
AR147800
LOCUS       AR147800                  19 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 7 from patent US 6225049.
ACCESSION   AR147800
VERSION     AR147800.1  GI:15111890
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Lan,M.S. and Notkins,A.L.
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  TITLE     Human insulinoma-associated cDNA
  JOURNAL   Patent: US 6225049-A 7 01-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        5 a      6 c      5 g      3 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 1.9e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        521 ACCTGCCGGAGGAGCAGCT 539
              |||||| |||||| || ||
Db          1 ACCTGCAGGAGGATCACCT 19


RESULT 130
BD178777/c
LOCUS       BD178777                 19 bp    DNA     linear   PAT 16-APR-2003
DEFINITION  Gene panel for genes involving liver regeneration.
ACCESSION   BD178777
VERSION     BD178777.1  GI:30016044
KEYWORDS    WO 02077222-A/115.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Yokoya,F., Okutsu,T., Mori,M., Yoshiyuki, Takahara, Fukuda,H.,
            Aburatani,H. and Sonaka,I.
  TITLE     Gene panel for genes involving liver regeneration
  JOURNAL   Patent: WO 02077222-A 115 03-OCT-2002;
            AJINOMOTO CO INC,FUMIHIKO YOKOYA,TOMOHISA OKUTSU,MAIKO MORI,
            YOSHIYUKI TAKAHARA,HISAO FUKUDA,HIROYUKI ABURATANI,ICHIRO SONAKA
COMMENT     OS   Artificial Sequence
            PN   WO 02077222-A/115
            PD   03-OCT-2002
            PF   13-MAR-2002 WO 2002JP002372
            PR   13-MAR-2001 JP 01P   070940
            PI   FUMIHIKO YOKOYA,TOMOHISA OKUTSU,MAIKO MORI,YOSHIYUKI PI
            TAKAHARA,HISAO FUKUDA,
            PI   HIROYUKI ABURATANI,ICHIRO SONAKA
            PC   C12N15/09,C12Q1/68,G01N33/15,G01N33/50,G01N37/00 CC
            Description of Artificial Sequence: primer
            FH   Key             Location/Qualifiers
            FT   source          1. .19
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        4 a      7 c      2 g      6 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 1.9e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        924 GATGGCAGATCTGGAGAAG 942
              ||| ||||| ||||||| |
Db         19 GATTGCAGAACTGGAGATG 1


RESULT 131
A62818/c
LOCUS       A62818                   20 bp    DNA     linear   PAT 12-MAR-1998
DEFINITION  Sequence 59 from Patent WO9719110.
ACCESSION   A62818
VERSION     A62818.1  GI:3716706
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Futreal,P.A., Wooster,R.F., Ashworth,A. and Stratton,M.R.
  TITLE     MATERIALS AND METHODS RELATING TO THE IDENTIFICATION AND SEQUENCING
            OF THE BRCA2 CANCER SUSCEPTIBILITY GENE AND USES THEREOF
  JOURNAL   Patent: WO 9719110-A 59 29-MAY-1997;
            CANCER RES CAMPAIGN TECH (GB)
COMMENT     Other publication AU 7635096 19970611
            Other publication GB 2307477 19970528.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        8 a      4 c      4 g      4 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1110 AGTTTTCTGTTTAATTGAA 1128
              |||  |||||||| |||||
Db         20 AGTCCTCTGTTTAGTTGAA 2


RESULT 132
AR067069
LOCUS       AR067069                 20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 417 from patent US 5851760.
ACCESSION   AR067069
VERSION     AR067069.1  GI:5998291
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Evans,G.A. and Smith,M.W.
  TITLE     Method for generation of sequence sampled maps of complex genomes
  JOURNAL   Patent: US 5851760-A 417 22-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT       11 a      4 c      4 g      1 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1159 AAGTAAAGCAGCTAAAACA 1177
              ||||||||| || ||| ||
Db          1 AAGTAAAGCCGCAAAAGCA 19


RESULT 133
AR073812/c
LOCUS       AR073812                 20 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 11 from patent US 5952202.
ACCESSION   AR073812
VERSION     AR073812.1  GI:10000572.
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Aoyagi,K. and Livak,K.J.
  TITLE     Methods using exogenous, internal controls and analogue blocks
            during nucleic acid amplification
  JOURNAL   Patent: US 5952202-A 11 14-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      6 c      5 g      5 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
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  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        620 TCAGGGACCAGCTCCAGGA 638
              ||||| ||| | |||||||
Db         20 TCAGGAACCTGGTCCAGGA 2


RESULT 134
AR082613/c
LOCUS       AR082613                  20 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 4 from patent US 5973225.
ACCESSION   AR082613
VERSION     AR082613.1  GI:10009333
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   D'Ovidio,R., Porceddu,E., Marchitelli,C. and Cardelli,L.Ercoli.
  TITLE     Isolation and characterization of a gene encoding a low molecular
            weight glutenin
  JOURNAL   Patent: US 5973225-A 4 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      7 c      6 g      3 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1011 GCACCTGAGATGGTGCCAA 1029
              ||||| ||| |||||||| |
Db         20 GCACCGGAGTTGGTGCCTA 2


RESULT 135
AR086110
LOCUS       AR086110                  20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 4 from patent US 5985556.
ACCESSION   AR086110
VERSION     AR086110.1  GI:10012876
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kambara,H. and Okano,K.
  TITLE     DNA sequencing method and DNA sample preparation method
  JOURNAL   Patent: US 5985556-A 4 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        1 a      1 c      3 g     15 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTGGAAGT 1162
              ||||||| |||||| | ||
Db          2 TTTTTTTTTTTTTGCAGGT 20


RESULT 136
AR116542
LOCUS       AR116542                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 123 from patent US 6133246.
ACCESSION   AR116542
VERSION     AR116542.1  GI:14096864
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   McKay,R.,, Dean,N., Monia,B.P., Nero,P.S. and Gaarde,W.A.
  TITLE     Antisense oligonucleotide compositions and methods for the
            modulation of JNK proteins
  JOURNAL   Patent: US 6133246-A 123 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        6 a      5 c      7 g      2 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        910 CTGGTCCTAAAGGAGATGG 928
              |||  |||||||||||| ||
Db          2 CTGCACCTAAAGGAGACGG 20


RESULT 137
AR120995/c
LOCUS       AR120995                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 16 from patent US 6159694.
ACCESSION   AR120995
VERSION     AR120995.1  GI:14104571
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Karras,J.G.
  TITLE     Antisense modulation of stat3 expression
  JOURNAL   Patent: US 6159694-A 16 12-DEC-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      3 c      8 g      5 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        628 CAGCTCCAGGAGCTCTGCA 646
              ||||||||  |||||| ||
Db         20 CAGCTCCATCAGCTCTACA 2


RESULT 138
AR121047/c
LOCUS       AR121047                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 68 from patent US 6159694.
ACCESSION   AR121047
VERSION     AR121047.1  GI:14104623
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Karras,J.G.
  TITLE     Antisense modulation of stat3 expression
  JOURNAL   Patent: US 6159694-A 68 12-DEC-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        5 a      7 c      5 g      3 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1256 GAGGCCAGGTTGAGGCCCT 1274
              |||| ||| ||||| ||||
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Db         20 GAGGGCAGTTTGAGTCCCT 2


RESULT 139
AR129648/c
LOCUS       AR129648                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 52 from patent US 6187545.
ACCESSION   AR129648
VERSION     AR129648.1  GI:14117545
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   McKay,R., Butler,M.M., Wyatt,J. and Cowsert,L.M.
  TITLE     Antisense modulation of pepck-cytosolic expression
  JOURNAL   Patent: US 6187545-A 52 13-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      3 c      10 g      3 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        512 TCAGCGCCAACCTGCCGGA 530
              ||| |||| ||||||| ||
Db         20 TCATCGCCCACCTGCCTGA 2


RESULT 140
AR229037/c
LOCUS       AR229037                  20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 47 from patent US 6448081.
ACCESSION   AR229037
VERSION     AR229037.1  GI:27268179
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F. and Freier,S.M.
  TITLE     Antisense modulation of interleukin 12 p40 subunit expression
  JOURNAL   Patent: US 6448081-A 47 10-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      4 c      9 g      3 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        227 CTCAGCCTCAGGCATCTGC 245
              ||||||| | | |||||||
Db         20 CTCAGCCACGGTCATCTGC 2


RESULT 141
AR232357/c
LOCUS       AR232357                  20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 52 from patent US 6455308.
ACCESSION   AR232357
VERSION     AR232357.1  GI:27274349
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Freier,S.M.
  TITLE     Antisense modulation of serum amyloid A4 expression
  JOURNAL   Patent: US 6455308-A 52 24-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      5 c      4 g      7 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        282 GGAAGCAGCAGCAATGTCT 300
              |||| |||||||| ||| |
Db         20 GGAAACAGCAGCACTGTAT 2


RESULT 142
AR261676/c
LOCUS       AR261676                  20 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 155 from patent US 6322976.
ACCESSION   AR261676
VERSION     AR261676.1  GI:28072754
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Aitman,T.J., Scott,J. and Stanton,L.W.
  TITLE     Compositions and methods of disease diagnosis and therapy
  JOURNAL   Patent: US 6322976-A 155 27-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        1 a      7 c      5 g      7 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        622 AGGGACCAGCTCCAGGAGC 640
              | ||||||| |||||| ||
Db         19 AAGGACCAGATCCAGGGGC 1


RESULT 143
AR294481/c
LOCUS       AR294481                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 6216 from patent US 6537751.
ACCESSION   AR294481
VERSION     AR294481.1  GI:31681765
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 6216 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        5 a      2 c      9 g      4 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1205 CACACCTCCCCTTCCCTGT 1223
              || |||||  |||||||||
Db         19 CAGACCTCAACTTCCCTGT 1


RESULT 144
AR299883/c
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LOCUS       AR299883                 20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 11618 from patent US 6537751.
ACCESSION   AR299883
VERSION     AR299883.1  GI:31687167
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 11618 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        7 a      9 c      2 g      2 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1232 CTTTGGTGCTGGACGTGGC 1250
              |||||||| |||| | |||
Db         20 CTTTGGTGTTGGAAGGGGC 2


RESULT 145
AR300301/c
LOCUS       AR300301                 20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 103 from patent US 6537775.
ACCESSION   AR300301
VERSION     AR300301.1  GI:31687720
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tournier-Lasserve,E., Joutel,A., Bousser,M.-G. and Bach,J.-F.
  TITLE     Gene involved in cadasil, method of diagnosis and therapeutic
            application
  JOURNAL   Patent: US 6537775-A 103 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        5 a      2 c     10 g      3 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1208 ACCTCCCCTTCCCTGTACA 1226
              ||||| |||||||| | ||
Db         20 ACCTCACCTTCCCTCTGCA 2


RESULT 146
AX056718
LOCUS       AX056718                 20 bp    DNA     linear   PAT 17-JAN-2001
DEFINITION  Sequence 50 from Patent WO0075317.
ACCESSION   AX056718
VERSION     AX056718.1  GI:12309697
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Botstein,D.A., Goddard,A., Gurney,A.L., Smith,V., Watanabe,C.K. and
            Wood,W.I.
  TITLE     Compositions and methods for the treatment of tumor
  JOURNAL   Patent: WO 0075317-A 50 14-DEC-2000;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide probe"
BASE COUNT        5 a      6 c      4 g      5 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        611 CTGACACCTTCAGGGACCA 629
              |||||| |||||||  |||
Db          2 CTGACAACTTCAGGTTCCA 20


RESULT 147
AX089272/c
LOCUS       AX089272                 20 bp    DNA     linear   PAT 21-MAR-2001
DEFINITION  Sequence 11 from Patent WO0116367.
ACCESSION   AX089272
VERSION     AX089272.1  GI:13443617
KEYWORDS    .
SOURCE      Escherichia coli
  ORGANISM  Escherichia coli
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE   1
  AUTHORS   Aoyagi,K. and Livak,K.J.
  TITLE     Methods for exogenous, internal controls during nucleic acid
            amplification
  JOURNAL   Patent: WO 0116367-A 11 08-MAR-2001;
            THE PERKIN-ELMER CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Escherichia coli"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:562"
BASE COUNT        4 a      6 c      5 g      5 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        620 TCAGGGACCAGCTCCAGGA 638
              ||||| ||| | |||||||
Db         20 TCAGGAACCTGGTCCAGGA 2


RESULT 148
AX167947
LOCUS       AX167947                 20 bp    DNA     linear   PAT 03-JUL-2001
DEFINITION  Sequence 131 from Patent WO0142307.
ACCESSION   AX167947
VERSION     AX167947.1  GI:14597267
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Saito,K., Ohe,N. and Satoh,H.
  TITLE     Mutant er_g(a) and test systems for transactivation
  JOURNAL   Patent: WO 0142307-A 131 14-JUN-2001;
            Sumitomo Chemical Company, Limited (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Designed oligonucleotide probe for Southern
                     hybridization"
BASE COUNT        6 a      4 c      7 g      3 t
```

```
  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1002 CTTGGACAGGCACCTGAGA 1020
              ||||||||||  ||| | ||
Db          2 CTTGGACAGGAACCAGGGA 20


RESULT 149
AX167955/c
LOCUS       AX167955                  20 bp    DNA     linear   PAT 03-JUL-2001
DEFINITION  Sequence 139 from Patent WO0142307.
ACCESSION   AX167955
VERSION     AX167955.1  GI:14597275
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Saito,K., Ohe,N. and Satoh,H.
  TITLE     Mutant er_g(a) and test systems for transactivation
  JOURNAL   Patent: WO 0142307-A 139 14-JUN-2001;
            Sumitomo Chemical Company, Limited (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Designed oligonucleotide probe for Southern
                     hybridization"
BASE COUNT        4 a      7 c      7 g      2 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        469 CTGCAGGGGGAGGACTGCC 487
              ||||||||  |||  |||||
Db         20 CTGCAGGGTCAGGCCTGCC 2


RESULT 150
AX296192
LOCUS       AX296192                  20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 7954 from Patent WO0179548.
ACCESSION   AX296192
VERSION     AX296192.1  GI:17057881
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 7954 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"
BASE COUNT        4 a     11 c      2 g      3 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1053 CAGCCCTGGCCTTCCCATC 1071
              |||||||  ||||||||  |
Db          1 CAGCCCTAACCTTCCCAGC 19


RESULT 151
AX298904
LOCUS       AX298904                  20 bp    DNA     linear   PAT 26-NOV-2001
DEFINITION  Sequence 538 from Patent WO0183749.
ACCESSION   AX298904
VERSION     AX298904.1  GI:17128894
KEYWORDS    .
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Bachmanov,A.A., Beauchamp,G.K., Chatterjee,A., de Jong,P.J., Li,S.,
            Li,X., Ohmen,J.D., Reed,D.R., Ross,D. and Tordoff,M.G.
  TITLE     Gene and sequence variation associated with sensing carbohydrate
            compounds and other sweeteners
  JOURNAL   Patent: WO 0183749-A 538 08-NOV-2001;
            WARNER-LAMBERT COMPANY (US) ; The Monell Chemical Senses Center
            (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10095"
BASE COUNT        5 a      3 c      8 g      4 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        879 CAAGTTCCAGGAGCTGCGG 897
              ||||||  ||||||||  ||
Db          2 CAAGTTTCAGGAGCTAGGG 20


RESULT 152
AX377027
LOCUS       AX377027                  20 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 22 from Patent WO0212890.
ACCESSION   AX377027
VERSION     AX377027.1  GI:19573321
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lamb,J.R., Hoyne,G.F., Dallman,M.J. and Champion,B.R.
  TITLE     Assay
  JOURNAL   Patent: WO 0212890-A 22 14-FEB-2002;
            Lorantis Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        5 a      5 c      6 g      4 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1081 CTTCAGTGAGTGTTTGAAC 1099
              ||||||  |||||  |||||
Db          2 CTTCAGCGAGTGCATGAAC 20


RESULT 153
AX511559/c
LOCUS       AX511559                  20 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 3 from Patent WO02057433.
ACCESSION   AX511559
```

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VERSION     AX511559.1  GI:23392398
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hofmann,T., Schmitz,L., Droege,W., Moeller,A., Will,H. and
            Hueseyin,S.
  TITLE     Homeodomain-interacting protein kinases and the use of the same for
            influencing cell division and cell proliferation
  JOURNAL   Patent: WO 02057433-A 3 25-JUL-2002;
            Deutsches Krebsforschungszentrum (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Primer fuer PCR (Beispiel 1)"
BASE COUNT        5 a      5 c      5 g      5 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1244 ACGTGGCCATGTGAGGCCA 1262
              || ||  ||||||||||||
Db         20 ACTTGCACATGTGAGGCCA 2


RESULT 154
AX742820/c
LOCUS       AX742820                 20 bp    DNA     linear   PAT 12-MAY-2003
DEFINITION  Sequence 623 from Patent EP1302550.
ACCESSION   AX742820
VERSION     AX742820.1  GI:30576809
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lin,C.Y., Lin,R.W., You,C.M., Huang,H.H., Lee,B.H., Lee,H.H.,
            Lin,Y.J., Fan,C.C., Hsu,H.C., Shih,C.W., Yeh,C.H., Kao,Y.F.,
            Pan,C.L. and Chan,P.
  TITLE     Method and detector for identifying subtypes of human papilloma
            viruses
  JOURNAL   Patent: EP 1302550-A 623 16-APR-2003;
            King Car Food Industrial Co., Ltd. (TW)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide for Identifying HPV 42"
BASE COUNT        6 a      9 c      2 g      3 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        443 AGTTGCTGAAGTTTGTGGT 461
              |||| |||||| | |||||
Db         20 AGTTCCTGAAGGTGGTGGT 2


RESULT 155
BD074699
LOCUS       BD074699                 20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Antisence oligonucleotide composition and modulation method of JNK
            protein.
ACCESSION   BD074699
VERSION     BD074699.1  GI:22620302
KEYWORDS    JP 2001514905-A/123.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mckay,R., Dean,N., Monia,B.P., Scott,P., Nero and Gaarde,W.A.
  TITLE     Antisence oligonucleotide composition and modulation method of JNK
            protein
  JOURNAL   Patent: JP 2001514905-A 123 18-SEP-2001;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001514905-A/123
            PD   18-SEP-2001
            PF   07-AUG-1998 JP 2000509875
            PR   13-AUG-1997 US    08/910629
            PI   ROBERT MCKAY,NICHOLAS DEAN,BRETT P MONIA,PAMELA SCOTT PI
            NERO,WILLIAM A GAARDE
            PC   C12Q1/68,A61K31/7088,A61K48/00,A61P35/00,C12N15/09,C12P19/34,
            PC   C12N15/00
            CC   antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        6 a      5 c      7 g      2 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         910 CTGGTCCTAAAGGAGATGG 928
               |||  |||||||||||  ||
Db           2 CTGCACCTAAAGGAGACGG 20


RESULT 156
BD090593
LOCUS       BD090593                 20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Drug containing humanized anti-Fas antibody.
ACCESSION   BD090593
VERSION     BD090593.1  GI:22636203
KEYWORDS    JP 2001342148-A/53.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I.
  TITLE     Drug containing humanized anti-Fas antibody
  JOURNAL   Patent: JP 2001342148-A 53 11-DEC-2001;
            SANKYO CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2001342148-A/53
            PD   11-DEC-2001
            PF   28-MAR-2001 JP 2001093106
            PI   NOBUFUSA SERIZAWA,HIDEYUKI HARUYAMA,KAORI NAKAHARA,IKUKO  PI
            TAMAKI
            PC   A61K39/395,A61K38/00,A61P1/16,A61P7/06,A61P9/00,A61P9/10, PC
            A61P13/12,
            PC   A61P19/02,A61P29/00,A61P37/00,A61P37/06,A61P37/08,A61P43/00//
            PC   C12N15/09,
            PC   A61K37/02,C12N15/00
            CC   Description of Artificial Sequence: Sequencing primer for a
            CC           DNA encoding
            CC   the heavy chain of a humanized anti-Fas antibody FH   Key
                   Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
```

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                     /db_xref="taxon:32630"
BASE COUNT        5 a      5 c      8 g      2 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        482 ACTGCCGAGACGGTGTGCA 500
              || |||| || ||||||||
Db          1 ACAGCCGGGAAGGTGTGCA 19


RESULT 157
BD090702
LOCUS       BD090702                 20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Drug containing humanized anti-Fas antibody.
ACCESSION   BD090702
VERSION     BD090702.1  GI:22636312
KEYWORDS    JP 2001342149-A/53.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Takahashi,W., Haruyama,H. and Serizawa,N.
  TITLE     Drug containing humanized anti-Fas antibody
  JOURNAL   Patent: JP 2001342149-A 53 11-DEC-2001;
            SANKYO CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2001342149-A/53
            PD   11-DEC-2001
            PF   28-MAR-2001 JP 2001093243
            PI   WATARU TAKAHASHI,HIDEYUKI HARUYAMA,NOBUFUSA SERIZAWA PC
           A61K39/395,A61K39/395,A61P1/16,A61P7/06,A61P9/00,A61P9/10, PC
           A61P13/12,
            PC   A61P17/00,A61P31/14,A61P31/18,A61P31/20,A61P37/00,A61P37/06,
            PC   A61P37/08,
            PC   A61P43/00//C12N15/02,C12N15/00
            CC   Description of Artificial Sequence: Sequencing primer for a
            CC          DNA encoding
            CC   the heavy chain of a humanized anti-Fas antibody FH   Key
              Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
BASE COUNT        5 a      5 c      8 g      2 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        482 ACTGCCGAGACGGTGTGCA 500
              || |||| || ||||||||
Db          1 ACAGCCGGGAAGGTGTGCA 19


RESULT 158
BD097485/c
LOCUS       BD097485                 20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Novel leukotrien B4 receptor.
ACCESSION   BD097485
VERSION     BD097485.1  GI:22643059
KEYWORDS    WO 0170815-A/9.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kamohara,M., Matsumoto,M., Takasaki,J., Saito,T. and Oishi,T.
  TITLE     Novel leukotrien B4 receptor
  JOURNAL   Patent: WO 0170815-A 9 27-SEP-2001;
            YAMANOUCHI PHARMACEUTICAL CO LTD,MASAZUMI KAMOHARA, MITSUYUKI
            MATSUMOTO, JUN TAKASAKI,TETSU SAITO,TAKAHIDE OISHI
COMMENT     OS   Rattus norvegicus (rat)
            PN   WO 0170815-A/9
            PD   27-SEP-2001
            PF   15-MAR-2001 WO 2001JP002060
            PR   21-MAR-2000 JP 00P    78992,22-JUN-2000 JP 00P   187978 PI
           MASAZUMI KAMOHARA,MITSUYUKI MATSUMOTO,JUN
           TAKASAKI,TETSU SAITO,
            PI   TAKAHIDE OISHI
            PC   C07K14/705,C12N15/12,C12N1/21,C12N1/19,C12N5/10,C12P21/02, PC
             C07K16/28,
            PC   C12Q1/02,G01N33/50,G01N33/15
            CC   Novel leukotrien B4 receptor
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Rattus norvegicus (rat)'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="Rattus norvegicus"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:10116"
BASE COUNT        5 a     11 c      4 g      0 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        723 GCAGCAGGGGGCCTGGCTG 741
              || || ||||| |||||||
Db         20 GCTGCTGGGGGTCTGGCTG 2


RESULT 159
BD174235
LOCUS       BD174235                 20 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Transgenic animal having drug-metabolizing enzyme gene and
            utilization thereof.
ACCESSION   BD174235
VERSION     BD174235.1  GI:28415574
KEYWORDS    WO 02066635-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Katsuki,M., Kamataki,T., Teranishi,Y., Ishida,M. and Kato,M.
  TITLE     Transgenic animal having drug-metabolizing enzyme gene and
            utilization thereof
  JOURNAL   Patent: WO 02066635-A 5 29-AUG-2002;
            GENCOM CORP,MOTOYA KATSUKI,TETSUYA KAMATAKI,YUTAKA TERANISHI,
            MITSUYOSHI ISHIDA,MINORU KATO
COMMENT     OS   Artificial Sequence
            PN   WO 02066635-A/5
            PD   29-AUG-2002
            PF   21-FEB-2002 WO 2002JP001555
            PR   23-FEB-2001 JP 01P   047735
            PI   MOTOYA KATSUKI,TETSUYA KAMATAKI,YUTAKA TERANISHI,MITSUYOSHI
            PI   ISHIDA,
            PI   MINORU KATO
            PC   C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/02,A01K67/
            PC   027,
            PC   A01K67/027,A61K45/00,A61P1/00,A61P3/10,A61P5/00,A61P9/00, PC
           A61P11/00,
            PC   A61P13/12,A61P19/00,A61P25/00,A61P31/00,A61P35/00,A61P37/08 CC
              Description of Artificial Sequence: Synthetic DNA FH   Key
              Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
```

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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT         2 a      8 c      7 g      3 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        381 TCCTCCAGAGGTGGCAGCA 399
              |||||| | | ||||||||
Db          2 TCCTCCCGGGCTGGCAGCA 20


RESULT 160
E13188
LOCUS       E13188                    20 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Oligonucleotide.
ACCESSION   E13188
VERSION     E13188.1  GI:3251993
KEYWORDS    JP 1997140400-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Okano,K. and Kanbara,H.
  TITLE     DETERMINATION OF BASE SEQUENCE
  JOURNAL   Patent: JP 1997140400-A 2 03-JUN-1997;
            HITACHI LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997140400-A/2
            PD   03-JUN-1997
            PF   13-SEP-1996 JP 1996242929
            PR   18-SEP-1995 JP 95P   238141
            PI   OKANO KAZUNOBU, KANBARA HIDEKI
            PC   C12Q1/68,G01N27/447,G01N33/58//C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES                Location/Qualifiers
     source             1. .20
                        /organism="unidentified"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32644"
BASE COUNT         1 a      1 c      3 g     15 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTGGAAGT 1162
              ||||||| |||||| | ||
Db          2 TTTTTTTTTTTTTGCAGGT 20


RESULT 161
E37452
LOCUS       E37452                    20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method for identifying animal hair fiber by DNA.
ACCESSION   E37452
VERSION     E37452.1  GI:18626704
KEYWORDS    JP 2000210084-A/1.
SOURCE      Bos sp.
  ORGANISM  Bos sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kato,M. and Takeuchi,A.
  TITLE     Method for identifying animal hair fiber by DNA
  JOURNAL   Patent: JP 2000210084-A 1 02-AUG-2000;
            NIPPON KAGAKU SENI KENSA KYOKAI
COMMENT     OS   Bos sp. (bovine)
            PN   JP 2000210084-A/1
            PD   02-AUG-2000
            PF   25-JAN-1999 JP 1999015616
            PR
            PI   MIKI KATO,AKIO TAKEUCHI
            PC   C12N15/09,C12Q1/68,G01N33/36,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Bos sp. (bovine)'.
FEATURES                Location/Qualifiers
     source             1. .20
                        /organism="Bos sp."
                        /mol_type="genomic DNA"
                        /db_xref="taxon:29061"
BASE COUNT         3 a      8 c      1 g      8 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          52 CATACTCCTCAATTACCCA 70
               ||| ||||||  |||||||
Db           1 CATTCTCCTCTGTTACCCA 19


RESULT 162
E37460
LOCUS       E37460                    20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method for identifying animal meat by DNA.
ACCESSION   E37460
VERSION     E37460.1  GI:18626712
KEYWORDS    JP 2000210085-A/1.
SOURCE      Bos sp.
  ORGANISM  Bos sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kato,M. and Takeuchi,A.
  TITLE     Method for identifying animal meat by DNA
  JOURNAL   Patent: JP 2000210085-A 1 02-AUG-2000;
            NIPPON KAGAKU SENI KENSA KYOKAI
COMMENT     OS   Bos sp. (bovine)
            PN   JP 2000210085-A/1
            PD   02-AUG-2000
            PF   25-JAN-1999 JP 1999015617
            PR
            PI   MIKI KATO,AKIO TAKEUCHI
            PC   C12N15/09,C12Q1/68,G01N33/12,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Bos sp. (bovine)'.
FEATURES                Location/Qualifiers
     source             1. .20
                        /organism="Bos sp."
                        /mol_type="genomic DNA"
                        /db_xref="taxon:29061"
BASE COUNT         3 a      8 c      1 g      8 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          52 CATACTCCTCAATTACCCA 70
               ||| ||||||  |||||||
Db           1 CATTCTCCTCTGTTACCCA 19
```

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RESULT 163
E40056
LOCUS       E40056                    20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Drug containing anti-Fas antibody.
ACCESSION   E40056
VERSION     E40056.1  GI:18627172
KEYWORDS    JP 2000169393-A/53.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Serizawa,N., Haruyama,H., Takahashi,W., Yoshida,H., Ichikawa,K.,
            Okuma,J., Otsuki,M., Shiraishi,A. and Yonehara,S.
  TITLE     Drug containing anti-Fas antibody
  JOURNAL   Patent: JP 2000169393-A 53 20-JUN-2000;
            SANKYO CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000169393-A/53
            PD   20-JUN-2000
            PF   30-SEP-1999 JP 1999278301
            PR
            PI   NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,WATARU TAKAHASHI, PI
            HIROKO YOSHIDA,
            PI   KIMIHISA ICHIKAWA,JUN OKUMA,MASAHIKO OTSUKI,AKIO SHIRAISHI, PI
              SHIN YONEHARA
            PC   A61K39/395,A61K39/395,A61K39/00,A61P1/16,A61P7/06,A61P9/00, PC
              A61P9/10,
            PC   A61P13/12,A61P31/18,A61P37/06,C12N5/10,C12N15/02,C12N15/09, PC
              C12P21/08//
            PC   C07K16/28,C12N5/00,C12N15/00,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        5 a      5 c      8 g      2 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        482 ACTGCCGAGACGGTGTGCA 500
              || |||| || ||||||||
Db          1 ACAGCCGGGAAGGTGTGCA 19


RESULT 164
E40864
LOCUS       E40864                    20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Humanized anti-Fas antibody.
ACCESSION   E40864
VERSION     E40864.1  GI:18627441
KEYWORDS    JP 2000166574-A/53.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I.
  TITLE     Humanized anti-Fas antibody
  JOURNAL   Patent: JP 2000166574-A 53 20-JUN-2000;
            SANKYO CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000166574-A/53
            PD   20-JUN-2000
            PF   29-SEP-1999 JP 1999275441
            PR
            PI   NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,KAORI NAKAHARA,IKUKO TAMAKI
            PC   C12N15/09,A61K39/00,A61K39/395,A61K39/395,A61P37/02,A61P43/00,
            PC   C07K16/18,
            PC   C12N1/21,C12N5/10,C12P21/08//(C12N1/21,C12R1:19),C12N15/00, PC
              C12N5/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        5 a      5 c      8 g      2 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        482 ACTGCCGAGACGGTGTGCA 500
              || |||| || ||||||||
Db          1 ACAGCCGGGAAGGTGTGCA 19


RESULT 165
E43410
LOCUS       E43410                    20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Humanized anti-Fas antibody.
ACCESSION   E43410
VERSION     E43410.1  GI:18627676
KEYWORDS    JP 2000166573-A/53.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Takahashi,W., Haruyama,H. and Serizawa,N.
  TITLE     Humanized anti-Fas antibody
  JOURNAL   Patent: JP 2000166573-A 53 20-JUN-2000;
            SANKYO CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000166573-A/53
            PD   20-JUN-2000
            PF   29-SEP-1999 JP 1999275440
            PR
            PI   WATARU TAKAHASHI,HIDEYUKI HARUYAMA,NOBUKI SERIZAWA PC
            C12N15/09,A61K38/00,A61K39/00,A61K39/395,A61K39/395,A61P37/00, PC
            A61P43/00,
            PC   C07K16/28,C12N1/21,C12N5/10,C12N15/02,C12P21/08//(C12P21/08,
            PC   C12R1:91),
            PC   C12N15/00,A61K37/02,C12N5/00,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        5 a      5 c      8 g      2 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        482 ACTGCCGAGACGGTGTGCA 500
              || |||| || ||||||||
Db          1 ACAGCCGGGAAGGTGTGCA 19


RESULT 166
I18763
LOCUS       I18763                    20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 18 from patent US 5498521.
ACCESSION   I18763
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VERSION     I18763.1  GI:1599118
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dryja,T.P. and Berson,E.L.
  TITLE     Diagnosis of hereditary retinal degenerative diseases
  JOURNAL   Patent: US 5498521-A 18 12-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      7 c      5 g      4 t

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        324 CCTGCATCATCCTGGTGAT 342
              ||||||  | |||||||||
Db          2 CCTGCACAACCCTGGTGAT 20


RESULT 167
AX272817/c
LOCUS       AX272817                 17 bp    mRNA    linear   PAT 29-OCT-2001
DEFINITION  Sequence 386 from Patent WO0162911.
ACCESSION   AX272817
VERSION     AX272817.1  GI:16545554
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
            Ellis,J.H.
  TITLE     Method and reagent for the inhibition of grid
  JOURNAL   Patent: WO 0162911-A 386 30-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      9 c      4 g      0 t

  Query Match             1.0%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        301 GCTGTGGGGGCTGC 314
              ||||||||||||||
Db         17 GCTGTGGGGGCTGC 4


RESULT 168
AX672484/c
LOCUS       AX672484                 17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 929 from Patent WO03004526.
ACCESSION   AX672484
VERSION     AX672484.1  GI:29330832
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 929 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT       11 a      3 c      2 g      1 t

  Query Match             1.0%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1146 TTTTTCTTTTTGGA 1159
              ||||||||||||||
Db         16 TTTTTCTTTTTGGA 3


RESULT 169
AX687585
LOCUS       AX687585                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 317 from Patent EP1281758.
ACCESSION   AX687585
VERSION     AX687585.1  GI:29410281
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 317 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      5 c      7 g      3 t

  Query Match             1.0%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        630 GCTCCAGGAGCTCT 643
              ||||||||||||||
Db          4 GCTCCAGGAGCTCT 17


RESULT 170
AX687589
LOCUS       AX687589                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 321 from Patent EP1281758.
ACCESSION   AX687589
VERSION     AX687589.1  GI:29410285
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 321 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      6 c      5 g      4 t
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  Query Match             1.0%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        631 CTCCAGGAGCTCTG 644
              ||||||||||||||
Db          1 CTCCAGGAGCTCTG 14


RESULT 171
AX688105
LOCUS       AX688105                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 837 from Patent EP1281758.
ACCESSION   AX688105
VERSION     AX688105.1  GI:29410803
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 837 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      8 c      4 g      4 t

  Query Match             1.0%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1055 GCCCTGGCCTTCCC 1068
              ||||||||||||||
Db          4 GCCCTGGCCTTCCC 17


RESULT 172
AX688106
LOCUS       AX688106                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 838 from Patent EP1281758.
ACCESSION   AX688106
VERSION     AX688106.1  GI:29410804
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 838 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      8 c      4 g      5 t

  Query Match             1.0%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1055 GCCCTGGCCTTCCC 1068
              ||||||||||||||
Db          3 GCCCTGGCCTTCCC 16


RESULT 173
AX688107
LOCUS       AX688107                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 839 from Patent EP1281758.
ACCESSION   AX688107
VERSION     AX688107.1  GI:29410805
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 839 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      8 c      5 g      4 t

  Query Match             1.0%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1055 GCCCTGGCCTTCCC 1068
              ||||||||||||||
Db          2 GCCCTGGCCTTCCC 15


RESULT 174
AX688108
LOCUS       AX688108                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 840 from Patent EP1281758.
ACCESSION   AX688108
VERSION     AX688108.1  GI:29410806
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 840 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      8 c      4 g      4 t

  Query Match             1.0%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1055 GCCCTGGCCTTCCC 1068
              ||||||||||||||
Db          1 GCCCTGGCCTTCCC 14


RESULT 175
AX690593
LOCUS       AX690593                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 3325 from Patent EP1281758.
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ACCESSION   AX690593
VERSION     AX690593.1  GI:29413474
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 3325 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      5 c      5 g      3 t

  Query Match             1.0%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        631 CTCCAGGAGCTCTG 644
              ||||||||||||||
Db          4 CTCCAGGAGCTCTG 17


RESULT 176
AX690597
LOCUS       AX690597                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 3329 from Patent EP1281758.
ACCESSION   AX690597
VERSION     AX690597.1  GI:29413478
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 3329 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      6 c      4 g      4 t

  Query Match             1.0%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        632 TCCAGGAGCTCTGC 645
              ||||||||||||||
Db          1 TCCAGGAGCTCTGC 14


RESULT 177
AR123497
LOCUS       AR123497                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 6 from patent US 6171779.
ACCESSION   AR123497
VERSION     AR123497.1  GI:14108858
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Chada,K.K., Ashar,H., Tkachenko,A. and Zhou,X.
  TITLE     HMGI proteins in cancer
  JOURNAL   Patent: US 6171779-A 6 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        8 a      5 c      6 g      0 t

  Query Match             1.0%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        282 GGAAGCAGCAGCAA 295
              ||||||||||||||
Db          1 GGAAGCAGCAGCAA 14


RESULT 178
AX129200
LOCUS       AX129200                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 418 from Patent WO0130362.
ACCESSION   AX129200
VERSION     AX129200.1  GI:14135505
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 418 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /note="Cdk4 ribozyme binding site"
BASE COUNT        4 a      7 c      5 g      3 t

  Query Match             1.0%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1060 GGCCTTCCCATCAG 1073
              ||||||||||||||
Db          5 GGCCTTCCCATCAG 18


RESULT 179
AX129201
LOCUS       AX129201                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 419 from Patent WO0130362.
ACCESSION   AX129201
VERSION     AX129201.1  GI:14135506
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 419 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
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```
                     /note="Cdk4 ribozyme binding site"
BASE COUNT        4 a      7 c      5 g      3 t

  Query Match             1.0%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1060 GGCCTTCCCATCAG 1073
              ||||||||||||||
Db          4 GGCCTTCCCATCAG 17


RESULT 180
AR059007
LOCUS       AR059007                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 14 from patent US 5837847.
ACCESSION   AR059007
VERSION     AR059007.1  GI:5984584
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Royer,J.C., Moyer,D.L., Wendy,Y.T. and Shuster,J.R.
  TITLE     Non-toxic, non-toxigenic, non-pathogenic fusarium expression system
            and promoters and terminators for use therein
  JOURNAL   Patent: US 5837847-A 14 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        9 a      3 c      6 g      2 t

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        387 AGAGGTGGCAGCAA 400
              ||||||||||||||
Db          5 AGAGGTGGCAGCAA 18


RESULT 181
AR295559/c
LOCUS       AR295559                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 7294 from patent US 6537751.
ACCESSION   AR295559
VERSION     AR295559.1  GI:31682843
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 7294 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        6 a      2 c      9 g      3 t

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        971 CCCTCACTTGACCA 984
              ||||||||||||||
Db         14 CCCTCACTTGACCA 1


RESULT 182
AR304363
LOCUS       AR304363                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 2 from patent US 6544774.
ACCESSION   AR304363
VERSION     AR304363.1  GI:31693480
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shuster,J.R. and Royer,J.C.
  TITLE     Morphological mutants of filamentous fungi
  JOURNAL   Patent: US 6544774-A 2 08-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        9 a      3 c      6 g      2 t

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        387 AGAGGTGGCAGCAA 400
              ||||||||||||||
Db          5 AGAGGTGGCAGCAA 18


RESULT 183
AX193676/c
LOCUS       AX193676                  20 bp    DNA     linear   PAT 15-AUG-2001
DEFINITION  Sequence 98 from Patent WO0140291.
ACCESSION   AX193676
VERSION     AX193676.1  GI:15211542
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Burgess,C.E., Prayaga,S.K., Shimkets,R.A., Rastelli,L.,
            Zerhusen,B.D. and Mezes,P.S.
  TITLE     Proteins and nucleic acids encoding the same
  JOURNAL   Patent: WO 0140291-A 98 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="chemically synthesized"
BASE COUNT        4 a      4 c      6 g      6 t

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        827 TGCAGCTGAAGCTT 840
              ||||||||||||||
Db         16 TGCAGCTGAAGCTT 3


RESULT 184
AX293574/c
LOCUS       AX293574                  20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 5336 from Patent WO0179548.
ACCESSION   AX293574
VERSION     AX293574.1  GI:17055257
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 5336 25-OCT-2001;
```

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          CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"
BASE COUNT        5 a      10 c       3 g       2 t

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        262 CTGGGCTGGCTGAT 275
              ||||||||||||||
Db         15 CTGGGCTGGCTGAT 2


RESULT 185
AX295621
LOCUS       AX295621                  20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 7383 from Patent WO0179548.
ACCESSION   AX295621
VERSION     AX295621.1  GI:17057310
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 7383 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"
BASE COUNT        6 a      5 c       5 g       4 t

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         40 GCAAAATCTTAGCA 53
              ||||||||||||||
Db          5 GCAAAATCTTAGCA 18


RESULT 186
AX472793/c
LOCUS       AX472793                  20 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 8 from Patent EP1213354.
ACCESSION   AX472793
VERSION     AX472793.1  GI:22207642
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Asako,H., Matsumura,K., Shimizu,M., Ito,N. and Wakita,R.
  TITLE     Process for producing optically active 4-halo-3-hydroxybutanoate
  JOURNAL   Patent: EP 1213354-A 8 12-JUN-2002;
            Sumitomo Chemical Company, Limited (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Designed oligonucleotide primer for PCR"
BASE COUNT        3 a      3 c       5 g       4 t      5 others

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   70.0%;  Pred. No. 2.2e+02;
  Matches   14;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        867 GGTCCCCACAGCCAAGTTCC 886
              ||| :||| | :||:|||||
Db         20 GGTWSCCARAAYCARGTTCC 1


RESULT 187
BD015231
LOCUS       BD015231                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Non-toxic, non-toxinogenic and non-phathogenic expression system,
            and promoter and terminator used therein.
ACCESSION   BD015231
VERSION     BD015231.1  GI:22556038
KEYWORDS    JP 2001169791-A/11.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Lowyer,J.C., Moeyer,D.L., Yoder,W. and Shuster,J.R.
  TITLE     Non-toxic, non-toxinogenic and non-phathogenic expression system,
            and promoter and terminator used therein
  JOURNAL   Patent: JP 2001169791-A 11 26-JUN-2001;
            NOVO NORDISK BIOTECH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001169791-A/11
            PD   26-JUN-2001
            PF   16-NOV-2000 JP 2000349977
            PR   30-JUN-1994 US    08/269449,15-MAR-1995 US    08/404678 PI
            JOHN C LOWYER,DONA L MOEYER,WENDY YODER,JEFFREY R SHUSTER PC
            C12N15/09,C12N1/15//C12N9/20,C12N9/24,C12N9/58,(C12N1/15,C12R1: PC
             77),
            PC   (C12N9/20,C12R1:77),(C12N9/24,C12R1:77),(C12N9/58,C12R1:77),
            PC   C12N15/00
            CC   Humicola insolens
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        9 a      3 c       6 g       2 t

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        387 AGAGGTGGCAGCAA 400
              ||||||||||||||
Db          5 AGAGGTGGCAGCAA 18


RESULT 188
E08868
LOCUS       E08868                    20 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  PCR primer.
ACCESSION   E08868
VERSION     E08868.1  GI:2176972
KEYWORDS    JP 1995067699-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Imamura,I., Kondo,S., Fukui,H., Shinomura,Y. and Matsuzawa,Y.
  TITLE     QUANTITATIVE DETERMINATION OF MRNA BY REVERSE TRANSCRIPTASE-PCR
  JOURNAL   Patent: JP 1995067699-A 1 14-MAR-1995;
            IATRON LAB INC
COMMENT     OS   None
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            OC   Artificial sequences.
            PN   JP 1995067699-A/1
            PD   14-MAR-1995
            PF   27-AUG-1993 JP 1993235681
            PI   IMAMURA IKUO, KONDO SHINYA, FUKUI HIROYUKI, SHINOMURA
            YUKIHISA, PI   MATSUZAWA YUJI
            PC   C12Q1/68;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        4 a      6 c      6 g      4 t

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        543 TGCCCTGCTGGCAG 556
              ||||||||||||||
Db          3 TGCCCTGCTGGCAG 16


RESULT 189
AR010206/c
LOCUS       AR010206                  17 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 4 from patent US 5756702.
ACCESSION   AR010206
VERSION     AR010206.1  GI:3969011
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Lohman,K.L., Ostrerova,N.V., Van Cleve,M. and Reid,R.Alan.
  TITLE     Detection of nucleic acids in cells by thermophilic strand
            displacement amplification
  JOURNAL   Patent: US 5756702-A 4 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        3 a      5 c      3 g      6 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGC 290
              ||||| |||||||| ||
Db         17 ATCAATGAGGAAGCTGC 1


RESULT 190
AR047236
LOCUS       AR047236                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2029 from patent US 5817796.
ACCESSION   AR047236
VERSION     AR047236.1  GI:5968701
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL   Patent: US 5817796-A 2029 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        6 a      0 c      3 g      8 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        1094 TTGAACGTAATTATGTA 1110
               ||||| || ||||||||
Db           1 TTGAAAGTTATTATGTA 17


RESULT 191
AR098727/c
LOCUS       AR098727                  17 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 2 from patent US 6077669.
ACCESSION   AR098727
VERSION     AR098727.1  GI:12808493
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Little,M.C. and Vonk,G.P.
  TITLE     Kit and method for fluorescence based detection assay
  JOURNAL   Patent: US 6077669-A 2 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        3 a      5 c      3 g      6 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGC 290
              ||||| |||||||| ||
Db         17 ATCAATGAGGAAGCTGC 1


RESULT 192
AR286312
LOCUS       AR286312                  17 bp    RNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 684 from patent US 6528640.
ACCESSION   AR286312
VERSION     AR286312.1  GI:29723908
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
            Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
  TITLE     Synthetic ribonucleic acids with RNAse activity
  JOURNAL   Patent: US 6528640-A 684 04-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        5 a      6 c      6 g      0 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        517 GCCAACCTGCCGGAGGA 533
              ||||||| ||| |||||
Db          1 GCCAACCGGCCAGAGGA 17


RESULT 193
AX010682
LOCUS       AX010682                  17 bp    DNA     linear   PAT 06-SEP-2000
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DEFINITION  Sequence 24 from Patent WO9958655.
ACCESSION   AX010682
VERSION     AX010682.1  GI:9997481
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kristensen,P., Jestin,J.L., Winter,G.P. and Riechmann,L.
  TITLE     Selection system
  JOURNAL   Patent: WO 9958655-A 24 18-NOV-1999;
            KRISTENSEN PETER (DK); JESTIN JEAN LUC (FR); MEDICAL RES COUNCIL
            (GB); WINTER GREGORY PAUL (GB); RIECHMANN LUTZ (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="PRIMER"
BASE COUNT        3 a      8 c      3 g      3 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        983 CAGTCCCATTCAGATCC 999
              | | ||||||||||||
Db          1 CGGCCCCATTCAGATCC 17


RESULT 194
AX074458
LOCUS       AX074458                 17 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 18 from Patent WO0104319.
ACCESSION   AX074458
VERSION     AX074458.1  GI:12710586
KEYWORDS    .
SOURCE      Infectious bursal disease virus (Gumboro virus)
  ORGANISM  Infectious bursal disease virus
            Viruses; dsRNA viruses; Birnaviridae; Avibirnavirus.
REFERENCE   1
  AUTHORS   Boot,H.J., ter Huurne,A.A. and Peeters,B.P.
  TITLE     Mosaic infectious bursal disease virus vaccines
  JOURNAL   Patent: WO 0104319-A 18 18-JAN-2001;
            Stichting Dienst Landbouwkundig Onderzoek (NL)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Infectious bursal disease virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10995"
BASE COUNT        3 a      4 c      7 g      3 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        485 GCCGAGACGGTGTGCAG 501
              ||| || ||||||||||
Db          1 GCCAAGTCGGTGTGCAG 17


RESULT 195
AX092631
LOCUS       AX092631                 17 bp    DNA     linear   PAT 21-MAR-2001
DEFINITION  Sequence 43 from Patent WO0115676.
ACCESSION   AX092631
VERSION     AX092631.1  GI:13444688
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M.
  TITLE     Compositions and methods for modulating hdl cholesterol and
            triglyceride levels
  JOURNAL   Patent: WO 0115676-A 43 08-MAR-2001;
            University of British Columbia (CA) ; Xenon Genetics Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      4 c      7 g      3 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        498 GCAGCGTCTTGGGGTCA 514
              |||| ||| ||||||||
Db          1 GCAGAGTCCTGGGGTCA 17


RESULT 196
AX217714/c
LOCUS       AX217714                 17 bp    mRNA    linear   PAT 07-SEP-2001
DEFINITION  Sequence 3156 from Patent WO0159103.
ACCESSION   AX217714
VERSION     AX217714.1  GI:15527775
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 3156 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
BASE COUNT        2 a      4 c      4 g      7 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        384 TCCAGAGGTGGCAGCAA 400
              ||||||  |||||||||
Db         17 TCCAGAAATGGCAGCAA 1


RESULT 197
AX264483/c
LOCUS       AX264483                 17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 1874 from Patent WO0173002.
ACCESSION   AX264483
VERSION     AX264483.1  GI:16513282
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 1874 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
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     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      4 c      4 g      7 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        600 CAGCCTGAAGCCTGACA 616
              |||| ||||| ||||||
Db         17 CAGCATGAAGACTGACA 1


RESULT 198
AX264484
LOCUS       AX264484                 17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 1875 from Patent WO0173002.
ACCESSION   AX264484
VERSION     AX264484.1  GI:16513283
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 1875 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        7 a      4 c      4 g      2 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        600 CAGCCTGAAGCCTGACA 616
              |||| ||||| ||||||
Db          1 CAGCATGAAGACTGACA 17


RESULT 199
AX272822/c
LOCUS       AX272822                 17 bp    mRNA    linear   PAT 29-OCT-2001
DEFINITION  Sequence 391 from Patent WO0162911.
ACCESSION   AX272822
VERSION     AX272822.1  GI:16545559
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
            Ellis,J.H.
  TITLE     Method and reagent for the inhibition of grid
  JOURNAL   Patent: WO 0162911-A 391 30-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      8 c      4 g      1 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        295 ATGTCTGCTGTGGGGGC 311
              ||  ||||||||||||||
Db         17 ATCGCTGCTGTGGGGGC 1


RESULT 200
AX422669
LOCUS       AX422669                 17 bp    mRNA    linear   PAT 18-JUN-2002
DEFINITION  Sequence 1005 from Patent WO0188124.
ACCESSION   AX422669
VERSION     AX422669.1  GI:21526051
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 1005 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      6 c      4 g      3 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        713 CTGTGGCCCAGCAGCAG 729
              |||||||||| || |||
Db          1 CTGTGGCCCATCAACAG 17


RESULT 201
AX423330/c
LOCUS       AX423330                 17 bp    mRNA    linear   PAT 18-JUN-2002
DEFINITION  Sequence 1666 from Patent WO0188124.
ACCESSION   AX423330
VERSION     AX423330.1  GI:21526712
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 1666 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        7 a      1 c      6 g      3 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         46 TCTTAGCATACTCCTCA 62
              | ||||||| |||||||
Db         17 TTTTAGCATCCTCCTCA 1
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RESULT 202
AX423645/c
LOCUS       AX423645                  17 bp    mRNA    linear   PAT 18-JUN-2002
DEFINITION  Sequence 1981 from Patent WO0188124.
ACCESSION   AX423645
VERSION     AX423645.1  GI:21527027
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 1981 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        7 a      1 c      6 g      3 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         48 TTAGCATACTCCTCAAT 64
              ||||||| ||||||| |
Db         17 TTAGCATCCTCCTCATT 1


RESULT 203
AX475190/c
LOCUS       AX475190                  17 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 411 from Patent WO0224750.
ACCESSION   AX475190
VERSION     AX475190.1  GI:22214475
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     Human kidney tumor overexpressed membrane protein 1
  JOURNAL   Patent: WO 0224750-A 411 28-MAR-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      9 c      5 g      1 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1248 GGCCATGTGAGGCCAGG 1264
              |||| |||| |||||||
Db         17 GGCCCTGTGGGGCCAGG 1


RESULT 204
AX531751/c
LOCUS       AX531751                  17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 1260 from Patent EP1239051.
ACCESSION   AX531751
VERSION     AX531751.1  GI:25255281
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 1260 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      7 c      3 g      4 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        267 CTGGCTGATCAAAGAGG 283
              |||| |||||| |||||
Db         17 CTGGGTGATCACAGAGG 1


RESULT 205
AX531752/c
LOCUS       AX531752                  17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 1261 from Patent EP1239051.
ACCESSION   AX531752
VERSION     AX531752.1  GI:25255283
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 1261 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      7 c      3 g      4 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        266 GCTGGCTGATCAAAGAG 282
              ||||| |||||| ||||
Db         17 GCTGGGTGATCACAGAG 1


RESULT 206
AX531753/c
LOCUS       AX531753                  17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 1262 from Patent EP1239051.
ACCESSION   AX531753
VERSION     AX531753.1  GI:25255285
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 1262 11-SEP-2002;
            Aeomica, Inc. (US)
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FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT         3 a      7 c      3 g      4 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        265 GGCTGGCTGATCAAAGA 281
              |||||| |||||| |||
Db         17 GGCTGGGTGATCACAGA 1


RESULT 207
AX531754/c
LOCUS       AX531754                  17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 1263 from Patent EP1239051.
ACCESSION   AX531754
VERSION     AX531754.1  GI:25255287
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 1263 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT         3 a      8 c      3 g      3 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        264 GGGCTGGCTGATCAAAG 280
              ||||||| |||||| ||
Db         17 GGGCTGGGTGATCACAG 1


RESULT 208
AX531755/c
LOCUS       AX531755                  17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 1264 from Patent EP1239051.
ACCESSION   AX531755
VERSION     AX531755.1  GI:25255289
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 1264 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT         4 a      7 c      3 g      3 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        263 TGGGCTGGCTGATCAAA 279
              ||||||| |||||| |
Db         17 TGGGCTGGGTGATCACA 1


RESULT 209
AX531757/c
LOCUS       AX531757                  17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 1266 from Patent EP1239051.
ACCESSION   AX531757
VERSION     AX531757.1  GI:25255293
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 1266 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT         4 a      7 c      3 g      3 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        261 CCTGGGCTGGCTGATCA 277
              | |||||||| ||||||
Db         17 CATGGGCTGGGTGATCA 1


RESULT 210
AX579223
LOCUS       AX579223                  17 bp    mRNA    linear   PAT 10-JAN-2003
DEFINITION  Sequence 1061 from Patent WO0211674.
ACCESSION   AX579223
VERSION     AX579223.1  GI:27648425
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
            and Grupe,A.
  TITLE     Method and reagent for the inhibition of calcium activated chloride
            channel-1 (clca-1)
  JOURNAL   Patent: WO 0211674-A 1061 14-FEB-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
            Thompson, James (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT         6 a      6 c      3 g      2 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        644 GCATCCCCCAAGACCTG 660
              | |||| ||||||||||
Db          1 GAATCCACCAAGACCTG 17
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RESULT 211
AX579976/c
LOCUS       AX579976                  17 bp    mRNA    linear   PAT 10-JAN-2003
DEFINITION  Sequence 1814 from Patent WO0211674.
ACCESSION   AX579976
VERSION     AX579976.1  GI:27649178
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
            and Grupe,A.
  TITLE     Method and reagent for the inhibition of calcium activated chloride
            channel-1 (clca-1)
  JOURNAL   Patent: WO 0211674-A 1814 14-FEB-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
            Thompson, James (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      7 c      3 g      2 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        661 GTCGGGGACTTGGCCAG 677
              ||||| || ||||||||
Db         17 GTCGGTGATTTGGCCAG 1


RESULT 212
AX671569
LOCUS       AX671569                  17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 14 from Patent WO03004526.
ACCESSION   AX671569
VERSION     AX671569.1  GI:29329917
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 14 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        9 a      3 c      4 g      1 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        273 GATCAAAGAGGAAGCAG 289
              ||||||| || ||||||
Db          1 GATCAAAAAGCAAGCAG 17


RESULT 213
AX671632
LOCUS       AX671632                  17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 77 from Patent WO03004526.
ACCESSION   AX671632
VERSION     AX671632.1  GI:29329980
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 77 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        8 a      1 c      6 g      2 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        273 GATCAAAGAGGAAGCAG 289
              ||||||| ||||| ||
Db          1 GATCAAAGTGGAAGAAG 17


RESULT 214
AX687555/c
LOCUS       AX687555                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 287 from Patent EP1281758.
ACCESSION   AX687555
VERSION     AX687555.1  GI:29410251
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 287 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      6 c      7 g      1 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        370 GGGGCCCAGCTTCCTCC 386
              |||| |||||| |||||
Db         17 GGGGTCCAGCTGCCTCC 1


RESULT 215
AX690655/c
LOCUS       AX690655                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 3387 from Patent EP1281758.
ACCESSION   AX690655
VERSION     AX690655.1  GI:29413536
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 3387 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      3 c      8 g      4 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        627 CCAGCTCCAGGAGCTCT 643
              ||||| |||| ||||||
Db         17 CCAGCACCAGCAGCTCT 1


RESULT 216
AX692662/c
LOCUS       AX692662                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5394 from Patent EP1281758.
ACCESSION   AX692662
VERSION     AX692662.1  GI:29415620
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5394 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      9 c      2 g      1 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        761 GGTGGCGGGTGGATGTA 777
              |||||||||||  ||||
Db         17 GGTGGCGGGTGCTTGTA 1


RESULT 217
AX729329
LOCUS       AX729329                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 963 from Patent WO03025175.
ACCESSION   AX729329
VERSION     AX729329.1  GI:30508672
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 963 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      10 c      1 g      4 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1199 GACCTTCACACCTCCCC 1215
              || |||| |||||||||
Db          1 GATCTTCCCACCTCCCC 17


RESULT 218
AX729717
LOCUS       AX729717                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 1351 from Patent WO03025175.
ACCESSION   AX729717
VERSION     AX729717.1  GI:30509060
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 1351 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        9 a      3 c      4 g      1 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        273 GATCAAAGAGGAAGCAG 289
              ||||||| || ||||||
Db          1 GATCAAAAAGCAAGCAG 17


RESULT 219
BD000130/c
LOCUS       BD000130                  17 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Detection of nucleic acid in cell by thermophilic strand
            substitutive  amplification.
ACCESSION   BD000130
VERSION     BD000130.1  GI:18623209
KEYWORDS    JP 2000300281-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Romains,K.L., Osutoreroba,N.V., Clive,M.V. and Lead,R.A.
  TITLE     Detection of nucleic acid in cell by thermophilic strand
            substitutive amplification
  JOURNAL   Patent: JP 2000300281-A 4 31-OCT-2000;
            BECTON DICKINSON & CO
COMMENT     OS   Artificial Sequence
            PN   JP 2000300281-A/4
            PD   31-OCT-2000
            PF   03-APR-2000 JP 2000101133
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            PR   21-SEP-1995 US    08/531747,21-SEP-1995 US    08/531749 PI
            KENTON L ROMAINS,NATARI V OSUTOREROBA,MARK VAN CLIVE, PI   ROBERT
            ALAN LEAD
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        3 a      5 c      3 g      6 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGC 290
              ||||| |||||||| ||
Db         17 ATCAATGAGGAAGCTGC 1


RESULT 220
BD067177/c
LOCUS       BD067177                 17 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors.
ACCESSION   BD067177
VERSION     BD067177.1  GI:22612780
KEYWORDS    JP 2001511003-A/17.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Akhtar,S., Fell,P. and Mcswiggen,J.A.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors
  JOURNAL   Patent: JP 2001511003-A 17 07-AUG-2001;
            RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT     OS   Unidentified
            PN   JP 2001511003-A/17
            PD   07-AUG-2001
            PF   14-JAN-1998 JP 1998532913
            PR   31-JAN-1997 US    60/036476,04-DEC-1997 US    08/985162 PI
            SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
            C12N9/00,C07K14/71
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                 related to
            CC   levels of epidermal growth factor receptors
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      7 c      6 g      3 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        629 AGCTCCAGGAGCTCTGC 645
              ||| |||||||| ||||
Db         17 AGCGCCAGGAGCGCTGC 1


RESULT 221
BD067805/c
LOCUS       BD067805                 17 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors.
ACCESSION   BD067805
VERSION     BD067805.1  GI:22613408
KEYWORDS    JP 2001511003-A/645.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Akhtar,S., Fell,P. and Mcswiggen,J.A.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors
  JOURNAL   Patent: JP 2001511003-A 645 07-AUG-2001;
            RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT     OS   Unidentified
            PN   JP 2001511003-A/645
            PD   07-AUG-2001
            PF   14-JAN-1998 JP 1998532913
            PR   31-JAN-1997 US    60/036476,04-DEC-1997 US    08/985162 PI
            SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
            C12N9/00,C07K14/71
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                 related to
            CC   levels of epidermal growth factor receptors
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"
BASE COUNT        4 a      4 c      2 g      7 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        916 CTAAAGGAGATGGCAGA 932
              |||||||||||  ||||
Db         17 CTAAAGGAGATTTCAGA 1


RESULT 222
E35686/c
LOCUS       E35686                   17 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Detection assay with the use of fluorescence and kit therefor.
ACCESSION   E35686
VERSION     E35686.1  GI:13019158
KEYWORDS    JP 1999225799-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Michael,C.L. and Gren,P.V.
  TITLE     Detection assay with the use of fluorescence and kit therefor
  JOURNAL   Patent: JP 1999225799-A 2 24-AUG-1999;
            BECTON DICKINSON & CO
COMMENT     OS   Artificial Sequence
            PN   JP 1999225799-A/2
            PD   24-AUG-1999
            PF   04-NOV-1998 JP 1998312790
            PR   04-NOV-1997 US    08/964020
            PI   MICHAEL C LITTLE,GREN P VONG
            PC   C12Q1/68,G01N21/78,G01N33/50//C12N15/09,C12N15/00 CC
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
```

```
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        3 a      5 c      3 g      6 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGC 290
              ||||| |||||||| ||
Db         17 ATCAATGAGGAAGCTGC 1


RESULT 223
I43322/c
LOCUS       I43322                   17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 4 from patent US 5631147.
ACCESSION   I43322
VERSION     I43322.1  GI:2468566
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Lohman,K.L., Ostrerova,N.V., Cleve,M.V. and Reid,R.A.
  TITLE     Detection of nucleic acids in cells by thermophilic strand
            displacement amplification
  JOURNAL   Patent: US 5631147-A 4 20-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        3 a      5 c      3 g      6 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGC 290
              ||||| |||||||| ||
Db         17 ATCAATGAGGAAGCTGC 1


RESULT 224
I54288
LOCUS       I54288                   17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 2029 from patent US 5646042.
ACCESSION   I54288
VERSION     I54288.1  GI:2475491
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 2029 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        6 a      0 c      3 g      8 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1094 TTGAACGTAATTATGTA 1110
              ||||| || ||||||||
Db          1 TTGAAAGTTATTATGTA 17


RESULT 225
I95825/c
LOCUS       I95825                   17 bp    DNA     linear   PAT 01-DEC-1998
DEFINITION  Sequence 4 from patent US 5733752.
ACCESSION   I95825
VERSION     I95825.1  GI:3940295
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Lohman,K.L., Ostrerova,N.V., Cleve,M.Van. and Reid,R.Alan.
  TITLE     Detection of nucleic acids in cells by thermophilic strand
            displacement amplification
  JOURNAL   Patent: US 5733752-A 4 31-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        3 a      5 c      3 g      6 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGC 290
              ||||| |||||||| ||
Db         17 ATCAATGAGGAAGCTGC 1


RESULT 226
A40561
LOCUS       A40561                   18 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 98 from Patent WO9425578.
ACCESSION   A40561
VERSION     A40561.1  GI:2296596
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   .
  TITLE     ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
            EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
  JOURNAL   Patent: WO 9425578-A 98 10-NOV-1994;
            BIOGNOSTIK GES (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        7 a      2 c      5 g      4 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1018 AGATGGTGCCAAAGTGC 1034
              ||||||| | |||||||
Db          2 AGATGGTACAAAAGTGC 18


RESULT 227
A89086
LOCUS       A89086                   18 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 1234 from Patent WO9833904.
ACCESSION   A89086
VERSION     A89086.1  GI:6737656
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
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  JOURNAL   Patent: WO 9833904-A 1234 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        7 a      2 c      5 g      4 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1018 AGATGGTGCCAAAGTGC 1034
              ||||||| | |||||||
Db          2 AGATGGTACAAAAGTGC 18


RESULT 228
AR070882/c
LOCUS       AR070882                 18 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 33 from patent US 5908839.
ACCESSION   AR070882
VERSION     AR070882.1  GI:7221770
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Levitt,R.Clifford. and Nicolaides,N.C.
  TITLE     Asthma associated factors as targets for treating atopic allergies
            including asthma and related disorders
  JOURNAL   Patent: US 5908839-A 33 01-JUN-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        2 a     11 c      2 g      3 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        464 GCAGCCTGCAGGGGGAG 480
              | || ||||||||||||
Db         17 GTAGGCTGCAGGGGGAG 1


RESULT 229
AR134123/c
LOCUS       AR134123                 18 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 2548 from patent US 6194150.
ACCESSION   AR134123
VERSION     AR134123.1  GI:14123028
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
  TITLE     Nucleic acid based inhibition of CD40
  JOURNAL   Patent: US 6194150-A 2548 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        2 a      6 c      2 g      8 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1157 GGAAGTAAAGCAGCTAA 1173
              ||||| ||||||| |||
Db         18 GGAAGCAAAGCAGGTAA 2


RESULT 230
AR196118
LOCUS       AR196118                 18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 583 from patent US 6350934.
ACCESSION   AR196118
VERSION     AR196118.1  GI:20245555
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
            Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
  TITLE     Nucleic acid encoding delta-9 desaturase
  JOURNAL   Patent: US 6350934-A 583 26-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        2 a      6 c      6 g      4 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        890 AGCTGCGGTACAGCGTG 906
              ||||||||| |||| ||
Db          1 AGCTGCGGTTCAGCCTG 17


RESULT 231
AR232841
LOCUS       AR232841                 18 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 98 from patent US 6455689.
ACCESSION   AR232841
VERSION     AR232841.1  GI:27275179
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
            Schlingensiepen,R. and Bogdahn,U.
  TITLE     Antisense-oligonucleotides for transforming growth factor-.beta.
            (TGF-.beta.)
  JOURNAL   Patent: US 6455689-A 98 24-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        7 a      2 c      5 g      4 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1018 AGATGGTGCCAAAGTGC 1034
              ||||||| | |||||||
Db          2 AGATGGTACAAAAGTGC 18


RESULT 232
AR233564
LOCUS       AR233564                 18 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 193 from patent US 6458532.
ACCESSION   AR233564
VERSION     AR233564.1  GI:27276155
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Detera-Wadleigh,S.D., Yoshikawa,T., Sanders,A.R. and Esterling,L.E.
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  TITLE     Polynucleotides encoding IMP.18p myo-inositol monophosphatase and
            methods of detecting said polynucleotides
  JOURNAL   Patent: US 6458532-A 193 01-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        2 a      4 c      4 g      8 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1319 GTGCTTTTGTAGATCTT 1335
              ||||||  |||||  ||||
Db          2 GTGCTTCTGTAGCTCTT 18


RESULT 233
AR292992
LOCUS       AR292992                 18 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4727 from patent US 6537751.
ACCESSION   AR292992
VERSION     AR292992.1  GI:31680276
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 4727 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        4 a      0 c      8 g      6 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        935 TGGAGAAGAGGTGTGAG 951
              ||||||||||| || |
Db          2 TGGAGAAGAGGTTTGTG 18


RESULT 234
AX030136
LOCUS       AX030136                 18 bp    DNA     linear   PAT 16-SEP-2000
DEFINITION  Sequence 98 from Patent EP1008649.
ACCESSION   AX030136
VERSION     AX030136.1  GI:10190353
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
            and Schlingensiepen,R.
  TITLE     Antisense-oligonucleotides for the treatment of immuno-suppressive
            effects of transforming growth factor-b2(tgf-b2)
  JOURNAL   Patent: EP 1008649-A 98 14-JUN-2000;
            BIOGNOSTIK GES (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        7 a      2 c      5 g      4 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1018 AGATGGTGCCAAAGTGC 1034
              |||||||  | |||||||
Db          2 AGATGGTACAAAAGTGC 18


RESULT 235
AX092632
LOCUS       AX092632                 18 bp    DNA     linear   PAT 21-MAR-2001
DEFINITION  Sequence 44 from Patent WO0115676.
ACCESSION   AX092632
VERSION     AX092632.1  GI:13444689
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M.
  TITLE     Compositions and methods for modulating hdl cholesterol and
            triglyceride levels
  JOURNAL   Patent: WO 0115676-A 44 08-MAR-2001;
            University of British Columbia (CA) ; Xenon Genetics Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      5 c      7 g      3 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        498 GCAGCGTCTTGGGGTCA 514
              |||| ||| ||||||||
Db          2 GCAGAGTCCTGGGGTCA 18


RESULT 236
AX100693/c
LOCUS       AX100693                 18 bp    DNA     linear   PAT 10-APR-2001
DEFINITION  Sequence 96 from Patent WO0121647.
ACCESSION   AX100693
VERSION     AX100693.1  GI:13619641
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Yen,F., Erickson,M.R., Fruebis,J. and Bihain,B.
  TITLE     Methods of screening for compounds that modulate the lsr-leptin
            interaction and their use in the prevention and treatment of
            obesity-related diseases
  JOURNAL   Patent: WO 0121647-A 96 29-MAR-2001;
            GENSET (FR)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide Zinc finger nuclotides of SEQID1"
BASE COUNT        1 a      4 c     12 g      1 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        192 CGCCCACCCGGACGCCG 208
              | |||||||||  |||||
Db         18 CTCCCACCCGGCCGCCG 2
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RESULT 237
AX250346/c
LOCUS       AX250346                  18 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 14 from Patent WO0168682.
ACCESSION   AX250346
VERSION     AX250346.1  GI:15984113
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Reinl,S.J. and Turpen,T.H.
  TITLE     Self antigen vaccines for treating b cell lymphomas and other
            cancers
  JOURNAL   Patent: WO 0168682-A 14 20-SEP-2001;
            Large Scale Biology Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
                     /note="primer"
BASE COUNT        4 a      7 c      5 g      2 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        262 CTGGGCTGGCTGATCAA 278
              ||||||||  ||| ||||
Db         18 CTGGGCTGCCTGGTCAA 2


RESULT 238
AX259209/c
LOCUS       AX259209                  18 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 7 from Patent WO0173087.
ACCESSION   AX259209
VERSION     AX259209.1  GI:16508455
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hohn,T., Stavolone,L., de Haan,P.T., Ligon,H.T. and Kononova,M.
  TITLE     Cestrum yellow leaf curling virus promoters
  JOURNAL   Patent: WO 0173087-A 7 04-OCT-2001;
            Syngenta Participations AG (CH)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
BASE COUNT        9 a      5 c      3 g      1 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        446 TGCTGAAGTTTGTGGTC 462
              | ||||  ||||||||||
Db         17 TTCTGATGTTTGTGGTC 1


RESULT 239
AX316457
LOCUS       AX316457                  18 bp    DNA     linear   PAT 14-DEC-2001
DEFINITION  Sequence 98 from Patent EP1160319.
ACCESSION   AX316457
VERSION     AX316457.1  GI:17899630
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
            Schlingensiepen,R. and Bogdahn,U.
  TITLE     Antisense-oligonucleotides for the treatment of immunosuppressive
            effects of transforming growth factor-beta (tgf-beta)
  JOURNAL   Patent: EP 1160319-A 98 05-DEC-2001;
            BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
                     /note="Description of unknown: unknown"
BASE COUNT        7 a      2 c      5 g      4 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1018 AGATGGTGCCAAAGTGC 1034
              ||||||| | |||||||
Db          2 AGATGGTACAAAAGTGC 18


RESULT 240
AX556571/c
LOCUS       AX556571                  18 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 84 from Patent WO02057453.
ACCESSION   AX556571
VERSION     AX556571.1  GI:25899747
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gangolli,E.A., Patturajan,M., Vernet,C.A., Malyankar,U.M.,
            Kekuda,R., Stone,D.J., Anderson,D., Shimkets,R.A., Burgess,C.E.,
            Zerhusen,B.D., Liu,X., Spytek,K.A., Casman,S.J., Boldog,F.L.,
            Smithson,G., Li,L. and Ji,W.
  TITLE     Polypetides and nucleic acids encoding same
  JOURNAL   Patent: WO 02057453-A 84 25-JUL-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="PCR primer"
BASE COUNT        3 a      8 c      5 g      2 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        725 AGCAGGGGGCCTGGCTG 741
              |||| || |||||||||
Db         18 AGCATGGCGCCTGGCTG 2


RESULT 241
AX718774/c
LOCUS       AX718774                  18 bp    DNA     linear   PAT 15-APR-2003
DEFINITION  Sequence 338 from Patent WO02103043.
ACCESSION   AX718774
VERSION     AX718774.1  GI:29891341
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
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  AUTHORS   Beimfohr,C. and Snaidr,J.
  TITLE     Method for the specific fast detection of bacteria which is harmful
            to beer
  JOURNAL   Patent: WO 02103043-A 338 27-DEC-2002;
            Vermicon AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonukleotid"
BASE COUNT        2 a      4 c      5 g      7 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         95 ACCGTACAACCCCGGAG 111
              |||||| |||| |||||
Db         18 ACCGTATAACCACGGAG 2


RESULT 242
BD066599
LOCUS       BD066599                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD066599
VERSION     BD066599.1  GI:22612202
KEYWORDS    JP 2001511000-A/1234.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 1234 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/1234
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unknown'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        7 a      2 c      5 g      4 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1018 AGATGGTGCCAAAGTGC 1034
              ||||||| | |||||||
Db          2 AGATGGTACAAAAGTGC 18


RESULT 243
BOVDIK13/c
LOCUS       BOVDIK13                 19 bp    DNA     linear   MAM 09-FEB-1999
DEFINITION  Bovine gene microsatellite DIK023 sense primer.
ACCESSION   D44514
VERSION     D44514.1  GI:624804
KEYWORDS    microsatellite.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (sites)
  AUTHORS   Watanabe,T., Hirano,T., Nakane,S., Inoue,M., Takeda,H.,
            Mizoshita,K., Ximin,L., Barendse,W. and Sugimoto,Y.
  TITLE     Five bovine polymorphic dinucleotide microsatellite loci (DIK021,
            DIK023, DIK024, DIK026 and DIK028)
  JOURNAL   Anim. Genet. 26 (6), 448-449 (1995)
  MEDLINE   96151441
   PUBMED   8572375
REFERENCE   2  (sites)
  AUTHORS   Hirano,T., Nakane,S., Mizoshita,K., Yamakuchi,H.,
            Inoue-Murayama,M., Watanabe,T., Barendse,W. and Sugimoto,Y.
  TITLE     Characterization of 42 highly polymorphic bovine microsatellite
            markers
  JOURNAL   Anim. Genet. 27 (5), 365-368 (1996)
  MEDLINE   97083737
   PUBMED   8930081
REFERENCE   3  (bases 1 to 19)
  AUTHORS   Inoue,M., Watanabe,T., Hirano,T., Yamakuchi,H., Tsukazawa,H.,
            Watanabe,E., Morita,M. and Sugimoto,Y.
  TITLE     Isolation of microsatellites from Japanese black cattle (Wagyu) and
            their application to individual identification and paternity
            exclusion
  JOURNAL   Unpublished
REFERENCE   4  (bases 1 to 19)
  AUTHORS   Sugimoto,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-DEC-1994) Yoshikazu Sugimoto, Japan Live Stock
            Technology Association, Shirakawa Institute of Animal Genetics;
            Nishigo Odakura, Nishishirakawa, Fukushima 961, Japan
            (E-mail:LDI03222@niftyserve.or.jp, Tel:0248-25-5641,
            Fax:0248-25-5725)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9913"
     misc_feature    <1. .19
                     /note="microsatellite DIK023 PCR sense primer"
BASE COUNT        3 a      9 c      3 g      4 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        716 TGGCCCAGCAGCAGGGG 732
              ||||  ||||||||||
Db         18 TGGCAGAGCAGCAGGGG 2


RESULT 244
AR019564/c
LOCUS       AR019564                 19 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 49 from patent US 5783666.
ACCESSION   AR019564
VERSION     AR019564.1  GI:3974678
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Albertsen,H., Anand,R., Carlson,M., Groden,J., Hedge,P.John.,
            Joslyn,G., Kinzler,K., Markham,A.Fred., Nakamura,Y., Thliveris,A.,
            Vogelstein,B. and White,R.L.
  TITLE     APC (adenomatous polyosis coli) protein
  JOURNAL   Patent: US 5783666-A 49 21-JUL-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        0 a      4 c      8 g      7 t
```

```
  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        100 ACAACCCCGGAGGCGCA 116
              ||||||| |||| ||||
Db         17 ACAACCCAGGAGCCGCA 1


RESULT 245
AR029157/c
LOCUS       AR029157                 19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 33 from patent US 5859221.
ACCESSION   AR029157
VERSION     AR029157.1  GI:5941130
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan. and Kawasaki,A.Mamoru.
  TITLE     2'-modified oligonucleotides
  JOURNAL   Patent: US 5859221-A 33 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT       13 a      4 c      2 g      0 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1141 GCCTTTTTTTCTTTTTG 1157
              || ||||||| ||||||
Db         19 GCGTTTTTTTTTTTTTG 3


RESULT 246
AR036541/c
LOCUS       AR036541                 19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 33 from patent US 5872232.
ACCESSION   AR036541
VERSION     AR036541.1  GI:5953209
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan. and Kawasaki,A.Mamoru.
  TITLE     2'-O-modified oligonucleotides
  JOURNAL   Patent: US 5872232-A 33 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT       13 a      4 c      2 g      0 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1141 GCCTTTTTTTCTTTTTG 1157
              || ||||||| ||||||
Db         19 GCGTTTTTTTTTTTTTG 3


RESULT 247
AR096074/c
LOCUS       AR096074                 19 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 33 from patent US 6005087.
ACCESSION   AR096074
VERSION     AR096074.1  GI:10024545
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan. and Kawasaki,A.Mamoru.
  TITLE     2'-modified oligonucleotides
  JOURNAL   Patent: US 6005087-A 33 21-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT       13 a      4 c      2 g      0 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1141 GCCTTTTTTTCTTTTTG 1157
              || ||||||| ||||||
Db         19 GCGTTTTTTTTTTTTTG 3


RESULT 248
AR109525/c
LOCUS       AR109525                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 49 from patent US 6114124.
ACCESSION   AR109525
VERSION     AR109525.1  GI:12825801
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Albertsen,H., Anand,R., Carlson,M., Groden,J., Hedge,P.John.,
            Joslyn,G., Kinzler,K., Markham,A.Fred., Nakamura,Y., Thliveris,A.,
            Vogelstein,B. and White,R.L.
  TITLE     Detection of APC proteins
  JOURNAL   Patent: US 6114124-A 49 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        0 a      4 c      8 g      7 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        100 ACAACCCCGGAGGCGCA 116
              ||||||| |||| ||||
Db         17 ACAACCCAGGAGCCGCA 1


RESULT 249
AR111930/c
LOCUS       AR111930                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 4 from patent US 6127533.
ACCESSION   AR111930
VERSION     AR111930.1  GI:12828778
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 4 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT       13 a      4 c      2 g      0 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy       1141 GCCTTTTTTTCTTTTTG 1157
              || ||||||| ||||||
Db         19 GCGTTTTTTTTTTTTTG 3


RESULT 250
AR124827/c
LOCUS       AR124827                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 4 from patent US 6172209.
ACCESSION   AR124827
VERSION     AR124827.1  GI:14110188
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 4 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT       13 a      4 c      2 g      0 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1141 GCCTTTTTTTCTTTTTG 1157
              || ||||||| ||||||
Db         19 GCGTTTTTTTTTTTTTG 3


RESULT 251
AR135275/c
LOCUS       AR135275                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 4 from patent US 6194598.
ACCESSION   AR135275
VERSION     AR135275.1  GI:14124180
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 4 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT       13 a      4 c      2 g      0 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1141 GCCTTTTTTTCTTTTTG 1157
              || ||||||| ||||||
Db         19 GCGTTTTTTTTTTTTTG 3


RESULT 252
AR141345/c
LOCUS       AR141345                 19 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 12 from patent US 6146829.
ACCESSION   AR141345
VERSION     AR141345.1  GI:15100861
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan. and Monia,B.P.
  TITLE     Gapped 2' modified oligonucleotides
  JOURNAL   Patent: US 6146829-A 12 14-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT       13 a      4 c      2 g      0 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1141 GCCTTTTTTTCTTTTTG 1157
              || ||||||| ||||||
Db         19 GCGTTTTTTTTTTTTTG 3


RESULT 253
AR148186/c
LOCUS       AR148186                 19 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 32 from patent US 6225063.
ACCESSION   AR148186
VERSION     AR148186.1  GI:15112276
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Khvorova,A. and Yarus,M.
  TITLE     RNA channels in biological membranes
  JOURNAL   Patent: US 6225063-A 32 01-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        2 a      6 c      7 g      4 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        196 CACCCGGACGCCGACGA 212
              ||||||||||||| | ||
Db         17 CACCCGGACGCCTAGGA 1


RESULT 254
AR179524/c
LOCUS       AR179524                 19 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 12 from patent US 6326199.
ACCESSION   AR179524
VERSION     AR179524.1  GI:20221079
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan. and Monia,B.P.
  TITLE     Gapped 2' modified oligonucleotides
  JOURNAL   Patent: US 6326199-A 12 04-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT       13 a      4 c      2 g      0 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1141 GCCTTTTTTTCTTTTTG 1157
              || ||||||| ||||||
Db         19 GCGTTTTTTTTTTTTTG 3


RESULT 255
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```
AR212307/c
LOCUS       AR212307                19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 33 from patent US 6399754.
ACCESSION   AR212307
VERSION     AR212307.1  GI:21515846
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan.
  TITLE     Sugar modified oligonucleotides
  JOURNAL   Patent: US 6399754-A 33 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT       13 a      4 c      2 g      0 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1141 GCCTTTTTTTCTTTTTG 1157
              || ||||||| ||||||
Db         19 GCGTTTTTTTTTTTTTG 3


RESULT 256
AR217038/c
LOCUS       AR217038                19 bp    mRNA    linear   PAT 25-SEP-2002
DEFINITION  Sequence 49 from patent US 6413727.
ACCESSION   AR217038
VERSION     AR217038.1  GI:23316395
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Albertsen,H., Anand,R., Carlson,M., Groden,J., Hedge,P.J.,
            Joslyn,G., Kinzler,K., Markham,A.F., Nakamura,Y., Thliveris,A.,
            Vogelstein,B. and White,R.L.
  TITLE     Diagnosis for mutant APC by immunoassay
  JOURNAL   Patent: US 6413727-A 49 02-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        0 a      4 c      8 g      7 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        100 ACAACCCCGGAGGCGCA 116
              ||||||| |||| ||||
Db         17 ACAACCCAGGAGCCGCA 1


RESULT 257
AR231437/c
LOCUS       AR231437                19 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 29 from patent US 6451991.
ACCESSION   AR231437
VERSION     AR231437.1  GI:27272520
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Martin,P., Altmann,K.-H., Cook,P.D. and Monia,B.P.
  TITLE     Sugar-modified gapped oligonucleotides
  JOURNAL   Patent: US 6451991-A 29 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT       13 a      4 c      2 g      0 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1141 GCCTTTTTTTCTTTTTG 1157
              || ||||||| ||||||
Db         19 GCGTTTTTTTTTTTTTG 3


RESULT 258
AR240864/c
LOCUS       AR240864                19 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 29 from patent US 6468791.
ACCESSION   AR240864
VERSION     AR240864.1  GI:27286065
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Tanzi,R.E., Schellenberg,G.D., Wasco,W., Levy-Lahad,E., Bird,T.D.
            and Galas,D.J.
  TITLE     Chromosone 1 gene and gene products related to Alzheimer's Disease
  JOURNAL   Patent: US 6468791-A 29 22-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        6 a      2 c     10 g      1 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        581 CCCTCCGTCTGCCCCCC 597
              | |||||||||||||| |
Db         17 CTCTCCGTCTGCCCCAC 1


RESULT 259
AR240876/c
LOCUS       AR240876                19 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 43 from patent US 6468791.
ACCESSION   AR240876
VERSION     AR240876.1  GI:27286077
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Tanzi,R.E., Schellenberg,G.D., Wasco,W., Levy-Lahad,E., Bird,T.D.
            and Galas,D.J.
  TITLE     Chromosone 1 gene and gene products related to Alzheimer's Disease
  JOURNAL   Patent: US 6468791-A 43 22-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        6 a      2 c     10 g      1 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        581 CCCTCCGTCTGCCCCCC 597
              | |||||||||||||| |
Db         17 CTCTCCGTCTGCCCCAC 1


RESULT 260
AX004623/c
LOCUS       AX004623                19 bp    DNA     linear   PAT 24-AUG-2000
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DEFINITION  Sequence 6 from Patent WO9915667.
ACCESSION   AX004623
VERSION     AX004623.1  GI:9928065
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Flintham,J.E. and Holdsworth,M.J.
  TITLE     Pre-harvest sprouting
  JOURNAL   Patent: WO 9915667-A 6 01-APR-1999;
            FLINTHAM JOHN ELLIS (GB); HOLDSWORTH MICHAEL JOHN (GB)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT        3 a      4 c     11 g      1 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        800 CTCGCTCCCTGCAGCCG 816
              ||||| |||||| ||||
Db         18 CTCGCACCCTGCTGCCG 2


RESULT 261
AX131128
LOCUS       AX131128                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 2346 from Patent WO0130362.
ACCESSION   AX131128
VERSION     AX131128.1  GI:14137433
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 2346 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /note="Cyclin F ribozyme binding site"
BASE COUNT        3 a      6 c      6 g      4 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        877 GCCAAGTTCCAGGAGCT 893
              ||||  ||||||||||
Db          3 GCCAGCTTCCAGGAGCT 19


RESULT 262
AX201281/c
LOCUS       AX201281                 19 bp    DNA     linear   PAT 29-AUG-2001
DEFINITION  Sequence 106 from Patent WO0142457.
ACCESSION   AX201281
VERSION     AX201281.1  GI:15391055
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Iversen,P.L.
  TITLE     Antisense antibacterial method and composition
  JOURNAL   Patent: WO 0142457-A 106 14-JUN-2001;
            Avi Biopharma, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="antisense oligomer"
BASE COUNT        4 a      5 c      8 g      2 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        685 TTTGGGAGCCAGCGGCC 701
              ||| |||||||||| |||
Db         17 TTTTGGAGCCAGCCGCC 1


RESULT 263
AX643312
LOCUS       AX643312                 19 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 178 from Patent WO02099099.
ACCESSION   AX643312
VERSION     AX643312.1  GI:28550940
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Penger,A., Sprenger,R. and Brinkmann,U.
  TITLE     Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
            and their use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 02099099-A 178 12-DEC-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        3 a      4 c      7 g      5 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        736 TGGCTGCCGCATGTTGC 752
              |||||||||  ||||||
Db          2 TGGCTGCCGAGTGTTGC 18


RESULT 264
AX643315/c
LOCUS       AX643315                 19 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 181 from Patent WO02099099.
ACCESSION   AX643315
VERSION     AX643315.1  GI:28550943
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Penger,A., Sprenger,R. and Brinkmann,U.
  TITLE     Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
            and their use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 02099099-A 181 12-DEC-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT         5 a      7 c      4 g      3 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        736 TGGCTGCCGCATGTTGC 752
              |||||||||  ||||||
Db         18 TGGCTGCCGAGTGTTGC 2


RESULT 265
I55696/c
LOCUS       I55696                   19 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 49 from patent US 5648212.
ACCESSION   I55696
VERSION     I55696.1  GI:2476490
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Albertsen,H., Anand,R., Carlson,M., Groden,J., Hedge,P.John.,
            Joslyn,G., Kinzler,K., Markham,A., Nakamura,Y., Thliveris,A.,
            Vogelstein,B. and White,R.L.
  TITLE     Detection of inherited and somatic mutations of APC gene in
            colorectal cancer of humans
  JOURNAL   Patent: US 5648212-A 49 15-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT         0 a      4 c      8 g      7 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        100 ACAACCCCGGAGGCGCA 116
              ||||||| |||| ||||
Db         17 ACAACCCAGGAGCCGCA 1


RESULT 266
I76473/c
LOCUS       I76473                   19 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 49 from patent US 5691454.
ACCESSION   I76473
VERSION     I76473.1  GI:3012627
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Albertsen,H., Anand,R., Carlson,M., Groden,J., Hedge,P.John.,
            Joslyn,G., Kinzler,K., Markham,A.Fred., Nakamura,Y., Thliveris,A.,
            Vogelstein,B. and White,R.L.
  TITLE     APC antibodies
  JOURNAL   Patent: US 5691454-A 49 25-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT         0 a      4 c      8 g      7 t

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 2.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        100 ACAACCCCGGAGGCGCA 116
              ||||||| |||| ||||
Db         17 ACAACCCAGGAGCCGCA 1


RESULT 267
AR224969
LOCUS       AR224969                 21 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 76 from patent US 6441149.
ACCESSION   AR224969
VERSION     AR224969.1  GI:23334086
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Herrnstadt,C., Ghosh,S.S., Clevenger,W., Fahy,E.D. and Davis,R.E.
  TITLE     Diagnostic method based on quantification of extramitochondrial DNA
  JOURNAL   Patent: US 6441149-A 76 27-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
BASE COUNT         5 a      2 c      8 g      6 t

  Query Match             1.0%;  Score 13.6;  DB 1;  Length 21;
  Best Local Similarity   80.0%;  Pred. No. 2.9e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        268 TGGCTGATCAAAGAGGAAGC 287
              ||||||||  ||||| | ||
Db          2 TGGCTGATTGAAGAGTATGC 21


RESULT 268
AX039751
LOCUS       AX039751                 21 bp    DNA     linear   PAT 18-NOV-2000
DEFINITION  Sequence 140 from Patent WO0063441.
ACCESSION   AX039751
VERSION     AX039751.1  GI:11229780
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Herrnstadt,C. and Davis,R.E.
  TITLE     Single nucleotide polymorphisms in mitochondrial genes that segreg
            ate with alzheimer's disease
  JOURNAL   Patent: WO 0063441-A 140 26-OCT-2000;
            MITOKOR (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="PCR primer"
BASE COUNT         5 a      2 c      8 g      6 t

  Query Match             1.0%;  Score 13.6;  DB 1;  Length 21;
  Best Local Similarity   80.0%;  Pred. No. 2.9e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        268 TGGCTGATCAAAGAGGAAGC 287
              ||||||||  ||||| | ||
Db          2 TGGCTGATTGAAGAGTATGC 21


RESULT 269
A02494
LOCUS       A02494                   15 bp    DNA     linear   PAT 21-MAY-1993
DEFINITION  Nucleotide sequence 2 from patent number EP0241210.
ACCESSION   A02494
VERSION     A02494.1  GI:410896
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
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  AUTHORS   .
  TITLE     Modified enzyme
  JOURNAL   Patent: EP 0241210-A 2 14-OCT-1987;
            BEECHAM GROUP PLC
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      5 c      5 g      4 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.7e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        903 CGTGGCCCTGGTCCT 917
              ||||||||||||  ||
Db          1 CGTGGCCCTGGTACT 15


RESULT 270
A10674/c
LOCUS       A10674                    15 bp    DNA     linear   PAT 02-DEC-1993
DEFINITION  Oligonucleotide (I5).
ACCESSION   A10674
VERSION     A10674.1  GI:490800
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Ueda,I., Niwa,M., Saito,Y., Sato,S., Ono,H. and Kitaguchi,T.
  TITLE     Process for production of gamma-interferon
  JOURNAL   Patent: EP 0176916-A 59 09-APR-1986;
            FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        1 a      4 c      3 g      7 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.7e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1165 AGCAGCTAAAACATG 1179
              |||||||||||||  |
Db         15 AGCAGCTAAAACAGG 1


RESULT 271
AX139176
LOCUS       AX139176                  15 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 24 from Patent EP1076099.
ACCESSION   AX139176
VERSION     AX139176.1  GI:14274849
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
            tuberculosis complex.
REFERENCE   1
  AUTHORS   Suzuki,Y., Nishida,M. and Takenishi,S.
  TITLE     Kit for diagnosis of tubercle bacilli
  JOURNAL   Patent: EP 1076099-A 24 14-FEB-2001;
            NISSHINBO INDUSTRIES, INC. (JP) ; System Research Incorporation
            (JP)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Mycobacterium tuberculosis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:1773"
                     /note="capture"
BASE COUNT        3 a      5 c      5 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.7e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        885 CCAGGAGCTGCGGTA 899
              ||||  ||||||||||
Db          1 CCAGCAGCTGCGGTA 15


RESULT 272
BD013460
LOCUS       BD013460                  15 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Diagnosis kit of tubercle bacillus.
ACCESSION   BD013460
VERSION     BD013460.1  GI:22553774
KEYWORDS    JP 2001103981-A/24.
SOURCE      Mycobacterium tuberculosis
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
            tuberculosis complex.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Suzuki,S., Nishida,M. and Takenishi,S.
  TITLE     Diagnosis kit of tubercle bacillus
  JOURNAL   Patent: JP 2001103981-A 24 17-APR-2001;
            NISSHINBO IND INC,SYSTEM RESEARCH CO LTD
COMMENT     OS   Mycobacterium tuberculosis
            PN   JP 2001103981-A/24
            PD   17-APR-2001
            PF   26-JUL-2000 JP 2000225985
            PI   SADAHIKO SUZUKI,MICHIO NISHIDA,SOICHIRO TAKENISHI PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68//(C12Q1/68,C12R1:32), PC
            (C12Q1/68,C12R1:325),(C12Q1/68,C12R1:33),C12N15/00,C12N15/00 CC
            capture
            FH   Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Mycobacterium tuberculosis'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Mycobacterium tuberculosis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:1773"
BASE COUNT        3 a      5 c      5 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.7e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        885 CCAGGAGCTGCGGTA 899
              ||||  ||||||||||
Db          1 CCAGCAGCTGCGGTA 15


RESULT 273
AR252725
LOCUS       AR252725                  17 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 493 from patent US 6478825.
ACCESSION   AR252725
VERSION     AR252725.1  GI:27300633
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
  TITLE     Implant, method of making same and use of the implant for the
            treatment of bone defects
  JOURNAL   Patent: US 6478825-A 493 12-NOV-2002;
FEATURES             Location/Qualifiers
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     source          1. .17
                     /organism="unknown"
BASE COUNT        1 a      4 c      7 g      5 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        494 GTGTGCAGCGTCTTG 508
              ||| ||||||||||||
Db          1 GTGGGCAGCGTCTTG 15


RESULT 274
AX201501
LOCUS       AX201501                 17 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 180 from Patent WO0153486.
ACCESSION   AX201501
VERSION     AX201501.1  GI:15391332
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
            Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Smith,V.,
            Stone,D.M., Watanabe,C.K. and Wood,W.I.
  TITLE     Compositions and methods for the treatment of tumour
  JOURNAL   Patent: WO 0153486-A 180 26-JUL-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Oligonucleotide Probe."
BASE COUNT        1 a      4 c      7 g      5 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        494 GTGTGCAGCGTCTTG 508
              ||| ||||||||||||
Db          1 GTGGGCAGCGTCTTG 15


RESULT 275
AX262644
LOCUS       AX262644                 17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 35 from Patent WO0173002.
ACCESSION   AX262644
VERSION     AX262644.1  GI:16511443
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 35 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      3 c      8 g      3 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        888 GGAGCTGCGGTACAG 902
              |||| ||||||||||
Db          1 GGAGGTGCGGTACAG 15


RESULT 276
AX262645/c
LOCUS       AX262645                 17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 36 from Patent WO0173002.
ACCESSION   AX262645
VERSION     AX262645.1  GI:16511444
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 36 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      8 c      3 g      3 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        888 GGAGCTGCGGTACAG 902
              |||| ||||||||||
Db         17 GGAGGTGCGGTACAG 3


RESULT 277
AX262648
LOCUS       AX262648                 17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 39 from Patent WO0173002.
ACCESSION   AX262648
VERSION     AX262648.1  GI:16511447
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 39 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      3 c      8 g      3 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        888 GGAGCTGCGGTACAG 902
              |||| ||||||||||
Db          1 GGAGGTGCGGTACAG 15
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RESULT 278
AX262649/c
LOCUS       AX262649                 17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 40 from Patent WO0173002.
ACCESSION   AX262649
VERSION     AX262649.1  GI:16511448
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 40 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      8 c      3 g      3 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        888 GGAGCTGCGGTACAG 902
              |||| ||||||||||
Db         17 GGAGGTGCGGTACAG 3


RESULT 279
AX262652
LOCUS       AX262652                 17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 43 from Patent WO0173002.
ACCESSION   AX262652
VERSION     AX262652.1  GI:16511451
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 43 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      2 c      8 g      4 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        888 GGAGCTGCGGTACAG 902
              |||| ||||||||||
Db          2 GGAGGTGCGGTACAG 16


RESULT 280
AX262653/c
LOCUS       AX262653                 17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 44 from Patent WO0173002.
ACCESSION   AX262653
VERSION     AX262653.1  GI:16511452
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 44 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      8 c      2 g      3 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        888 GGAGCTGCGGTACAG 902
              |||| ||||||||||
Db         16 GGAGGTGCGGTACAG 2


RESULT 281
AX266427/c
LOCUS       AX266427                 17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 3818 from Patent WO0173002.
ACCESSION   AX266427
VERSION     AX266427.1  GI:16515226
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 3818 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        6 a      4 c      4 g      3 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        745 CATGTTGCTGACTTT 759
              |||||||| ||||||
Db         15 CATGTTGCAGACTTT 1


RESULT 282
AX266428
LOCUS       AX266428                 17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 3819 from Patent WO0173002.
ACCESSION   AX266428
VERSION     AX266428.1  GI:16515227
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
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            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 3819 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      4 c      4 g      6 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        745 CATGTTGCTGACTTT 759
              ||||||| ||||||
Db          3 CATGTTGCAGACTTT 17


RESULT 283
AX403606
LOCUS       AX403606                 17 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 493 from Patent WO0073454.
ACCESSION   AX403606
VERSION     AX403606.1  GI:21437079
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
            Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
            Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,
            Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
            Williams,P., Wood,W.I. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0073454-A 493 07-DEC-2000;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide probe"
BASE COUNT        1 a      4 c      7 g      5 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        494 GTGTGCAGCGTCTTG 508
              ||| ||||||||||||
Db          1 GTGGGCAGCGTCTTG 15


RESULT 284
AX422720
LOCUS       AX422720                 17 bp    mRNA    linear   PAT 18-JUN-2002
DEFINITION  Sequence 1056 from Patent WO0188124.
ACCESSION   AX422720
VERSION     AX422720.1  GI:21526102
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 1056 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        6 a      5 c      2 g      4 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         21 TTAAACCAAACCCAG 35
              ||| ||||||||||||
Db          3 TTATACCAAACCCAG 17


RESULT 285
AX422721
LOCUS       AX422721                 17 bp    mRNA    linear   PAT 18-JUN-2002
DEFINITION  Sequence 1057 from Patent WO0188124.
ACCESSION   AX422721
VERSION     AX422721.1  GI:21526103
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 1057 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        6 a      5 c      2 g      4 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         21 TTAAACCAAACCCAG 35
              ||| ||||||||||||
Db          2 TTATACCAAACCCAG 16


RESULT 286
AX423646/c
LOCUS       AX423646                 17 bp    mRNA    linear   PAT 18-JUN-2002
DEFINITION  Sequence 1982 from Patent WO0188124.
ACCESSION   AX423646
VERSION     AX423646.1  GI:21527028
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 1982 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        7 a      1 c      6 g      3 t
```

```
  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         48 TTAGCATACTCCTCA 62
              ||||||| |||||||
Db         16 TTAGCATCCTCCTCA 2


RESULT 287
AX499076
LOCUS       AX499076                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 383 from Patent EP1229046.
ACCESSION   AX499076
VERSION     AX499076.1  GI:23381369
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 383 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      6 c      7 g      1 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        522 CCTGCCGGAGGAGCA 536
              ||||||||||||| |
Db          3 CCTGCCGGAGGAGGA 17


RESULT 288
AX499077
LOCUS       AX499077                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 384 from Patent EP1229046.
ACCESSION   AX499077
VERSION     AX499077.1  GI:23381370
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 384 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      5 c      7 g      1 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        522 CCTGCCGGAGGAGCA 536
              ||||||||||||| |
Db          2 CCTGCCGGAGGAGGA 16


RESULT 289
AX499078
LOCUS       AX499078                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 385 from Patent EP1229046.
ACCESSION   AX499078
VERSION     AX499078.1  GI:23381371
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 385 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      4 c      7 g      1 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        522 CCTGCCGGAGGAGCA 536
              ||||||||||||| |
Db          1 CCTGCCGGAGGAGGA 15


RESULT 290
AX530985/c
LOCUS       AX530985                  17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 494 from Patent EP1239051.
ACCESSION   AX530985
VERSION     AX530985.1  GI:25253757
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 494 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      4 c      9 g      1 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        631 CTCCAGGAGCTCTGC 645
              |||| ||||||||||
Db         17 CTCCCGGAGCTCTGC 3


RESULT 291
AX530986/c
LOCUS       AX530986                  17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 495 from Patent EP1239051.
ACCESSION   AX530986
VERSION     AX530986.1  GI:25253759
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
```

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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 495 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      4 c      8 g      1 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        631 CTCCAGGAGCTCTGC 645
              |||| ||||||||||
Db         16 CTCCCGGAGCTCTGC 2


RESULT 292
AX530987/c
LOCUS       AX530987                 17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 496 from Patent EP1239051.
ACCESSION   AX530987
VERSION     AX530987.1  GI:25253761
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 496 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      4 c      8 g      1 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        631 CTCCAGGAGCTCTGC 645
              |||| ||||||||||
Db         15 CTCCCGGAGCTCTGC 1


RESULT 293
AX531756/c
LOCUS       AX531756                 17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 1265 from Patent EP1239051.
ACCESSION   AX531756
VERSION     AX531756.1  GI:25255291
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 1265 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      7 c      3 g      3 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        263 TGGGCTGGCTGATCA 277
              |||||||| ||||||
Db         16 TGGGCTGGGTGATCA 2


RESULT 294
AX579224
LOCUS       AX579224                 17 bp    mRNA    linear   PAT 10-JAN-2003
DEFINITION  Sequence 1062 from Patent WO0211674.
ACCESSION   AX579224
VERSION     AX579224.1  GI:27648426
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
            and Grupe,A.
  TITLE     Method and reagent for the inhibition of calcium activated chloride
            channel-1 (clca-1)
  JOURNAL   Patent: WO 0211674-A 1062 14-FEB-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
            Thompson, James (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        7 a      6 c      2 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        646 ATCCCCCAAGACCTG 660
              |||| ||||||||||
Db          2 ATCCACCAAGACCTG 16


RESULT 295
AX648753/c
LOCUS       AX648753                 17 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 593 from Patent EP1273660.
ACCESSION   AX648753
VERSION     AX648753.1  GI:29151571
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y.
  TITLE     Human sodium-hydrogen exchanger like protein 1
  JOURNAL   Patent: EP 1273660-A 593 08-JAN-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      6 c      4 g      4 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
```

```
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        920 AGGAGATGGCAGATC 934
              ||||||||||||| ||
Db         17 AGGAGATGGCAGTTC 3


RESULT 296
AX648754/c
LOCUS       AX648754                 17 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 594 from Patent EP1273660.
ACCESSION   AX648754
VERSION     AX648754.1  GI:29151572
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y.
  TITLE     Human sodium-hydrogen exchanger like protein 1
  JOURNAL   Patent: EP 1273660-A 594 08-JAN-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      6 c      4 g      4 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        920 AGGAGATGGCAGATC 934
              ||||||||||||| ||
Db         16 AGGAGATGGCAGTTC 2


RESULT 297
AX648755/c
LOCUS       AX648755                 17 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 595 from Patent EP1273660.
ACCESSION   AX648755
VERSION     AX648755.1  GI:29151573
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y.
  TITLE     Human sodium-hydrogen exchanger like protein 1
  JOURNAL   Patent: EP 1273660-A 595 08-JAN-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      7 c      3 g      4 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        920 AGGAGATGGCAGATC 934
              ||||||||||||| ||
Db         15 AGGAGATGGCAGTTC 1


RESULT 298
AX693203/c
LOCUS       AX693203                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5935 from Patent EP1281758.
ACCESSION   AX693203
VERSION     AX693203.1  GI:29416167
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5935 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      3 c      9 g      1 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        571 CTCCAGCAGGCCCTC 585
              ||||||| |||||||
Db         17 CTCCAGCTGGCCCTC 3


RESULT 299
AX693204/c
LOCUS       AX693204                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5936 from Patent EP1281758.
ACCESSION   AX693204
VERSION     AX693204.1  GI:29416168
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5936 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      3 c      8 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        571 CTCCAGCAGGCCCTC 585
              ||||||| |||||||
Db         16 CTCCAGCTGGCCCTC 2


RESULT 300
AX693205/c
LOCUS       AX693205                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5937 from Patent EP1281758.
ACCESSION   AX693205
VERSION     AX693205.1  GI:29416169
KEYWORDS    .
SOURCE      Homo sapiens (human)
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5937 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      4 c      8 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        571 CTCCAGCAGGCCCTC 585
              ||||||| |||||||
Db         15 CTCCAGCTGGCCCTC 1


RESULT 301
AX727414/c
LOCUS       AX727414                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 5101 from Patent WO03025176.
ACCESSION   AX727414
VERSION     AX727414.1  GI:30506757
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 5101 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
BASE COUNT       11 a      2 c      2 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1145 TTTTTTCTTTTTGGA 1159
              |||| ||||||||||
Db         17 TTTTATCTTTTTGGA 3


RESULT 302
AX733233
LOCUS       AX733233                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 4867 from Patent WO03025175.
ACCESSION   AX733233
VERSION     AX733233.1  GI:30512576
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 4867 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        8 a      3 c      4 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        273 GATCAAAGAGGAAGC 287
              ||||||||||  ||||
Db          1 GATCAAAGAGTAAGC 15


RESULT 303
AX733988/c
LOCUS       AX733988                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 5622 from Patent WO03025175.
ACCESSION   AX733988
VERSION     AX733988.1  GI:30513331
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 5622 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a     10 c      3 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        760 CGGTGGCGGGTGGAT 774
              ||| ||||||||||
Db         16 CGGAGGCGGGTGGAT 2


RESULT 304
AX735372/c
LOCUS       AX735372                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 962 from Patent WO03025177.
ACCESSION   AX735372
VERSION     AX735372.1  GI:30514649
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 962 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
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     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      9 c      3 g      1 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        760 CGGTGGCGGGTGGAT 774
              | ||||||||||||||
Db         16 CTGTGGCGGGTGGAT 2


RESULT 305
AX736910/c
LOCUS       AX736910                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 2500 from Patent WO03025177.
ACCESSION   AX736910
VERSION     AX736910.1  GI:30516198
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 2500 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a     10 c      3 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        760 CGGTGGCGGGTGGAT 774
              ||| ||||||||||||
Db         16 CGGAGGCGGGTGGAT 2


RESULT 306
A26386/c
LOCUS       A26386                    18 bp    DNA     linear   PAT 07-APR-1995
DEFINITION  probe no.4.
ACCESSION   A26386
VERSION     A26386.1  GI:904943
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   .
  TITLE     ANTIGEN PROCESSING
  JOURNAL   Patent: WO 9211289-A 12 09-JUL-1992;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        3 a      6 c      6 g      3 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        625 GACCAGCTCCAGGAG 639
              | ||||||||||||||
Db         16 GCCCAGCTCCAGGAG 2


RESULT 307
AR087097/c
LOCUS       AR087097                  18 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 47 from patent US 5985664.
ACCESSION   AR087097
VERSION     AR087097.1  GI:10013863
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Baker,B.F. and Cowsert,L.M.
  TITLE     Antisense modulation of Sentrin expression
  JOURNAL   Patent: US 5985664-A 47 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        4 a      5 c      3 g      6 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        440 GAAAGTTGCTGAAGT 454
              ||||||| |||||||
Db         18 GAAAGTTACTGAAGT 4


RESULT 308
AR096634/c
LOCUS       AR096634                  18 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 18 from patent US 6008048.
ACCESSION   AR096634
VERSION     AR096634.1  GI:10025604
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Monia,B.P. and Cowsert,L.M.
  TITLE     Antisense inhibition of EGR-1 expression
  JOURNAL   Patent: US 6008048-A 18 28-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        4 a      8 c      3 g      3 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        348 CAGTGGCCGAGTGAG 362
              |||||||| ||||||
Db         15 CAGTGGCCTAGTGAG 1


RESULT 309
AR106763/c
LOCUS       AR106763                  18 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 11 from patent US 6107091.
ACCESSION   AR106763
VERSION     AR106763.1  GI:12821293
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
```

```
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of G-alpha-16 expression
  JOURNAL   Patent: US 6107091-A 11 22-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        4 a      8 c      2 g      4 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1336 GTGTTTCAGGCAGGG 1350
              ||||||||||||| ||
Db         16 GTGTTTCAGGCAAGG 2


RESULT 310
AR134170
LOCUS       AR134170                 18 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 2595 from patent US 6194150.
ACCESSION   AR134170
VERSION     AR134170.1  GI:14123075
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
  TITLE     Nucleic acid based inhibition of CD40
  JOURNAL   Patent: US 6194150-A 2595 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        3 a      3 c      2 g     10 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1111 GTTTTCTGTTTAATT 1125
              ||||||||| |||||
Db          1 GTTTTCTGTCTAATT 15


RESULT 311
AR160830
LOCUS       AR160830                 18 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 34 from patent US 6255111.
ACCESSION   AR160830
VERSION     AR160830.1  GI:16225621
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Bennett,C.Frank. and Cowsert,L.M.
  TITLE     Antisense modulation of Her-4 expression
  JOURNAL   Patent: US 6255111-A 34 03-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        5 a      6 c      6 g      1 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        552 GGCAGGCATGCACAC 566
              ||||||| ||||||
Db          4 GGCAGGCACGCACAC 18


RESULT 312
AX080166
LOCUS       AX080166                 18 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 4 from Patent WO0107665.
ACCESSION   AX080166
VERSION     AX080166.1  GI:13159647
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Umek,R.M.
  TITLE     Sequence determination of nucleic acids using electronic detection
  JOURNAL   Patent: WO 0107665-A 4 01-FEB-2001;
            Clinical Micro Sensors, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic."
BASE COUNT        3 a      2 c      7 g      6 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCAGTTGAGGTGGAT 21
              |||||||| ||||||
Db          4 GCAGTTGACGTGGAT 18


RESULT 313
AX080169/c
LOCUS       AX080169                 18 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 7 from Patent WO0107665.
ACCESSION   AX080169
VERSION     AX080169.1  GI:13159650
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Umek,R.M.
  TITLE     Sequence determination of nucleic acids using electronic detection
  JOURNAL   Patent: WO 0107665-A 7 01-FEB-2001;
            Clinical Micro Sensors, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic."
BASE COUNT        6 a      7 c      2 g      3 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GCAGTTGAGGTGGAT 21
              |||||||| ||||||
Db         15 GCAGTTGACGTGGAT 1


RESULT 314
AX100688/c
LOCUS       AX100688                 18 bp    DNA     linear   PAT 10-APR-2001
DEFINITION  Sequence 91 from Patent WO0121647.
ACCESSION   AX100688
VERSION     AX100688.1  GI:13619636
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
```

```
            artificial sequences.
REFERENCE   1
  AUTHORS   Yen,F., Erickson,M.R., Fruebis,J. and Bihain,B.
  TITLE     Methods of screening for compounds that modulate the lsr-leptin
            interaction and their use in the prevention and treatment of
            obesity-related diseases
  JOURNAL   Patent: WO 0121647-A 91 29-MAR-2001;
            GENSET (FR)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide Zinc finger nuclotides of SEQID1"
BASE COUNT        2 a      2 c     12 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        186 CCCCGCCGCCCACCC 200
              ||||||||| |||||
Db         18 CCCCGCCGCTCACCC 4


RESULT 315
AX164295
LOCUS       AX164295                  18 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 125 from Patent WO0138564.
ACCESSION   AX164295
VERSION     AX164295.1  GI:14545229
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Rouleau,G.A., Lafreniere,R.G., Rochefort,D., Cossette,P. and
            Ragsdale,D.
  TITLE     Loci for idiopathic generalized epilepsy, mutations thereof and
            method using same to assess, diagnose, prognose or treat epilepsy
  JOURNAL   Patent: WO 0138564-A 125 31-MAY-2001;
            McGill University (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic oligonucleotide"
BASE COUNT        4 a      6 c      6 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1068 CATCAGGCAGGCTCT 1082
              || ||||||||||||
Db          2 CAGCAGGCAGGCTCT 16


RESULT 316
AX427087/c
LOCUS       AX427087                  18 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 51 from Patent WO0196604.
ACCESSION   AX427087
VERSION     AX427087.1  GI:21530470
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bee,G., Kohne,D.E., Korb,L., Peterson,T. and Yguerabide,J.
  TITLE     Assay for genetic polymorphisms using scattered light detectable
            labels
  JOURNAL   Patent: WO 0196604-A 51 20-DEC-2001;
            Genicon Sciences Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Exemplary probe for CYP2D6 allele detection"
BASE COUNT        4 a      3 c      8 g      3 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        562 CACACACTGCTCCAG 576
              ||| ||||||||||||
Db         15 CACCCACTGCTCCAG 1


RESULT 317
AX599642/c
LOCUS       AX599642                  18 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 982 from Patent WO02077272.
ACCESSION   AX599642
VERSION     AX599642.1  GI:28399790
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pelet,C. and Ziebarth,H.
  TITLE     Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
  JOURNAL   Patent: WO 02077272-A 982 03-OCT-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for PITX2"
BASE COUNT        6 a      0 c      7 g      5 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         54 TACTCCTCAATTACC 68
              ||||||||||||| |
Db         17 TACTCCTCAATTAAC 3


RESULT 318
AX710932/c
LOCUS       AX710932                  18 bp    RNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 232 from Patent EP1288296.
ACCESSION   AX710932
VERSION     AX710932.1  GI:29787313
KEYWORDS    .
SOURCE      Human herpesvirus 5
  ORGANISM  Human herpesvirus 5
            Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
            Betaherpesvirinae; Cytomegalovirus.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 232 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
```

```
     source          1. .18
                     /organism="Human herpesvirus 5"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:10359"
BASE COUNT        8 a      4 c      4 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        703 CTCCTTGATTCTGTG 717
              ||||||||||||| ||
Db         15 CTCCTTGATTCTATG 1


RESULT 319
BD001073/c
LOCUS       BD001073                 18 bp    RNA     linear   PAT 31-JAN-2002
DEFINITION  Method and reagent for inhibiting viral replication.
ACCESSION   BD001073
VERSION     BD001073.1  GI:18625632
KEYWORDS    JP 2000342285-A/233.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
            Holesek,J.J. and Mamone,A.J.
  TITLE     Method and reagent for inhibiting viral replication
  JOURNAL   Patent: JP 2000342285-A 233 12-DEC-2000;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000342285-A/233
            PD   12-DEC-2000
            PF   01-MAY-2000 JP 2000132616
            PR   11-MAY-1992 US    07/882689,14-MAY-1992 US    07/882712 PR
            14-MAY-1992 US    07/882713,14-MAY-1992 US    07/882714 PR
            14-MAY-1992 US    07/882823,14-MAY-1992 US    07/882824 PR
            14-MAY-1992 US    07/882886,14-MAY-1992 US    07/882888 PR
            14-MAY-1992 US    07/882889,14-MAY-1992 US    07/882921 PR
            14-MAY-1992 US    07/882922,14-MAY-1992 US    07/883823 PR
            14-MAY-1992 US    07/883849,14-MAY-1992 US    07/884073 PR
            14-MAY-1992 US    07/884074,14-MAY-1992 US    07/884333 PR
            14-MAY-1992 US    07/884422,14-MAY-1992 US    07/884431 PR
            14-MAY-1992 US    07/884436,14-MAY-1992 US    07/884521 PR
            31-JUL-1992 US    07/923738,26-AUG-1992 US    07/935854 PR
            26-AUG-1992 US    07/936086,18-SEP-1992 US    07/948359 PR
            15-OCT-1992 US    07/963322,07-DEC-1992 US    07/987129 PR
            07-DEC-1992 US    07/987130,07-DEC-1992 US    07/987133 PI
            KENNETH G DRAPER,LEC W DADYKTZ,JAMES A MACSWIGEN, PI   DENNIS G
            MAYSEJAK,
            PI   JAMES J HOLESEK,ANTHONY J MAMONE
            PC   C12N15/09,C12N5/10,C12N7/00,C12N9/22//(C12N5/10,C12R1:91), PC
             C12N15/00,
            PC   C12N5/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic RNA"
                      /db_xref="taxon:32630"
BASE COUNT        8 a      4 c      4 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        703 CTCCTTGATTCTGTG 717
              ||||||||||||| ||
Db         15 CTCCTTGATTCTATG 1


RESULT 320
BD001502/c
LOCUS       BD001502                 18 bp    RNA     linear   PAT 31-JAN-2002
DEFINITION  Method and reagent for inhibiting viral replication.
ACCESSION   BD001502
VERSION     BD001502.1  GI:18626061
KEYWORDS    JP 2000342286-A/233.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
            Holesek,J.J. and Mamone,A.J.
  TITLE     Method and reagent for inhibiting viral replication
  JOURNAL   Patent: JP 2000342286-A 233 12-DEC-2000;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000342286-A/233
            PD   12-DEC-2000
            PF   01-MAY-2000 JP 2000132651
            PR   11-MAY-1992 US    07/882689,14-MAY-1992 US    07/882712 PR
            14-MAY-1992 US    07/882713,14-MAY-1992 US    07/882714 PR
            14-MAY-1992 US    07/882823,14-MAY-1992 US    07/882824 PR
            14-MAY-1992 US    07/882886,14-MAY-1992 US    07/882888 PR
            14-MAY-1992 US    07/882889,14-MAY-1992 US    07/882921 PR
            14-MAY-1992 US    07/882922,14-MAY-1992 US    07/883823 PR
            14-MAY-1992 US    07/883849,14-MAY-1992 US    07/884073 PR
            14-MAY-1992 US    07/884074,14-MAY-1992 US    07/884333 PR
            14-MAY-1992 US    07/884422,14-MAY-1992 US    07/884431 PR
            14-MAY-1992 US    07/884436,14-MAY-1992 US    07/884521 PR
            31-JUL-1992 US    07/923738,26-AUG-1992 US    07/935854 PR
            26-AUG-1992 US    07/936086,18-SEP-1992 US    07/948359 PR
            15-OCT-1992 US    07/963322,07-DEC-1992 US    07/987129 PR
            07-DEC-1992 US    07/987130,07-DEC-1992 US    07/987133 PI
            KENNETH G DRAPER,LEC W DADYKTZ,JAMES A MACSWIGEN, PI   DENNIS G
            MAYSEJAK,
            PI   JAMES J HOLESEK,ANTHONY J MAMONE
            PC   C12N15/09,C12N5/10,C12N7/00//A61K38/43,A61K39/125,A61K39/13,
            PC   A61K39/135,
            PC   A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
            PC   A61P1/16,
            PC   A61P31/14,A61P31/16,A61P31/18,A61P31/22,A61P35/02,C12Q1/68, PC
              (C12N15/09,C12R1:93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00, PC
             C12R1:93)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic RNA"
                      /db_xref="taxon:32630"
BASE COUNT        8 a      4 c      4 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        703 CTCCTTGATTCTGTG 717
              ||||||||||||| ||
Db         15 CTCCTTGATTCTATG 1


RESULT 321
E32451
LOCUS       E32451                   18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32451
VERSION     E32451.1  GI:13018687
KEYWORDS    JP 2000037190-A/11.
```

```
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 11 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/11
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES            Location/Qualifiers
     source         1. .18
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"
BASE COUNT       0 a      0 c      3 g     15 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTGG 1158
              ||||||| |||||||
Db          4 TTTTTTTTTTTTTGG 18


RESULT 322
S83625/c
LOCUS       S83625                   18 bp    DNA     linear   PRI 07-MAY-1993
DEFINITION  HuP2=DNA binding protein [human, Genomic Mutant, 18 nt].
ACCESSION   S83625
VERSION     S83625.1  GI:245865
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Baldwin,C.T., Hoth,C.F., Amos,J.A., da-Silva,E.O. and Milunsky,A.
  TITLE     An exonic mutation in the HuP2 paired domain gene causes
            Waardenburg's syndrome
  JOURNAL   Nature 355 (6361), 637-638 (1992)
  MEDLINE   92168114
   PUBMED   1347149
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 83625] from the original journal article.
            This sequence comes from Fig. 3.
FEATURES            Location/Qualifiers
     source         1. .18
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
     gene           1. .18
                    /partial
                    /gene="HuP2"
                    /note="DNA binding protein"
     CDS            1. .18
                    /partial
                    /gene="HuP2"
                    /note="DNA binding protein; This sequence comes from Fig.
                    3"
                    /codon_start=1
                    /protein_id="AAB21477.1"
                    /db_xref="GI:245866"
                    /translation="GRLLPN"
BASE COUNT       3 a      7 c      6 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        458 TGGTCAGCAGCCTGC 472
              ||| ||||||||||||
Db         16 TGGGCAGCAGCCTGC 2


RESULT 323
AR021368
LOCUS       AR021368                 19 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 16 from patent US 5789650.
ACCESSION   AR021368
VERSION     AR021368.1  GI:3975983
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Lonberg,N. and Kay,R.M.
  TITLE     Transgenic non-human animals for producing heterologous antibodies
  JOURNAL   Patent: US 5789650-A 16 04-AUG-1998;
FEATURES            Location/Qualifiers
     source         1. .19
                    /organism="unknown"
BASE COUNT       3 a      7 c      7 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        391 GTGGCAGCAATGGCC 405
              ||||| |||||||||
Db          4 GTGGCCGCAATGGCC 18


RESULT 324
AR042930
LOCUS       AR042930                 19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 16 from patent US 5814318.
ACCESSION   AR042930
VERSION     AR042930.1  GI:5963938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Lonberg,N. and Kay,R.M.
  TITLE     Transgenic non-human animals for producing heterologous antibodies
  JOURNAL   Patent: US 5814318-A 16 29-SEP-1998;
FEATURES            Location/Qualifiers
     source         1. .19
                    /organism="unknown"
BASE COUNT       3 a      7 c      7 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        391 GTGGCAGCAATGGCC 405
              ||||| |||||||||
Db          4 GTGGCCGCAATGGCC 18


RESULT 325
AR161238
```

```
LOCUS       AR161238                19 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 184 from patent US 6255458.
ACCESSION   AR161238
VERSION     AR161238.1  GI:16227013
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Lonberg,N. and Kay,R.M.
  TITLE     High affinity human antibodies and human antibodies against digoxin
  JOURNAL   Patent: US 6255458-A 184 03-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        3 a      7 c      7 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        391 GTGGCAGCAATGGCC 405
              ||||| |||||||||
Db          4 GTGGCCGCAATGGCC 18


RESULT 326
AR230749
LOCUS       AR230749                19 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 9 from patent US 6451602.
ACCESSION   AR230749
VERSION     AR230749.1  GI:27271536
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Popoff,I. and Cowsert,L.M.
  TITLE     Antisense modulation of PARP expression
  JOURNAL   Patent: US 6451602-A 9 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        4 a      9 c      3 g      3 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        229 CAGCCTCAGGCATCT 243
              ||||| |||||||||
Db          5 CAGCCACAGGCATCT 19


RESULT 327
AX352891/c
LOCUS       AX352891                19 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 97 from Patent EP1174518.
ACCESSION   AX352891
VERSION     AX352891.1  GI:18617973
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Loukachov,V.V., van Gemen,B. and Goudsmit,J.
  TITLE     Collection of binding molecules
  JOURNAL   Patent: EP 1174518-A 97 23-JAN-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="position 65"
BASE COUNT       13 a      3 c      2 g      1 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTGG 1158
              ||||||||||| |||
Db         15 TTTTTTTCTTTATGG 1


RESULT 328
AX362736/c
LOCUS       AX362736                19 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 97 from Patent WO0208463.
ACCESSION   AX362736
VERSION     AX362736.1  GI:18694876
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Loukachov,V.V., Goudsmit,J. and van Gemen,B.
  TITLE     Collection of binding molecules
  JOURNAL   Patent: WO 0208463-A 97 31-JAN-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="position 65"
BASE COUNT       13 a      3 c      2 g      1 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTGG 1158
              ||||||||||| |||
Db         15 TTTTTTTCTTTATGG 1


RESULT 329
AX643313
LOCUS       AX643313                19 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 179 from Patent WO02099099.
ACCESSION   AX643313
VERSION     AX643313.1  GI:28550941
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Penger,A., Sprenger,R. and Brinkmann,U.
  TITLE     Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
            and their use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 02099099-A 179 12-DEC-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="r=g or a"
BASE COUNT        3 a      4 c      6 g      5 t      1 others

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   82.4%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy        736 TGGCTGCCGCATGTTGC 752
              |||||||:  ||||||
Db          2 TGGCTGCCRAGTGTTGC 18


RESULT 330
AX643316/c
LOCUS       AX643316                19 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 182 from Patent WO02099099.
ACCESSION   AX643316
VERSION     AX643316.1  GI:28550945
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Penger,A., Sprenger,R. and Brinkmann,U.
  TITLE     Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
            and their use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 02099099-A 182 12-DEC-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="y=t or c"
BASE COUNT        5 a      6 c      4 g      3 t      1 others

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   82.4%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        736 TGGCTGCCGCATGTTGC 752
              |||||||:  ||||||
Db         18 TGGCTGCCRAGTGTTGC 2


RESULT 331
AX699142/c
LOCUS       AX699142                19 bp    DNA     linear   PAT 02-APR-2003
DEFINITION  Sequence 83 from Patent WO03000727.
ACCESSION   AX699142
VERSION     AX699142.1  GI:29499792
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Zhang,Y., Moffatt,M., Cookson,W. and Tinsley,J.
  TITLE     Atopy
  JOURNAL   Patent: WO 03000727-A 83 03-JAN-2003;
            ISIS INNOVATION LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT        7 a      3 c      6 g      3 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1216 TTCCCTGTACATTTG 1230
              ||||||||||| |||
Db         16 TTCCCTGTACACTTG 2


RESULT 332
AX700717/c
LOCUS       AX700717                19 bp    DNA     linear   PAT 03-APR-2003
DEFINITION  Sequence 4 from Patent WO03012100.
ACCESSION   AX700717
VERSION     AX700717.1  GI:29536539
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Koltermann,A., Kettling,U., Greiner-Stoeffele,T. and Spangenberg,O.
  TITLE     Method for the production of nucleic acids consisting of
            stochastically combined parts of source nucleic acids
  JOURNAL   Patent: WO 03012100-A 4 13-FEB-2003;
            Direvo Biotech AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="PrimerHR"
BASE COUNT        7 a      2 c      8 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        317 CTCCATACCTGCATC 331
              ||||||||||||| ||
Db         15 CTCCATACCTGCTTC 1


RESULT 333
BD096500
LOCUS       BD096500                19 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Transgenic non-human animals capable of producing heterologous
            antibodies.
ACCESSION   BD096500
VERSION     BD096500.1  GI:22642088
KEYWORDS    JP 2001527386-A/27.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Lonberg,N. and Kay,R.M.
  TITLE     Transgenic non-human animals capable of producing heterologous
            antibodies
  JOURNAL   Patent: JP 2001527386-A 27 25-DEC-2001;
            GENPHARM INTERNATIONAL
COMMENT     OS   Unidentified
            PN   JP 2001527386-A/27
            PD   25-DEC-2001
            PF   01-DEC-1997 JP 1998525687
            PR   02-DEC-1996 US    08/758417
            PI   NILS LONBERG,ROBERT M KAY
            PC   C12N5/00,C12N5/28,C12N5/24,C12N5/10,C07K16/00,A61K39/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            CC   Transgenic non-human animals capable of
            producing heterologous
            CC            antibodies
            FH   Key             Location/Qualifiers
            FT   source          1. .19
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        3 a      7 c      7 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy        391 GTGGCAGCAATGGCC 405
              ||||| |||||||||
Db          4 GTGGCCGCAATGGCC 18


RESULT 334
I43919
LOCUS       I43919                    19 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 8 from patent US 5633425.
ACCESSION   I43919
VERSION     I43919.1  GI:2469017
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Lonberg,N. and Kay,R.M.
  TITLE     Transgenic non-human animals capable of producing heterologous
            antibodies
  JOURNAL   Patent: US 5633425-A 8 27-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        3 a      7 c      7 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        391 GTGGCAGCAATGGCC 405
              ||||| |||||||||
Db          4 GTGGCCGCAATGGCC 18


RESULT 335
I62921
LOCUS       I62921                    19 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 16 from patent US 5661016.
ACCESSION   I62921
VERSION     I62921.1  GI:2480629
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Lonberg,N. and Kay,R.M.
  TITLE     Transgenic non-human animals capable of producing heterologous
            antibodies of various isotypes
  JOURNAL   Patent: US 5661016-A 16 26-AUG-1997;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        3 a      7 c      7 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        391 GTGGCAGCAATGGCC 405
              ||||| |||||||||
Db          4 GTGGCCGCAATGGCC 18


RESULT 336
I88674
LOCUS       I88674                    19 bp    DNA     linear   PAT 10-AUG-1998
DEFINITION  Sequence 16 from patent US 5719032.
ACCESSION   I88674
VERSION     I88674.1  GI:3408614
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Vielkind,J.R.
  TITLE     Melanoma and prostate cancer specific antibodies for
            immunodetection and immunotherapy
  JOURNAL   Patent: US 5719032-A 16 17-FEB-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
BASE COUNT        3 a      7 c      7 g      2 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        391 GTGGCAGCAATGGCC 405
              ||||| |||||||||
Db          4 GTGGCCGCAATGGCC 18


RESULT 337
MMTC4F3
LOCUS       MMTC4F3                   19 bp    DNA     linear   ROD 06-DEC-1995
DEFINITION  M.musculus partial gene for T cell receptor gamma-chain (clone
            4F3).
ACCESSION   Z49028
VERSION     Z49028.1  GI:1107755
KEYWORDS    joining region; T cell receptor; T cell receptor gamma; variable
            region.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Roger,T.T.
  TITLE     extensive TCR-g gene analysis in ab+ T cells indicates selective
            rearrangement and expression of particular Vg genes
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 19)
  AUTHORS   Roger,T.T.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-APR-1995) Thierry T.R. Roger, Lab.
            d'immunodifferenciation, Pr Seman, Universite Denis Diderot, 2,
            place Jussieu, Paris, Paris, 75251, Paris cedex 05, France
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="DBA/2"
                     /db_xref="taxon:10090"
                     /chromosome="13"
                     /cell_line="4F3"
                     /cell_type="T-cell"
                     /tissue_type="Spleen"
                     /clone_lib="library M13mp19"
                     /dev_stage="Seed, cell expansion stage"
     misc_recomb     1. .19
                     /note="out of frame messenger"
                     /organism="Mus musculus domesticus"
     V_region        1. .7
                     /product="end of Tcrg-V2 gene segment"
     misc_recomb     8. .12
                     /note="N region"
                     /organism="Mus musculus domesticus"
     J_segment       13. .19
                     /product="beginning of Tcrg-J2 gene segment"
     terminator      13. .15
BASE COUNT        2 a      5 c      6 g      6 t

  Query Match             1.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        495 TGTGCAGCGTCTTGG 509
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                ||||||||||||| |
Db          1 TGTGCAGCGTCTTAG 15


RESULT 338
AR112529
LOCUS       AR112529                  18 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 31 from patent US 6130071.
ACCESSION   AR112529
VERSION     AR112529.1  GI:14092429
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Alitalo,K. and Joukov,V.
  TITLE     Vascular endothelial growth factor C (VEGF-C) .DELTA.Cys.sub.156
            protein and gene, and uses thereof
  JOURNAL   Patent: US 6130071-A 31 10-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        4 a      4 c      4 g      6 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        380 TTCCTCCAGAGGTGGCAG 397
              ||| |||| ||||| |||
Db          1 TTCTTCCAAAGGTGTCAG 18


RESULT 339
AR121114
LOCUS       AR121114                  18 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 10 from patent US 6159697.
ACCESSION   AR121114
VERSION     AR121114.1  GI:14104690
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Monia,B.P. and Cowsert,L.M.
  TITLE     Antisense modulation of Smad7 expression
  JOURNAL   Patent: US 6159697-A 10 12-DEC-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        1 a      12 c      3 g      2 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        583 CTCCGTCTGCCCCCCACC 600
              ||||| ||||||| | ||
Db          1 CTCCGGCTGCCCCACCCC 18


RESULT 340
AR187495
LOCUS       AR187495                  18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2983 from patent US 6346398.
ACCESSION   AR187495
VERSION     AR187495.1  GI:20233460
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2983 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        0 a      11 c      3 g      4 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        142 CCGCTCGGCTCCGCTCCG 159
              || |||||||| | |||
Db          1 CCTCTCGGCTCCTCCCCG 18


RESULT 341
AR188966
LOCUS       AR188966                  18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 4454 from patent US 6346398.
ACCESSION   AR188966
VERSION     AR188966.1  GI:20234931
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 4454 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        0 a      7 c      7 g      4 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1239 GCTGGACGTGGCCATGTG 1256
              ||||| ||| ||| ||||
Db          1 GCTGGCCGTCGCCCTGTG 18


RESULT 342
AR192905
LOCUS       AR192905                  18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 8393 from patent US 6346398.
ACCESSION   AR192905
VERSION     AR192905.1  GI:20238870
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 8393 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        3 a      7 c      4 g      4 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1053 CAGCCCTGGCCTTCCCAT 1070
              ||| |||| ||||| |||
Db          1 CAGGCCTGACCTTCGCAT 18
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RESULT 343
AR202005
LOCUS       AR202005                 18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 31 from patent US 6361946.
ACCESSION   AR202005
VERSION     AR202005.1  GI:20256544
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Alitalo,K. and Joukov,V.
  TITLE     Vascular endothelial growth factor C (VEGF-C) protein and gene,
            mutants thereof, and uses thereof
  JOURNAL   Patent: US 6361946-A 31 26-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        4 a      4 c      4 g      6 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        380 TTCCTCCAGAGGTGGCAG 397
              ||| |||| ||||| |||
Db          1 TTCTTCCAAAGGTGTCAG 18


RESULT 344
AR211095
LOCUS       AR211095                 18 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 8 from patent US 6399297.
ACCESSION   AR211095
VERSION     AR211095.1  GI:21514326
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 8 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        2 a      5 c      9 g      2 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        471 GCAGGGGGAGGACTGCCG 488
              || ||| |||||||||  |
Db          1 GCCGGGCGAGGACTGCTG 18


RESULT 345
AR231296
LOCUS       AR231296                 18 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 33 from patent US 6451968.
ACCESSION   AR231296
VERSION     AR231296.1  GI:27272227
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
            Coull,J.M., Kiely,J. and Griffith,M.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6451968-A 33 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        0 a      2 c      0 g     16 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1138 TATGCCTTTTTTTCTTTT 1155
              | | | ||||||||||||
Db          1 TTTTCTTTTTTTTCTTTT 18


RESULT 346
AR294304/c
LOCUS       AR294304                 18 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 6039 from patent US 6537751.
ACCESSION   AR294304
VERSION     AR294304.1  GI:31681588
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 6039 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        7 a      0 c      8 g      3 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         56 CTCCTCAATTACCCACAT 73
              ||||||  ||| ||||||
Db         18 CTCCTCTCTTATCCACAT 1


RESULT 347
AX009054
LOCUS       AX009054                 18 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 87 from Patent WO9963975.
ACCESSION   AX009054
VERSION     AX009054.1  GI:9996428
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
  TITLE     A method for stimulating the immune system
  JOURNAL   Patent: WO 9963975-A 87 16-DEC-1999;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
            HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      9 c      7 g      1 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
```

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Qy        191 CCGCCCACCCGGACGCCG 208
              ||| |||||||| ||| |
Db          1 CCGGCCACCCGGTCGCGG 18


RESULT 348
AX114414
LOCUS       AX114414                 18 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 83 from Patent WO0129257.
ACCESSION   AX114414
VERSION     AX114414.1  GI:14031378
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Schork,N. and Skierczynski,B.
  TITLE     Methods of genetic cluster analysis and use thereof
  JOURNAL   Patent: WO 0129257-A 83 26-APR-2001;
            GENSET (FR)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     primer_bind     1. .18
                     /note="upstream amplification primer 4-58 for SEQ 20"
BASE COUNT        5 a      8 c      3 g      2 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        869 TCCCCACAGCCAAGTTCC 886
              |||||||||| |||  ||
Db          1 TCCCCACAGCTAAGAGCC 18


RESULT 349
AX147861
LOCUS       AX147861                 18 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 106 from Patent WO0136473.
ACCESSION   AX147861
VERSION     AX147861.1  GI:14346857
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Vogeli,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
            Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
            Sejlitz,T. and Huff,R.M.
  TITLE     Novel g protein-coupled receptors
  JOURNAL   Patent: WO 0136473-A 106 25-MAY-2001;
            PHARMACIA & UPJOHN COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Novel Sequence"
BASE COUNT        1 a      5 c      8 g      4 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        524 TGCCGGAGGAGCAGCTGG 541
              |||| | ||||| |||||
Db          1 TGCCTGTGGAGCCGCTGG 18


RESULT 350
AX226473
LOCUS       AX226473                 18 bp    DNA     linear   PAT 10-SEP-2001
DEFINITION  Sequence 129 from Patent WO0155179.
ACCESSION   AX226473
VERSION     AX226473.1  GI:15555687
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Prayaga,S.K., Padigaru,M., Spytek,K.A., Li,L., Tchernev,V.T.,
            Vernet,C.A., Peyman,J.A. and Macdougall,J.
  TITLE     Nucleic acids encoding polypeptides with homology to olfactory
            receptors
  JOURNAL   Patent: WO 0155179-A 129 02-AUG-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="NOV12 Reverse Primer Sequence"
BASE COUNT        5 a      5 c      7 g      1 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        906 GGCCCTGGTCCTAAAGGA 923
              ||||| || ||| |||||
Db          1 GGCCCAGGACCTGAAGGA 18


RESULT 351
AX282820/c
LOCUS       AX282820                 18 bp    DNA     linear   PAT 02-NOV-2001
DEFINITION  Sequence 34 from Patent WO0164238.
ACCESSION   AX282820
VERSION     AX282820.1  GI:16609820
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Zehentner,B., Leser-Reiff,U. and Burtscher,H.
  TITLE     Methods and compositions for regulating adipocytes
  JOURNAL   Patent: WO 0164238-A 34 07-SEP-2001;
            Curis, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="primer"
BASE COUNT        4 a      5 c      6 g      3 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        304 GTGGGGGCTGCAACTCCA 321
              |||| | ||||| |||||
Db         18 GTGGAGCCTGCATCTCCA 1


RESULT 352
AX357992/c
LOCUS       AX357992                 18 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 38 from Patent WO0194413.
ACCESSION   AX357992
VERSION     AX357992.1  GI:18674763
KEYWORDS    .
```

```
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mikesell,G.E., Chang,H., Finger,J.N., Yang,G., Lu,P., Zhou,X.D. and
            Peach,R.
  TITLE     B7-related nucleic acids and polypeptides and their uses for
            immunomodulation
  JOURNAL   Patent: WO 0194413-A 38 13-DEC-2001;
            Bristol-Myers Squibb Company (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT        4 a      7 c      3 g      4 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1014 CCTGAGATGGTGCCAAAG 1031
              |||| ||||||| || ||
Db         18 CCTGTGATGGTGACAGAG 1


RESULT 353
AX521910
LOCUS       AX521910                  18 bp    DNA     linear   PAT 24-OCT-2002
DEFINITION  Sequence 106 from Patent WO02064789.
ACCESSION   AX521910
VERSION     AX521910.1  GI:24410809
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lind,P., Parodi,L.A., Vogeli,G. and Wood,L.S.
  TITLE     G protein-coupled receptor
  JOURNAL   Patent: WO 02064789-A 106 22-AUG-2002;
            PHARMACIA & UPJOHN COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Novel Sequence"
BASE COUNT        1 a      5 c      8 g      4 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        524 TGCCGGAGGAGCAGCTGG 541
              |||| | ||||| |||||
Db          1 TGCCTGTGGAGCCGCTGG 18


RESULT 354
AX554246
LOCUS       AX554246                  18 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 75 from Patent WO02057299.
ACCESSION   AX554246
VERSION     AX554246.1  GI:25898103
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Alitalo,K., Koivunen,E. and Kubo,H.
  TITLE     Vegfr-3 inhibitor materials and methods
  JOURNAL   Patent: WO 02057299-A 75 25-JUL-2002;
            LUDWIG INSTITUTE FOR CANCER RESEARCH (US) ; Licentia Ltd. (FI)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="primer"
BASE COUNT        1 a      10 c      5 g      2 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        686 TTGGGAGCCAGCGGCCCC 703
              || ||  ||||||||||
Db          1 TTCGGCCCCAGCGGCCCC 18


RESULT 355
AX590584/c
LOCUS       AX590584                  18 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 24 from Patent WO02086113.
ACCESSION   AX590584
VERSION     AX590584.1  GI:27949193
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Cookson,W.O., Moffat,M.F., Allen,M. and Lench,N.
  TITLE     Enzyme and snp marker for disease
  JOURNAL   Patent: WO 02086113-A 24 31-OCT-2002;
            Isis Innovation Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT        2 a      7 c      3 g      6 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        935 TGGAGAAGAGGTGTGAGC 952
              |||||||||| |  ||||
Db         18 TGGAGAAGAGCTACGAGC 1


RESULT 356
AX599245/c
LOCUS       AX599245                  18 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 585 from Patent WO02077272.
ACCESSION   AX599245
VERSION     AX599245.1  GI:28399387
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pelet,C. and Ziebarth,H.
  TITLE     Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
  JOURNAL   Patent: WO 02077272-A 585 03-OCT-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
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                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for CDC25A"
BASE COUNT        1 a      1 c      8 g      8 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         24 AACCAAACCCAGCTACGC 41
              ||||||||| | |||| |
Db         18 AACCAAACCGACCTACAC 1


RESULT 357
AX599246/c
LOCUS       AX599246                 18 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 586 from Patent WO02077272.
ACCESSION   AX599246
VERSION     AX599246.1  GI:28399388
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pelet,C. and Ziebarth,H.
  TITLE     Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
  JOURNAL   Patent: WO 02077272-A 586 03-OCT-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for CDC25A"
BASE COUNT        1 a      0 c      8 g      9 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         24 AACCAAACCCAGCTACGC 41
              ||||||||| | |||| |
Db         18 AACCAAACCAACCTACAC 1


RESULT 358
AX599819/c
LOCUS       AX599819                 18 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 1159 from Patent WO02077272.
ACCESSION   AX599819
VERSION     AX599819.1  GI:28399967
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pelet,C. and Ziebarth,H.
  TITLE     Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
  JOURNAL   Patent: WO 02077272-A 1159 03-OCT-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for CDC25A"
BASE COUNT        1 a      1 c      8 g      8 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         24 AACCAAACCCAGCTACGC 41
              ||||||||| | |||| |
Db         18 AACCAAACCGACCTACAC 1


RESULT 359
AX599820/c
LOCUS       AX599820                 18 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 1160 from Patent WO02077272.
ACCESSION   AX599820
VERSION     AX599820.1  GI:28399968
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pelet,C. and Ziebarth,H.
  TITLE     Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
  JOURNAL   Patent: WO 02077272-A 1160 03-OCT-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for CDC25A"
BASE COUNT        1 a      0 c      8 g      9 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         24 AACCAAACCCAGCTACGC 41
              ||||||||| | |||| |
Db         18 AACCAAACCAACCTACAC 1


RESULT 360
AX599821
LOCUS       AX599821                 18 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 1161 from Patent WO02077272.
ACCESSION   AX599821
VERSION     AX599821.1  GI:28399969
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pelet,C. and Ziebarth,H.
  TITLE     Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
  JOURNAL   Patent: WO 02077272-A 1161 03-OCT-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for CDC25A"
```

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BASE COUNT        8 a      8 c      1 g      1 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         24 AACCAAACCCAGCTACGC 41
              ||||||||| | |||| |
Db          1 AACCAAACCGACCTACAC 18


RESULT 361
AX599822
LOCUS       AX599822                 18 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 1162 from Patent WO02077272.
ACCESSION   AX599822
VERSION     AX599822.1  GI:28399970
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pelet,C. and Ziebarth,H.
  TITLE     Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
  JOURNAL   Patent: WO 02077272-A 1162 03-OCT-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for CDC25A"
BASE COUNT        9 a      8 c      0 g      1 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         24 AACCAAACCCAGCTACGC 41
              ||||||||| | |||| |
Db          1 AACCAAACCAACCTACAC 18


RESULT 362
AX601190/c
LOCUS       AX601190                 18 bp    DNA     linear   PAT 17-FEB-2003
DEFINITION  Sequence 285 from Patent WO02092851.
ACCESSION   AX601190
VERSION     AX601190.1  GI:28401273
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Binns,M.M. and Swinburne,J.E.
  TITLE     Genetic typing
  JOURNAL   Patent: WO 02092851-A 285 21-NOV-2002;
            ANIMAL HEALTH TRUST (GB) ; The British Horseracing Board (GB)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT        2 a     12 c      2 g      2 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        528 GGAGGAGCAGCTGGGTGC 545
              || ||||||| |||| ||
Db         18 GGTGGAGCAGGTGGGGGC 1


RESULT 363
AX708070/c
LOCUS       AX708070                 18 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 6 from Patent WO03014387.
ACCESSION   AX708070
VERSION     AX708070.1  GI:29564021
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wojnowski,L. and Presecan-Siedel,E.
  TITLE     Polymorphisms in the human gene for cyp1a2 and their use in
            diagnostic and therapeutic applications
  JOURNAL   Patent: WO 03014387-A 6 20-FEB-2003;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        2 a      4 c      8 g      4 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        557 GCATGCACACACTGCTCC 574
              |||||| ||||| ||| |
Db         18 GCATGCCCACACAGCTGC 1


RESULT 364
AX718771/c
LOCUS       AX718771                 18 bp    DNA     linear   PAT 15-APR-2003
DEFINITION  Sequence 335 from Patent WO02103043.
ACCESSION   AX718771
VERSION     AX718771.1  GI:29891338
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Beimfohr,C. and Snaidr,J.
  TITLE     Method for the specific fast detection of bacteria which is harmful
            to beer
  JOURNAL   Patent: WO 02103043-A 335 27-DEC-2002;
            Vermicon AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonukleotid"
BASE COUNT        2 a      4 c      6 g      6 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         96 CCGTACAACCCCGGAGGC 113
              ||||| |||| ||||| |
Db         18 CCGTATAACCACGGAGAC 1


RESULT 365
BD064468/c
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```
LOCUS       BD064468                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Covalent joining of DNA strands to RNA strands catalyzed by vaccine
            topoisomerase.
ACCESSION   BD064468
VERSION     BD064468.1  GI:22610071
KEYWORDS    JP 2001507241-A/16.
SOURCE      Vaccinia virus
  ORGANISM  Vaccinia virus
            Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
            Orthopoxvirus.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Shuman,S., Sekiguchi,J., Fernandez,J., Marcil,R., Hoeffler,J. and
            Comisky,J.
  TITLE     Covalent joining of DNA strands to RNA strands catalyzed by vaccine
            topoisomerase
  JOURNAL   Patent: JP 2001507241-A 16 05-JUN-2001;
            SLOAN KETTERING INSTITUTE FOR CANCER RESEARCH,INVITROGEN CORP
COMMENT     OS   Vaccinia virus
            PN   JP 2001507241-A/16
            PD   05-JUN-2001
            PF   12-JUN-1998 JP 1999503313
            PR   12-JUN-1997 US    60/049405
            PI   STEWART SHUMAN,JOANN SEKIGUCHI,JOSEPH FERNANDEZ,ROBERT MARCIL,
            PI   JAMES HOEFFLER,JOHN COMISKY
            PC   C12P19/34,C12Q1/68,C12N15/11
            CC
            FH   Key             Location/Qualifiers.
FEATURES                 Location/Qualifiers
     source              1. .18
                         /organism="Vaccinia virus"
                         /mol_type="genomic DNA"
                         /db_xref="taxon:10245"
BASE COUNT        4 a      7 c      3 g      4 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        677 GCGTGGTATTTGGGAGCC 694
              | || |||| ||||||||
Db         18 GAGTCGTATATGGGAGCC 1


RESULT 366
BD082178
LOCUS       BD082178                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Vascular endothelial growth factor C (VEGF-C) protein and gene,
            mutants thereof, and uses thereof.
ACCESSION   BD082178
VERSION     BD082178.1  GI:22627788
KEYWORDS    JP 2001523951-A/24.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Alitalo,K. and Joukov,V.
  TITLE     Vascular endothelial growth factor C (VEGF-C) protein and gene,
            mutants thereof, and uses thereof
  JOURNAL   Patent: JP 2001523951-A 24 27-NOV-2001;
            THE LUDWIG INSTITUTE FOR CANCER RESEARCH, HELSINKI UNIVERSITY
            LICENSING LTD
COMMENT     PN   JP 2001523951-A/24
            PD   27-NOV-2001
            PF   02-FEB-1998 JP 1998533178
            PR   05-FEB-1997 US    08/795430
            PI   KARI ALITALO,VLADIMIR JOUKOV
            PC   C12N15/12,C07K14/52,C12N15/10,C07K16/24,C12Q1/68,C12N15/62, PC
              G01N33/50,
            PC   A01K67/027
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES                 Location/Qualifiers
     source              1. .18
                         /organism="Zea mays"
                         /mol_type="genomic DNA"
                         /db_xref="taxon:4577"
BASE COUNT        4 a      4 c      4 g      6 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        380 TTCCTCCAGAGGTGGCAG 397
              ||| |||| ||||| |||
Db          1 TTCTTCCAAAGGTGTCAG 18


RESULT 367
BD088488
LOCUS       BD088488                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD088488
VERSION     BD088488.1  GI:22634098
KEYWORDS    JP 2001321190-A/732.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 732 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/732
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                   Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES                 Location/Qualifiers
     source              1. .18
                         /organism="synthetic construct"
                         /mol_type="genomic DNA"
                         /db_xref="taxon:32630"
BASE COUNT        5 a      7 c      4 g      2 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        559 ATGCACACACTGCTCCAG 576
              | |  ||||||||||||||
Db          1 AAGGCCACACTGCTCCAG 18


RESULT 368
I40172
LOCUS       I40172                   18 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 2 from patent US 5618796.
ACCESSION   I40172
VERSION     I40172.1  GI:2083177
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Iversen,P.L.
```

```
  TITLE     Metal binding oligonucleotide and methods and compositions for
            their use to treat metal toxicity
  JOURNAL   Patent: US 5618796-A 2 08-APR-1997;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        3 a      3 c     10 g      2 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        525 GCCGGAGGAGCAGCTGGG 542
              | || |||||||| ||||
Db          1 GGCGCAGGAGCAGTTGGG 18


RESULT 369
I40173/c
LOCUS       I40173                  18 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 3 from patent US 5618796.
ACCESSION   I40173
VERSION     I40173.1  GI:2083178
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Iversen,P.L.
  TITLE     Metal binding oligonucleotide and methods and compositions for
            their use to treat metal toxicity
  JOURNAL   Patent: US 5618796-A 3 08-APR-1997;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        2 a      10 c      3 g      3 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        525 GCCGGAGGAGCAGCTGGG 542
              | || |||||||| ||||
Db         18 GGCGCAGGAGCAGTTGGG 1


RESULT 370
HSRETPO16
LOCUS       HSRETPO16               18 bp    DNA     linear   PRI 13-DEC-1994
DEFINITION  H.sapiens Ret Proto-Oncogene, Intron 16 (3').
ACCESSION   X79755
VERSION     X79755.1  GI:601967
KEYWORDS    intron; ret gene; ret proto-oncogene.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Mulligan,L.M., Eng,C., Attie,T., Lyonnet,S., Marsh,D.J.,
            Hyland,V.J., Robinson,B.G., Frilling,A., Verellen-Dumoulin,C.,
            Safar,A., Venter,D.J., Munnich,A. and Ponder,B.A.J.
  TITLE     Diverse phenotypes associated with exon 10 mutations of the RET
            proto-oncogene
  JOURNAL   Hum. Mol. Genet. 3 (12), 2163-2167 (1994)
  MEDLINE   95187155
   PUBMED   7881414
REFERENCE   2  (bases 1 to 18)
  AUTHORS   Eng,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUN-1994) C. Eng, University of Cambridge, Dept of
            Pathology, Tennis Court Road, Cambridge CB2 1QP, UK
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="10"
                     /map="q11.2"
                     /germline
     gene            1. .18
                     /gene="RET"
     intron          <1. .18
                     /gene="RET"
                     /note="3' end"
                     /number=16
BASE COUNT        2 a      3 c      9 g      4 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1248 GGCCATGTGAGGCCAGGT 1265
              |||  ||||||| |||||
Db          1 GGCTCTGTGAGGGCAGGT 18


RESULT 371
A17234/c
LOCUS       A17234                  20 bp    DNA     linear   PAT 31-MAR-1994
DEFINITION  Oligonucleotide 20-mer BB9513 (SEQ ID NO: 134).
ACCESSION   A17234
VERSION     A17234.1  GI:513003
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   .
  TITLE     STEM CELL INHIBITING PROTEINS
  JOURNAL   Patent: WO 9313206-A 134 08-JUL-1993;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        4 a      6 c      4 g      6 t

  Query Match             1.0%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        820 GTCCTGATGCAGCTGAAG 837
              || |||| ||| ||||||
Db         20 GTGCTGACGCATCTGAAG 3


RESULT 372
AR027617/c
LOCUS       AR027617                20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 134 from patent US 5856301.
ACCESSION   AR027617
VERSION     AR027617.1  GI:5938437
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Craig,S., Hunter,M.George., Edwards,R.Mark., Czaplewski,L.George.
            and Gilbert,R.James.
  TITLE     Stem cell inhibiting proteins
  JOURNAL   Patent: US 5856301-A 134 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      6 c      4 g      6 t
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  Query Match             1.0%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        820 GTCCTGATGCAGCTGAAG 837
              || |||| ||| ||||||
Db         20 GTGCTGACGCATCTGAAG 3


RESULT 373
AX636077
LOCUS       AX636077                  15 bp    mRNA    linear   PAT 21-FEB-2003
DEFINITION  Sequence 3216 from Patent EP1260586.
ACCESSION   AX636077
VERSION     AX636077.1  GI:28471691
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 3216 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="mRNA"
                     /db_xref="taxon:32644"
BASE COUNT        4 a      5 c      5 g      1 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1066 CCCATCAGGCAGG 1078
              |||||||||||||
Db          3 CCCATCAGGCAGG 15


RESULT 374
I61757
LOCUS       I61757                    15 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 311 from patent US 5658780.
ACCESSION   I61757
VERSION     I61757.1  GI:2479705
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
  TITLE     Rel a targeted ribozymes
  JOURNAL   Patent: US 5658780-A 311 19-AUG-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
BASE COUNT        4 a      5 c      5 g      1 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1066 CCCATCAGGCAGG 1078
              |||||||||||||
Db          3 CCCATCAGGCAGG 15


RESULT 375
AR014264
LOCUS       AR014264                  17 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 29 from patent US 5773278.
ACCESSION   AR014264
VERSION     AR014264.1  GI:3971718
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Schuchman,E.H. and Desnick,R.J.
  TITLE     Acid sphingomyelinase gene
  JOURNAL   Patent: US 5773278-A 29 30-JUN-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        4 a      6 c      3 g      4 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        631 CTCCAGGAGCTCT 643
              |||||||||||||
Db          5 CTCCAGGAGCTCT 17


RESULT 376
AR302290
LOCUS       AR302290                  17 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 29 from patent US 6541218.
ACCESSION   AR302290
VERSION     AR302290.1  GI:31690529
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Schuchman,E.H. and Desnick,R.J.
  TITLE     Acid sphingomyelinase protein and methods of treating type B
            Niemann-Pick disease
  JOURNAL   Patent: US 6541218-A 29 01-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        4 a      6 c      3 g      4 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        631 CTCCAGGAGCTCT 643
              |||||||||||||
Db          5 CTCCAGGAGCTCT 17


RESULT 377
AX361147
LOCUS       AX361147                  17 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 31 from Patent EP1177789.
ACCESSION   AX361147
VERSION     AX361147.1  GI:18693793
KEYWORDS    .
SOURCE      Rattus sp.
  ORGANISM  Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
  AUTHORS   Fluehmann,B., Heim,M., Hunziker,W. and Weber,P.
  TITLE     Use of phytanic acid for the treatment of diabetes
  JOURNAL   Patent: EP 1177789-A 31 06-FEB-2002;
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            Roche Vitamins AG (CH)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Rattus sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10118"
BASE COUNT        2 a      6 c      6 g      3 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        457 GTGGTCAGCAGCC 469
              |||||||||||||
Db          2 GTGGTCAGCAGCC 14


RESULT 378
AX499074
LOCUS       AX499074                 17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 381 from Patent EP1229046.
ACCESSION   AX499074
VERSION     AX499074.1  GI:23381367
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 381 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      7 c      6 g      1 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        522 CCTGCCGGAGGAG 534
              |||||||||||||
Db          5 CCTGCCGGAGGAG 17


RESULT 379
AX499075
LOCUS       AX499075                 17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 382 from Patent EP1229046.
ACCESSION   AX499075
VERSION     AX499075.1  GI:23381368
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 382 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      6 c      7 g      1 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        522 CCTGCCGGAGGAG 534
              |||||||||||||
Db          4 CCTGCCGGAGGAG 16


RESULT 380
AX687584
LOCUS       AX687584                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 316 from Patent EP1281758.
ACCESSION   AX687584
VERSION     AX687584.1  GI:29410280
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 316 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      5 c      8 g      2 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        630 GCTCCAGGAGCTC 642
              |||||||||||||
Db          5 GCTCCAGGAGCTC 17


RESULT 381
AX687590
LOCUS       AX687590                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 322 from Patent EP1281758.
ACCESSION   AX687590
VERSION     AX687590.1  GI:29410286
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 322 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      5 c      5 g      5 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        632 TCCAGGAGCTCTG 644
              |||||||||||||
Db          1 TCCAGGAGCTCTG 13
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RESULT 382
AX688104
LOCUS       AX688104                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 836 from Patent EP1281758.
ACCESSION   AX688104
VERSION     AX688104.1  GI:29410802
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 836 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      7 c      4 g      5 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1055 GCCCTGGCCTTCC 1067
              |||||||||||||
Db          5 GCCCTGGCCTTCC 17


RESULT 383
AX688109
LOCUS       AX688109                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 841 from Patent EP1281758.
ACCESSION   AX688109
VERSION     AX688109.1  GI:29410807
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 841 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      8 c      4 g      4 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1056 CCCTGGCCTTCCC 1068
              |||||||||||||
Db          1 CCCTGGCCTTCCC 13


RESULT 384
AX690592
LOCUS       AX690592                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 3324 from Patent EP1281758.
ACCESSION   AX690592
VERSION     AX690592.1  GI:29413473
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 3324 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      5 c      4 g      3 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        631 CTCCAGGAGCTCT 643
              |||||||||||||
Db          5 CTCCAGGAGCTCT 17


RESULT 385
AX690598
LOCUS       AX690598                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 3330 from Patent EP1281758.
ACCESSION   AX690598
VERSION     AX690598.1  GI:29413479
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 3330 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      7 c      4 g      3 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        633 CCAGGAGCTCTGC 645
              |||||||||||||
Db          1 CCAGGAGCTCTGC 13


RESULT 386
AX726504
LOCUS       AX726504                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 4191 from Patent WO03025176.
ACCESSION   AX726504
VERSION     AX726504.1  GI:30505847
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
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```
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 4191 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
BASE COUNT        1 a      5 c      6 g      5 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        260 TCCTGGGCTGGCT 272
              |||||||||||||
Db          3 TCCTGGGCTGGCT 15


RESULT 387
AX737849/c
LOCUS       AX737849                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3439 from Patent WO03025177.
ACCESSION   AX737849
VERSION     AX737849.1  GI:30517137
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 3439 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      3 c      7 g      5 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        649 CCCCAAGACCTGG 661
              |||||||||||||
Db         16 CCCCAAGACCTGG 4


RESULT 388
BD067164/c
LOCUS       BD067164                 17 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors.
ACCESSION   BD067164
VERSION     BD067164.1  GI:22612767
KEYWORDS    JP 2001511003-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Akhtar,S., Fell,P. and Mcswiggen,J.A.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors
  JOURNAL   Patent: JP 2001511003-A 4 07-AUG-2001;
            RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT     OS   Unidentified
            PN   JP 2001511003-A/4
            PD   07-AUG-2001
            PF   14-JAN-1998 JP 1998532913
            PR   31-JAN-1997 US    60/036476,04-DEC-1997 US    08/985162 PI
            SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
            C12N9/00,C07K14/71
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                 related to
            CC   levels of epidermal growth factor receptors
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      8 c      5 g      3 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        200 CGGACGCCGACGA 212
              |||||||||||||
Db         17 CGGACGCCGACGA 5


RESULT 389
BD144764
LOCUS       BD144764                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Use of phytanic acid for the treatment of diabetes.
ACCESSION   BD144764
VERSION     BD144764.1  GI:27850522
KEYWORDS    JP 2002104964-A/31.
SOURCE      Rattus sp.
  ORGANISM  Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Fluehmann,B., Helm,M., Hunziker,W. and Weber,P.
  TITLE     Use of phytanic acid for the treatment of diabetes
  JOURNAL   Patent: JP 2002104964-A 31 10-APR-2002;
            ROCHE VITAMINS AG
COMMENT     OS   Rattus sp. (rat)
            PN   JP 2002104964-A/31
            PD   10-APR-2002
            PF   01-AUG-2001 JP 2001233070
            PR   04-AUG-2000 EP   00116848.3
            PI   BEAT FLUEHMANN,MANUEL HELM,WILLI HUNZIKER,PETER WEBER PC
            A61K31/20,A23L1/30,A61K31/16,A61K31/201,A61K31/215,A61P3/00, PC
            A61P3/04,
            PC   A61P3/06,A61P3/10
            CC   Rat primary hepatocytes
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Rattus sp. (rat)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Rattus sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10118"
BASE COUNT        2 a      6 c      6 g      3 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        457 GTGGTCAGCAGCC 469
              |||||||||||||
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Db          2 GTGGTCAGCAGCC 14


RESULT 390
I26888
LOCUS       I26888                    17 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 111 from patent US 5561041.
ACCESSION   I26888
VERSION     I26888.1  GI:1606758
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sidransky,D.
  TITLE     Nucleic acid mutation detection by analysis of sputum
  JOURNAL   Patent: US 5561041-A 111 01-OCT-1996;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        3 a      9 c      3 g      2 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        589 CTGCCCCCCACCA 601
              |||||||||||||
Db          2 CTGCCCCCCACCA 14


RESULT 391
I73171
LOCUS       I73171                    17 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 23 from patent US 5686240.
ACCESSION   I73171
VERSION     I73171.1  GI:3009310
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Schuchman,E.H. and Desnick,R.J.
  TITLE     Acid sphingomyelinase gene and diagnosis of Niemann-Pick disease
  JOURNAL   Patent: US 5686240-A 23 11-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        4 a      6 c      3 g      4 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        631 CTCCAGGAGCTCT 643
              |||||||||||||
Db          5 CTCCAGGAGCTCT 17


RESULT 392
I91629
LOCUS       I91629                    17 bp    DNA     linear   PAT 01-DEC-1998
DEFINITION  Sequence 111 from patent US 5726019.
ACCESSION   I91629
VERSION     I91629.1  GI:3936099
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sidransky,D.
  TITLE     Analysis of sputum by amplification and detection of mutant nucleic
            acid sequences
  JOURNAL   Patent: US 5726019-A 111 10-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        3 a      9 c      3 g      2 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        589 CTGCCCCCCACCA 601
              |||||||||||||
Db          2 CTGCCCCCCACCA 14


RESULT 393
DOGP43402
LOCUS       DOGP43402                 18 bp    DNA     linear   MAM 07-MAR-1996
DEFINITION  Dog (Clone: CXX.434) primer for STS 434, 3' end.
ACCESSION   L24317
VERSION     L24317.1  GI:402018
KEYWORDS    PCR identification; PCR primer; STS.
SEGMENT     2 of 2
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Ostrander,E.A., Mapa,F.A., Yee,M. and Rine,J.
  TITLE     One hundred and one new simple sequence repeat-based markers for
            the canine genome
  JOURNAL   Mamm. Genome 6 (3), 192-195 (1995)
  MEDLINE   95268214
   PUBMED   7749226
COMMENT     Original source text: Canis familiaris (library: E. Ostrander, in
            pBluescript+) adult spleen DNA.
            Submitted by:
            Fred Hutchinson Cancer Research Center
            Transplantation Biology Dept
            1124 Columbia; Mailstop M318
            Seattle, WA 98104, USA
            e-mail: EAOstrander@lbl.gov
            PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
            PCR Profile:  Denaturation:    94 degrees C for 1.00 minute
            Annealing:       55 or 59 degrees C for 0.45 minutes
            Polymerization:  74 degrees C for 1.00 minutes
            PCR Cycles:      33
            Final Extension:  74 degrees C for 5.00 minutes.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9615"
                     /tissue_type="spleen"
                     /dev_stage="adult"
                     /tissue_lib="E. Ostrander, in pBluescript+"
     primer_bind     complement(1. .18)
BASE COUNT        4 a     10 c      1 g      3 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1207 CACCTCCCCTTCC 1219
              |||||||||||||
Db          6 CACCTCCCCTTCC 18


RESULT 394
A17235/c
LOCUS       A17235                    18 bp    DNA     linear   PAT 31-MAR-1994
DEFINITION  Oligonucleotide 18-mer BB9516 (SEQ ID NO: 135).
ACCESSION   A17235
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VERSION     A17235.1  GI:513004
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   .
  TITLE     STEM CELL INHIBITING PROTEINS
  JOURNAL   Patent: WO 9313206-A 135 08-JUL-1993;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT         7 a      4 c      2 g      5 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        746 ATGTTGCTGACTT 758
              |||||||||||||
Db         14 ATGTTGCTGACTT 2


RESULT 395
A17407
LOCUS       A17407                   18 bp    DNA     linear   PAT 29-MAR-1994
DEFINITION  oligonucleotides.
ACCESSION   A17407
VERSION     A17407.1  GI:513898
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Schumacher,G. and Dony,C.
  TITLE     Mutein of granulocyte colony stimulating factor (G-CSF)
  JOURNAL   Patent: EP 0456200-A 4 13-NOV-1991;
            BOEHRINGER MANNHEIM GMBH
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT         2 a      6 c      7 g      3 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        259 CTCCTGGGCTGGC 271
              |||||||||||||
Db          2 CTCCTGGGCTGGC 14


RESULT 396
AR002274/c
LOCUS       AR002274                 18 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 13 from patent US 5741645.
ACCESSION   AR002274
VERSION     AR002274.1  GI:3963828
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Orr,H.T., Ranum,L.P.W., Chung,M.-Y. and Zoghbi,H.Y.
  TITLE     Gene sequence for spinocerebellar ataxia type 1 and method for
            diagnosis
  JOURNAL   Patent: US 5741645-A 13 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT         0 a      2 c     12 g      4 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        592 CCCCCCACCAGCC 604
              |||||||||||||
Db         18 CCCCCCACCAGCC 6


RESULT 397
AR027618/c
LOCUS       AR027618                 18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 135 from patent US 5856301.
ACCESSION   AR027618
VERSION     AR027618.1  GI:5938438
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Craig,S., Hunter,M.George., Edwards,R.Mark., Czaplewski,L.George.
            and Gilbert,R.James.
  TITLE     Stem cell inhibiting proteins
  JOURNAL   Patent: US 5856301-A 135 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT         7 a      4 c      2 g      5 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        746 ATGTTGCTGACTT 758
              |||||||||||||
Db         14 ATGTTGCTGACTT 2


RESULT 398
AR053125/c
LOCUS       AR053125                 18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 31 from patent US 5834183.
ACCESSION   AR053125
VERSION     AR053125.1  GI:5977987
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Orr,H.T., Ranum,L.P.W., Chung,M.-y. and Zoghbi,H.Y.
  TITLE     Gene sequence for spinocerebellar ataxia type 1 and method for
            diagnosis
  JOURNAL   Patent: US 5834183-A 31 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT         0 a      2 c     12 g      4 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        592 CCCCCCACCAGCC 604
              |||||||||||||
Db         18 CCCCCCACCAGCC 6


RESULT 399
AR085593
LOCUS       AR085593                 18 bp    DNA     linear   PAT 01-SEP-2000
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DEFINITION  Sequence 29 from patent US 5981732.
ACCESSION   AR085593
VERSION     AR085593.1  GI:10012360
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense modulation of G-alpha-13 expression
  JOURNAL   Patent: US 5981732-A 29 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        4 a      7 c      6 g      1 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        718 GCCCAGCAGCAGG 730
              |||||||||||||
Db          4 GCCCAGCAGCAGG 16


RESULT 400
AR297049/c
LOCUS       AR297049                 18 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 8784 from patent US 6537751.
ACCESSION   AR297049
VERSION     AR297049.1  GI:31684333
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 8784 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT       10 a      2 c      6 g      0 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1140 TGCCTTTTTTTCT 1152
              |||||||||||||
Db         17 TGCCTTTTTTTCT 5


RESULT 401
AX378610/c
LOCUS       AX378610                 18 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 399 from Patent WO0206525.
ACCESSION   AX378610
VERSION     AX378610.1  GI:19574463
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cohen,D., Blumenfeld,M., Chumakov,I., Abderrahim,H. and Bihain,B.
  TITLE     Obesity associated biallelic marker maps
  JOURNAL   Patent: WO 0206525-A 399 24-JAN-2002;
            GENSET (FR)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     primer_bind     1. .18
                     /note="downstream amplification primer 99-27595 for SEQ
                     57, in complement"
BASE COUNT        6 a      3 c      5 g      4 t

  Query Match             1.0%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        325 CTGCATCATCCTG 337
              |||||||||||||
Db         18 CTGCATCATCCTG 6


RESULT 402
BD096968
LOCUS       BD096968                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  SAG:apoptosis sensitivity gene.
ACCESSION   BD096968
VERSION     BD096968.1  GI:22642556
KEYWORDS    JP 2001526063-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Sun,Y.
  TITLE     SAG:apoptosis sensitivity gene
  JOURNAL   Patent: JP 2001526063-A 3 18-DEC-2001;
            WARNER LAMBERT CO
COMMENT     OS   Unidentified
            PN   JP 2001526063-A/3
            PD   18-DEC-2001
            PF   15-DEC-1998 JP 2000525451
            PR   19-DEC-1997 US    60/068179,11-SEP-1998 US    60/099840 PI
            YI SUN
            PC   C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61P35/00,
            PC   A61P39/06,
            PC   A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12Q1/68,
            PC   G01N33/50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            CC   /desc = 'oligonucleotide P1 downstream primer' FH   Key
                 Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      1 c      1 g     13 t      1 others

  Query Match             1.0%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 2.8e+02;
  Matches   13;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTTG 1157
              |||||||| |||||:
Db         4 CTTTTTTTTTTTTTR 18


RESULT 403
A57738
LOCUS       A57738                   16 bp    DNA     linear   PAT 03-MAR-1998
DEFINITION  Sequence 1 from Patent WO9633287.
ACCESSION   A57738
VERSION     A57738.1  GI:3713562
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
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            unclassified.
REFERENCE   1
  AUTHORS   Garchon,H. and Bach,J.
  TITLE     JUVENILE GLAUCOMA DETECTION PROCESS
  JOURNAL   Patent: WO 9633287-A 1 24-OCT-1996;
            INST NAT SANTE RECH MED (FR)
COMMENT     Other publication FR 2733251 961025.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      9 c      1 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 2.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1042 TCTTCCCACGACAGCC 1057
              ||||||||| || |||
Db          1 TCTTCCCACCACTGCC 16


RESULT 404
AX359760/c
LOCUS       AX359760                  16 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 64 from Patent WO0200691.
ACCESSION   AX359760
VERSION     AX359760.1  GI:18675467
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vernet,C.A., Tchernev,V., Putturajan,M., Malyankar,U.M., Gusev,V.,
            Herrmann,J.L., Macdougall,J.R., Rastelli,L., Zhong,H., Spytek,K.A.,
            Shenoy,S., Gerlach,V.L., Gangolli,E.A., Stone,D.J. and Smithson,G.
  TITLE     Novel polynucleotides and polypeptides encoded thereby
  JOURNAL   Patent: WO 0200691-A 64 03-JAN-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT       14 a      1 c      1 g      0 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 2.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1141 GCCTTTTTTTCTTTTT 1156
              || ||||||| |||||
Db         16 GCTTTTTTTTTTTTT 1


RESULT 405
AX663407
LOCUS       AX663407                  16 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 33 from Patent WO02097126.
ACCESSION   AX663407
VERSION     AX663407.1  GI:29163747
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weizenegger,M.
  TITLE     Method for detecting gram-positive bacteria
  JOURNAL   Patent: WO 02097126-A 33 05-DEC-2002;
            Hain Lifeschience GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Sonde"
BASE COUNT        4 a      6 c      4 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 2.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        598 ACCAGCCTGAAGCCTG 613
              |||| ||||||||| ||
Db          1 ACCACCCTGAAGCGTG 16


RESULT 406
BD145086
LOCUS       BD145086                  16 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145086
VERSION     BD145086.1  GI:27850844
KEYWORDS    JP 2002119291-A/67.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 67 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/67
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                 examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probec labeled with BODIBY FL/C6 upon the  CC
                 hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        0 a      6 c      2 g      8 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 2.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1214 CCTTCCCTGTACATTT 1229
              |||||||||| | |||
Db          1 CCTTCCCTGTTCGTTT 16


RESULT 407
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BD166093
LOCUS       BD166093                 16 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166093
VERSION     BD166093.1  GI:27871905
KEYWORDS    JP 2002191372-A/73.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 73 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/73
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                  labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        0 a      6 c      2 g      8 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 2.5e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1214 CCTTCCCTGTACATTT 1229
              |||||||||| | |||
Db          1 CCTTCCCTGTTCGTTT 16


RESULT 408
AR039807
LOCUS       AR039807                 17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 655 from patent US 5807743.
ACCESSION   AR039807
VERSION     AR039807.1  GI:5959170
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T. and McSwiggen,J.A.
  TITLE     Interleukin-2 receptor gamma-chain ribozymes
  JOURNAL   Patent: US 5807743-A 655 15-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        4 a      7 c      4 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        227 CTCAGCCTCAGGCATC 242
              || |||||||||| |
Db          1 CTGAGCCTCAGGCAAC 16


RESULT 409
AR039873
LOCUS       AR039873                 17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 721 from patent US 5807743.
ACCESSION   AR039873
VERSION     AR039873.1  GI:5959236
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T. and McSwiggen,J.A.
  TITLE     Interleukin-2 receptor gamma-chain ribozymes
  JOURNAL   Patent: US 5807743-A 721 15-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        3 a      8 c      4 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        625 GACCAGCTCCAGGAGC 640
              | ||||||||||||| |
Db          1 GTCCAGCTCCAGGACC 16


RESULT 410
AR045627
LOCUS       AR045627                 17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 420 from patent US 5817796.
ACCESSION   AR045627
VERSION     AR045627.1  GI:5967092
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL   Patent: US 5817796-A 420 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        1 a      8 c      3 g      5 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        795 CCTGGCTCGCTCCCTG 810
              |||||||| || ||||
Db          2 CCTGGCTCCCTACCTG 17


RESULT 411
AR047238
LOCUS       AR047238                 17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2031 from patent US 5817796.
ACCESSION   AR047238
VERSION     AR047238.1  GI:5968703
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL   Patent: US 5817796-A 2031 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        6 a      0 c      3 g      8 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1095 TGAACGTAATTATGTA 1110
              |||| || ||||||||
Db          1 TGAAAGTTATTATGTA 16


RESULT 412
AR057523/c
LOCUS       AR057523                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1727 from patent US 5837542.
ACCESSION   AR057523
VERSION     AR057523.1  GI:5983100
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
  JOURNAL   Patent: US 5837542-A 1727 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        4 a      3 c      7 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        334 CCTGGTGATAGTCACA 349
              |||||||||| || ||
Db         17 CCTGGTGATACTCCCA 2


RESULT 413
AR057733/c
LOCUS       AR057733                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1937 from patent US 5837542.
ACCESSION   AR057733
VERSION     AR057733.1  GI:5983310
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
  JOURNAL   Patent: US 5837542-A 1937 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        4 a      3 c      7 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        334 CCTGGTGATAGTCACA 349
              |||||||||| || ||
Db         17 CCTGGTGATACTCCCA 2


RESULT 414
AR091870
LOCUS       AR091870                  17 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 79 from patent US 5994524.
ACCESSION   AR091870
VERSION     AR091870.1  GI:10018624
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Matsushima,K., Matsumoto,Y., Yamada,Y., Sato,K., Tsuchiya,M. and
            Yamazaki,T.
  TITLE     Polynucleotides which encode reshaped IL-8-specific antibodies and
            methods to produce the same
  JOURNAL   Patent: US 5994524-A 79 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        5 a      7 c      4 g      1 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        870 CCCCACAGCCAAGTTC 885
              ||||| ||||||| ||
Db          2 CCCCAAAGCCAAGGTC 17


RESULT 415
AR115281/c
LOCUS       AR115281                  17 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 1727 from patent US 6132967.
ACCESSION   AR115281
VERSION     AR115281.1  GI:14095603
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
  JOURNAL   Patent: US 6132967-A 1727 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        4 a      3 c      7 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        334 CCTGGTGATAGTCACA 349
              |||||||||| || ||
Db         17 CCTGGTGATACTCCCA 2


RESULT 416
AR115491/c
LOCUS       AR115491                  17 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 1937 from patent US 6132967.
ACCESSION   AR115491
VERSION     AR115491.1  GI:14095813
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
  JOURNAL   Patent: US 6132967-A 1937 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        4 a      3 c      7 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        334 CCTGGTGATAGTCACA 349
              ||||||||||  || ||
Db         17 CCTGGTGATACTCCCA 2


RESULT 417
AR157778
LOCUS       AR157778                  17 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 79 from patent US 6245894.
ACCESSION   AR157778
VERSION     AR157778.1  GI:16218788
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Matsushima,K., Matsumoto,Y., Yamada,Y., Sato,K., Tsuchiya,M. and
            Yamazaki,T.
  TITLE     Reshaped human antibody to human interleukin-8
  JOURNAL   Patent: US 6245894-A 79 12-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        5 a      7 c      4 g      1 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        870 CCCCACAGCCAAGTTC 885
              |||||  |||||||  ||
Db          2 CCCCAAAGCCAAGGTC 17


RESULT 418
AR188886/c
LOCUS       AR188886                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 4374 from patent US 6346398.
ACCESSION   AR188886
VERSION     AR188886.1  GI:20234851
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 4374 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        2 a      3 c      5 g      7 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         41 CAAAATCTTAGCATAC 56
              ||||||| |||| ||
Db         17 CAAAATCTGAGCAGAC 2


RESULT 419
AR192436
LOCUS       AR192436                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 7924 from patent US 6346398.
ACCESSION   AR192436
VERSION     AR192436.1  GI:20238401
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 7924 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        3 a      7 c      2 g      5 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         47 CTTAGCATACTCCTCA 62
              ||| ||||||| ||||
Db          1 CTTCGCATACTGCTCA 16


RESULT 420
AR195610
LOCUS       AR195610                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 75 from patent US 6350934.
ACCESSION   AR195610
VERSION     AR195610.1  GI:20245047
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
            Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
  TITLE     Nucleic acid encoding delta-9 desaturase
  JOURNAL   Patent: US 6350934-A 75 26-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        1 a      6 c      6 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        891 GCTGCGGTACAGCGTG 906
              |||||||| |||| ||
Db          1 GCTGCGGTTCAGCCTG 16


RESULT 421
AR196421
LOCUS       AR196421                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 886 from patent US 6350934.
ACCESSION   AR196421
VERSION     AR196421.1  GI:20245858
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
            Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
  TITLE     Nucleic acid encoding delta-9 desaturase
  JOURNAL   Patent: US 6350934-A 886 26-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        2 a      1 c      2 g     12 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1103 ATTATGTAGTTTTCTG 1118
              ||| |||| |||||||
Db          2 ATTTTGTATTTTTCTG 17


RESULT 422
AR286016
LOCUS       AR286016                 17 bp    RNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 388 from patent US 6528640.
ACCESSION   AR286016
VERSION     AR286016.1  GI:29723612
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
            Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
  TITLE     Synthetic ribonucleic acids with RNAse activity
  JOURNAL   Patent: US 6528640-A 388 04-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        2 a     10 c      3 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        589 CTGCCCCCCACCAGCC 604
              ||||||| | ||||||
Db          2 CTGCCCCGCTCCAGCC 17


RESULT 423
AX217713/c
LOCUS       AX217713                 17 bp    mRNA    linear   PAT 07-SEP-2001
DEFINITION  Sequence 3155 from Patent WO0159103.
ACCESSION   AX217713
VERSION     AX217713.1  GI:15527774
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 3155 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
BASE COUNT        1 a      4 c      4 g      8 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        385 CCAGAGGTGGCAGCAA 400
              |||||  |||||||||
Db         17 CCAGAAATGGCAGCAA 2


RESULT 424
AX218185/c
LOCUS       AX218185                 17 bp    mRNA    linear   PAT 07-SEP-2001
DEFINITION  Sequence 3627 from Patent WO0159103.
ACCESSION   AX218185
VERSION     AX218185.1  GI:15528246
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 3627 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
BASE COUNT        4 a      3 c      2 g      8 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        437 TCAGAAAGTTGCTGAA 452
              | |||||||||| ||
Db         17 TAAGAAAGTTGCTCAA 2


RESULT 425
AX266451/c
LOCUS       AX266451                 17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 3842 from Patent WO0173002.
ACCESSION   AX266451
VERSION     AX266451.1  GI:16515250
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 3842 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      3 c      7 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
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  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        974 TCACTTGACCAGTCCC 989
              |||  ||||||||||||
Db         17 TCATCTGACCAGTCCC 2


RESULT 426
AX266452
LOCUS       AX266452                 17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 3843 from Patent WO0173002.
ACCESSION   AX266452
VERSION     AX266452.1  GI:16515251
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 3843 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      7 c      3 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        974 TCACTTGACCAGTCCC 989
              |||  ||||||||||||
Db          1 TCATCTGACCAGTCCC 16


RESULT 427
AX266703
LOCUS       AX266703                 17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 4094 from Patent WO0173002.
ACCESSION   AX266703
VERSION     AX266703.1  GI:16515502
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 4094 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      2 c      9 g      6 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1235 TGGTGCTGGACGTGGC 1250
              |||||  ||| ||||||
Db          1 TGGTGGTGGTCGTGGC 16


RESULT 428
AX266704/c
LOCUS       AX266704                 17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 4095 from Patent WO0173002.
ACCESSION   AX266704
VERSION     AX266704.1  GI:16515503
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 4095 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        6 a      9 c      2 g      0 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1235 TGGTGCTGGACGTGGC 1250
              |||||  ||| ||||||
Db         17 TGGTGGTGGTCGTGGC 2


RESULT 429
AX272956
LOCUS       AX272956                 17 bp    mRNA    linear   PAT 29-OCT-2001
DEFINITION  Sequence 525 from Patent WO0162911.
ACCESSION   AX272956
VERSION     AX272956.1  GI:16545693
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
            Ellis,J.H.
  TITLE     Method and reagent for the inhibition of grid
  JOURNAL   Patent: WO 0162911-A 525 30-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      5 c      4 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        287 CAGCAGCAATGTCTGC 302
              |||||||  || |||||
Db          2 CAGCAGCGATATCTGC 17


RESULT 430
AX273048/c
LOCUS       AX273048                 17 bp    mRNA    linear   PAT 29-OCT-2001
DEFINITION  Sequence 617 from Patent WO0162911.
ACCESSION   AX273048
VERSION     AX273048.1  GI:16545785
KEYWORDS    .
```

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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
            Ellis,J.H.
  TITLE     Method and reagent for the inhibition of grid
  JOURNAL   Patent: WO 0162911-A 617 30-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      8 c      3 g      1 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        295 ATGTCTGCTGTGGGGG 310
              ||  ||||||||||||
Db         16 ATCGCTGCTGTGGGGG 1


RESULT 431
AX273142
LOCUS       AX273142                 17 bp    mRNA    linear   PAT 29-OCT-2001
DEFINITION  Sequence 711 from Patent WO0162911.
ACCESSION   AX273142
VERSION     AX273142.1  GI:16545879
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
            Ellis,J.H.
  TITLE     Method and reagent for the inhibition of grid
  JOURNAL   Patent: WO 0162911-A 711 30-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      5 c      4 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        287 CAGCAGCAATGTCTGC 302
              |||||||  || |||||
Db          1 CAGCAGCGATATCTGC 16


RESULT 432
AX324733/c
LOCUS       AX324733                 17 bp    DNA     linear   PAT 02-SEP-2002
DEFINITION  Sequence 871 from Patent WO0192512.
ACCESSION   AX324733
VERSION     AX324733.1  GI:18095486
KEYWORDS    .
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
  TITLE     Targeted chromosomal genomic alterations in plants using modified
            single stranded oligonucleotides
  JOURNAL   Patent: WO 0192512-A 871 06-DEC-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4577"
BASE COUNT        5 a      3 c      5 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        164 GATCCTCAAGGTCTCG 179
              |||||||  || |||||
Db         17 GATCCTCTAGATCTCG 2


RESULT 433
AX324734
LOCUS       AX324734                 17 bp    DNA     linear   PAT 02-SEP-2002
DEFINITION  Sequence 872 from Patent WO0192512.
ACCESSION   AX324734
VERSION     AX324734.1  GI:18095487
KEYWORDS    .
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
  TITLE     Targeted chromosomal genomic alterations in plants using modified
            single stranded oligonucleotides
  JOURNAL   Patent: WO 0192512-A 872 06-DEC-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4577"
BASE COUNT        4 a      5 c      3 g      5 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        164 GATCCTCAAGGTCTCG 179
              |||||||  || |||||
Db          1 GATCCTCTAGATCTCG 16


RESULT 434
AX324749/c
LOCUS       AX324749                 17 bp    DNA     linear   PAT 02-SEP-2002
DEFINITION  Sequence 887 from Patent WO0192512.
ACCESSION   AX324749
VERSION     AX324749.1  GI:18095502
KEYWORDS    .
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
  TITLE     Targeted chromosomal genomic alterations in plants using modified
            single stranded oligonucleotides
  JOURNAL   Patent: WO 0192512-A 887 06-DEC-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
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     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4530"
BASE COUNT        5 a      3 c      5 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        164 GATCCTCAAGGTCTCG 179
              ||||||| || |||||
Db         17 GATCCTCTAGATCTCG 2


RESULT 435
AX324750
LOCUS       AX324750                 17 bp    DNA     linear   PAT 02-SEP-2002
DEFINITION  Sequence 888 from Patent WO0192512.
ACCESSION   AX324750
VERSION     AX324750.1  GI:18095503
KEYWORDS    .
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
  TITLE     Targeted chromosomal genomic alterations in plants using modified
            single stranded oligonucleotides
  JOURNAL   Patent: WO 0192512-A 888 06-DEC-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4530"
BASE COUNT        4 a      5 c      3 g      5 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        164 GATCCTCAAGGTCTCG 179
              ||||||| || |||||
Db          1 GATCCTCTAGATCTCG 16


RESULT 436
AX422141
LOCUS       AX422141                 17 bp    mRNA    linear   PAT 18-JUN-2002
DEFINITION  Sequence 477 from Patent WO0188124.
ACCESSION   AX422141
VERSION     AX422141.1  GI:21525523
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 477 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      0 c      5 g     10 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1325 TTGTAGATCTTGTGTT 1340
              |||| ||| |||||||
Db          1 TTGTGGATTTTGTGTT 16


RESULT 437
AX422668
LOCUS       AX422668                 17 bp    mRNA    linear   PAT 18-JUN-2002
DEFINITION  Sequence 1004 from Patent WO0188124.
ACCESSION   AX422668
VERSION     AX422668.1  GI:21526050
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 1004 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      6 c      3 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        713 CTGTGGCCCAGCAGCA 728
              |||||||||| || ||
Db          2 CTGTGGCCCATCAACA 17


RESULT 438
AX422670
LOCUS       AX422670                 17 bp    mRNA    linear   PAT 18-JUN-2002
DEFINITION  Sequence 1006 from Patent WO0188124.
ACCESSION   AX422670
VERSION     AX422670.1  GI:21526052
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 1006 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      5 c      4 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        714 TGTGGCCCAGCAGCAG 729
              ||||||||| || |||
Db          1 TGTGGCCCATCAACAG 16
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RESULT 439
AX423116/c
LOCUS       AX423116                  17 bp    mRNA    linear   PAT 18-JUN-2002
DEFINITION  Sequence 1452 from Patent WO0188124.
ACCESSION   AX423116
VERSION     AX423116.1  GI:21526498
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 1452 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      7 c      2 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        824 TGATGCAGCTGAAGCT 839
              ||||||||||| || |
Db         17 TGATGCAGCTGGAGTT 2


RESULT 440
AX423597
LOCUS       AX423597                  17 bp    mRNA    linear   PAT 18-JUN-2002
DEFINITION  Sequence 1933 from Patent WO0188124.
ACCESSION   AX423597
VERSION     AX423597.1  GI:21526979
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 1933 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        8 a      5 c      3 g      1 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         66 ACCCACATAGGATGAA 81
              ||||||| | ||||||
Db          2 ACCCACAGAAGATGAA 17


RESULT 441
AX423644/c
LOCUS       AX423644                  17 bp    mRNA    linear   PAT 18-JUN-2002
DEFINITION  Sequence 1980 from Patent WO0188124.
ACCESSION   AX423644
VERSION     AX423644.1  GI:21527026
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 1980 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        6 a      1 c      7 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         50 AGCATACTCCTCAATT 65
              ||||| |||||| ||
Db         17 AGCATCCTCCTCATTT 2


RESULT 442
AX475189/c
LOCUS       AX475189                  17 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 410 from Patent WO0224750.
ACCESSION   AX475189
VERSION     AX475189.1  GI:22214474
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     Human kidney tumor overexpressed membrane protein 1
  JOURNAL   Patent: WO 0224750-A 410 28-MAR-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      8 c      5 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1249 GCCATGTGAGGCCAGG 1264
              ||| |||| |||||||
Db         17 GCCCTGTGGGGCCAGG 2


RESULT 443
AX475191/c
LOCUS       AX475191                  17 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 412 from Patent WO0224750.
ACCESSION   AX475191
VERSION     AX475191.1  GI:22214476
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
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  TITLE     Human kidney tumor overexpressed membrane protein 1
  JOURNAL   Patent: WO 0224750-A 412 28-MAR-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      9 c      5 g      1 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1248 GGCCATGTGAGGCCAG 1263
              |||| |||| ||||||
Db         16 GGCCCTGTGGGGCCAG 1


RESULT 444
AX500509/c
LOCUS       AX500509                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 1816 from Patent EP1229046.
ACCESSION   AX500509
VERSION     AX500509.1  GI:23382802
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 1816 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      4 c      4 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       239 CATCTGCATCTGGGAC 254
             ||| | ||||||||||
Db        17 CATGTTCATCTGGGAC 2


RESULT 445
AX500510/c
LOCUS       AX500510                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 1817 from Patent EP1229046.
ACCESSION   AX500510
VERSION     AX500510.1  GI:23382803
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 1817 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      4 c      5 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       239 CATCTGCATCTGGGAC 254
             ||| | ||||||||||
Db        16 CATGTTCATCTGGGAC 1


RESULT 446
AX502777
LOCUS       AX502777                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 4084 from Patent EP1229046.
ACCESSION   AX502777
VERSION     AX502777.1  GI:23385070
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 4084 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      4 c      2 g      9 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1137 CTATGCCTTTTTTTCT 1152
              |||||| ||| |||||
Db          2 CTATGCATTTGTTTCT 17


RESULT 447
AX502778
LOCUS       AX502778                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 4085 from Patent EP1229046.
ACCESSION   AX502778
VERSION     AX502778.1  GI:23385071
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 4085 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      3 c      2 g      9 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1137 CTATGCCTTTTTTTCT 1152
              |||||| ||| |||||
Db          1 CTATGCATTTGTTTCT 16
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RESULT 448
AX530711
LOCUS       AX530711                  17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 220 from Patent EP1239051.
ACCESSION   AX530711
VERSION     AX530711.1  GI:25253227
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 220 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      7 c      4 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        160 CGCTGATCCTCAAGGT 175
              ||||| ||||| ||||
Db          2 CGCTGCTCCTCCAGGT 17


RESULT 449
AX530712
LOCUS       AX530712                  17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 221 from Patent EP1239051.
ACCESSION   AX530712
VERSION     AX530712.1  GI:25253229
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 221 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      7 c      5 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        160 CGCTGATCCTCAAGGT 175
              ||||| ||||| ||||
Db          1 CGCTGCTCCTCCAGGT 16


RESULT 450
AX531738
LOCUS       AX531738                  17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 1247 from Patent EP1239051.
ACCESSION   AX531738
VERSION     AX531738.1  GI:25255259
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 1247 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      9 c      2 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        570 GCTCCAGCAGGCCCTC 585
              |||||||||  |||||
Db          2 GCTCCAGCAACCCCTC 17


RESULT 451
AX531739
LOCUS       AX531739                  17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 1248 from Patent EP1239051.
ACCESSION   AX531739
VERSION     AX531739.1  GI:25255261
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 1248 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      9 c      2 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        570 GCTCCAGCAGGCCCTC 585
              |||||||||  |||||
Db          1 GCTCCAGCAACCCCTC 16


RESULT 452
AX531750/c
LOCUS       AX531750                  17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 1259 from Patent EP1239051.
ACCESSION   AX531750
VERSION     AX531750.1  GI:25255279
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 1259 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
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     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      8 c      2 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        268 TGGCTGATCAAAGAGG 283
              ||| |||||| |||||
Db         17 TGGGTGATCACAGAGG 2


RESULT 453
AX531758/c
LOCUS       AX531758                  17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 1267 from Patent EP1239051.
ACCESSION   AX531758
VERSION     AX531758.1  GI:25255295
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 1267 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      7 c      4 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        261 CCTGGGCTGGCTGATC 276
              | |||||||| |||||
Db         16 CATGGGCTGGGTGATC 1


RESULT 454
AX532257/c
LOCUS       AX532257                  17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 1766 from Patent EP1239051.
ACCESSION   AX532257
VERSION     AX532257.1  GI:25256299
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 1766 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      3 c      5 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        906 GGCCCTGGTCCTAAAG 921
              | |||| |||||||||
Db         17 GACCCTTGTCCTAAAG 2


RESULT 455
AX532258/c
LOCUS       AX532258                  17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 1767 from Patent EP1239051.
ACCESSION   AX532258
VERSION     AX532258.1  GI:25256301
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 1767 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      3 c      5 g      5 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        906 GGCCCTGGTCCTAAAG 921
              | |||| |||||||||
Db         16 GACCCTTGTCCTAAAG 1


RESULT 456
AX578402
LOCUS       AX578402                  17 bp    mRNA    linear   PAT 10-JAN-2003
DEFINITION  Sequence 240 from Patent WO0211674.
ACCESSION   AX578402
VERSION     AX578402.1  GI:27647604
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
            and Grupe,A.
  TITLE     Method and reagent for the inhibition of calcium activated chloride
            channel-1 (clca-1)
  JOURNAL   Patent: WO 0211674-A 240 14-FEB-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
            Thompson, James (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      3 c      7 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CAGGCAGTTGAGGTGG 19
              ||| |||||||| |||
Db          1 CAGACAGTTGAGCTGG 16
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RESULT 457
AX578578/c
LOCUS       AX578578                 17 bp    mRNA    linear   PAT 10-JAN-2003
DEFINITION  Sequence 416 from Patent WO0211674.
ACCESSION   AX578578
VERSION     AX578578.1  GI:27647780
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
            and Grupe,A.
  TITLE     Method and reagent for the inhibition of calcium activated chloride
            channel-1 (clca-1)
  JOURNAL   Patent: WO 0211674-A 416 14-FEB-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
            Thompson, James (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      7 c      3 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        660 GGTCGGGGACTTGGCC 675
              |||||| || ||||||
Db         16 GGTCGGTGATTTGGCC 1


RESULT 458
AX579153/c
LOCUS       AX579153                 17 bp    mRNA    linear   PAT 10-JAN-2003
DEFINITION  Sequence 991 from Patent WO0211674.
ACCESSION   AX579153
VERSION     AX579153.1  GI:27648355
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
            and Grupe,A.
  TITLE     Method and reagent for the inhibition of calcium activated chloride
            channel-1 (clca-1)
  JOURNAL   Patent: WO 0211674-A 991 14-FEB-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
            Thompson, James (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        7 a      4 c      3 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1149 TTCTTTTTGGAAGTAA 1164
              ||| |||||||||| |
Db         17 TTCGTTTTGGAAGTCA 2


RESULT 459
AX579154/c
LOCUS       AX579154                 17 bp    mRNA    linear   PAT 10-JAN-2003
DEFINITION  Sequence 992 from Patent WO0211674.
ACCESSION   AX579154
VERSION     AX579154.1  GI:27648356
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
            and Grupe,A.
  TITLE     Method and reagent for the inhibition of calcium activated chloride
            channel-1 (clca-1)
  JOURNAL   Patent: WO 0211674-A 992 14-FEB-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
            Thompson, James (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        7 a      5 c      2 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1149 TTCTTTTTGGAAGTAA 1164
              ||| |||||||||| |
Db         16 TTCGTTTTGGAAGTCA 1


RESULT 460
AX579663
LOCUS       AX579663                 17 bp    mRNA    linear   PAT 10-JAN-2003
DEFINITION  Sequence 1501 from Patent WO0211674.
ACCESSION   AX579663
VERSION     AX579663.1  GI:27648865
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
            and Grupe,A.
  TITLE     Method and reagent for the inhibition of calcium activated chloride
            channel-1 (clca-1)
  JOURNAL   Patent: WO 0211674-A 1501 14-FEB-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
            Thompson, James (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      3 c      6 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GCAGGCAGTTGAGGTG 18
              |||| |||||||| ||
Db          2 GCAGACAGTTGAGCTG 17


RESULT 461
AX579937/c
LOCUS       AX579937                 17 bp    mRNA    linear   PAT 10-JAN-2003
DEFINITION  Sequence 1775 from Patent WO0211674.
ACCESSION   AX579937
VERSION     AX579937.1  GI:27649139
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KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
            and Grupe,A.
  TITLE     Method and reagent for the inhibition of calcium activated chloride
            channel-1 (clca-1)
  JOURNAL   Patent: WO 0211674-A 1775 14-FEB-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
            Thompson, James (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        8 a      5 c      2 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1146 TTTTTCTTTTTGGAAG 1161
                || ||| |||||||||
Db         16 TTGTTCGTTTTGGAAG 1


RESULT 462
AX615895/c
LOCUS       AX615895                  17 bp    DNA     linear   PAT 20-FEB-2003
DEFINITION  Sequence 702 from Patent EP1262488.
ACCESSION   AX615895
VERSION     AX615895.1  GI:28446941
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y. and Nguyen,C.T.
  TITLE     Human lccl-domain containing protein
  JOURNAL   Patent: EP 1262488-A 702 04-DEC-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      8 c      3 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        525 GCCGGAGGAGCAGCTG 540
                | | ||||||||||||
Db         17 GGCTGAGGAGCAGCTG 2


RESULT 463
AX615896/c
LOCUS       AX615896                  17 bp    DNA     linear   PAT 20-FEB-2003
DEFINITION  Sequence 703 from Patent EP1262488.
ACCESSION   AX615896
VERSION     AX615896.1  GI:28446942
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y. and Nguyen,C.T.
  TITLE     Human lccl-domain containing protein
  JOURNAL   Patent: EP 1262488-A 703 04-DEC-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      9 c      3 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        525 GCCGGAGGAGCAGCTG 540
                | | ||||||||||||
Db         16 GGCTGAGGAGCAGCTG 1


RESULT 464
AX634594/c
LOCUS       AX634594                  17 bp    mRNA    linear   PAT 21-FEB-2003
DEFINITION  Sequence 1733 from Patent EP1260586.
ACCESSION   AX634594
VERSION     AX634594.1  GI:28470208
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 1733 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="mRNA"
                     /db_xref="taxon:32644"
BASE COUNT        4 a      3 c      7 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        334 CCTGGTGATAGTCACA 349
                ||||||||||  || ||
Db         17 CCTGGTGATACTCCCA 2


RESULT 465
AX634818/c
LOCUS       AX634818                  17 bp    mRNA    linear   PAT 21-FEB-2003
DEFINITION  Sequence 1957 from Patent EP1260586.
ACCESSION   AX634818
VERSION     AX634818.1  GI:28470432
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
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genes
JOURNAL Patent: EP 1260586-A 1957 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
source 1. .17
/organism="unidentified"
/mol_type="mRNA"
/db_xref="taxon:32644"
BASE COUNT 4 a 3 c 7 g 3 t

Query Match 0.9%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 334 CCTGGTGATAGTCACA 349
|||||||||| || ||
Db 17 CCTGGTGATACTCCCA 2

RESULT 466
AX671731
LOCUS AX671731 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 176 from Patent WO03004526.
ACCESSION AX671731
VERSION AX671731.1 GI:29330079
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines
JOURNAL Patent: WO 03004526-A 176 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 5 a 5 c 4 g 3 t

Query Match 0.9%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1069 ATCAGGCAGGCTCTTC 1084
|||| |||||| ||||
Db 2 ATCAAGCAGGCACTTC 17

RESULT 467
AX671969
LOCUS AX671969 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 414 from Patent WO03004526.
ACCESSION AX671969
VERSION AX671969.1 GI:29330317
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines
JOURNAL Patent: WO 03004526-A 414 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 2 a 3 c 1 g 11 t

Query Match 0.9%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1139 ATGCCTTTTTTTCTTT 1154
|| ||||||||||||
Db 2 ATCACTTTTTTTCTTT 17

RESULT 468
AX672540
LOCUS AX672540 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 985 from Patent WO03004526.
ACCESSION AX672540
VERSION AX672540.1 GI:29330888
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines
JOURNAL Patent: WO 03004526-A 985 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 8 a 2 c 5 g 2 t

Query Match 0.9%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 273 GATCAAAGAGGAAGCA 288
|||| ||||||||| |
Db 1 GATCCAAGAGGAAGAA 16

RESULT 469
AX672632/c
LOCUS AX672632 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 1077 from Patent WO03004526.
ACCESSION AX672632
VERSION AX672632.1 GI:29330980
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines
JOURNAL Patent: WO 03004526-A 1077 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 3 a 8 c 3 g 3 t

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  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GGCAGTTGAGGTGGAT 21
              ||||| | ||||||||
Db         17 GGCAGGTCAGGTGGAT 2


RESULT 470
AX673167
LOCUS       AX673167                 17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 1612 from Patent WO03004526.
ACCESSION   AX673167
VERSION     AX673167.1  GI:29331515
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 1612 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      3 c      1 g     11 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1139 ATGCCTTTTTTTCTTT 1154
              || |||||||||  |||
Db          2 ATCCCTTTTTTTATTT 17


RESULT 471
AX673340/c
LOCUS       AX673340                 17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 1785 from Patent WO03004526.
ACCESSION   AX673340
VERSION     AX673340.1  GI:29331688
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 1785 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      5 c      6 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1066 CCCATCAGGCAGGCTC 1081
              |||||||| ||| ||
Db         16 CCCATCAGGGAGGATC 1


RESULT 472
AX674420
LOCUS       AX674420                 17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 2865 from Patent WO03004526.
ACCESSION   AX674420
VERSION     AX674420.1  GI:29332768
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 2865 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      4 c      7 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        684 ATTTGGGAGCCAGCGG 699
              || |||||||||||  |
Db          2 ATCTGGGAGCCAGCAG 17


RESULT 473
AX687431
LOCUS       AX687431                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 163 from Patent EP1281758.
ACCESSION   AX687431
VERSION     AX687431.1  GI:29410125
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 163 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      6 c      4 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        222 AGCTCCTCAGCCTCAG 237
              ||||||||||  |||
Db          2 AGCTCCTCAGCAGCAG 17


RESULT 474
AX687432
```

```
LOCUS       AX687432                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 164 from Patent EP1281758.
ACCESSION   AX687432
VERSION     AX687432.1  GI:29410126
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 164 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      6 c      4 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        222 AGCTCCTCAGCCTCAG 237
              ||||||||||| |||
Db          1 AGCTCCTCAGCAGCAG 16


RESULT 475
AX687554/c
LOCUS       AX687554                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 286 from Patent EP1281758.
ACCESSION   AX687554
VERSION     AX687554.1  GI:29410250
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 286 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      5 c      7 g      1 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        371 GGGCCCAGCTTCCTCC 386
              ||| |||||| |||||
Db         17 GGGTCCAGCTGCCTCC 2


RESULT 476
AX687556/c
LOCUS       AX687556                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 288 from Patent EP1281758.
ACCESSION   AX687556
VERSION     AX687556.1  GI:29410252
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 288 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      6 c      6 g      1 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        370 GGGGCCCAGCTTCCTC 385
              |||| |||||| ||||
Db         16 GGGGTCCAGCTGCCTC 1


RESULT 477
AX687640/c
LOCUS       AX687640                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 372 from Patent EP1281758.
ACCESSION   AX687640
VERSION     AX687640.1  GI:29410336
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 372 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      5 c      5 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        626 ACCAGCTCCAGGAGCT 641
              | |||||||||| ||
Db         17 AGCAGCTCCAGGATCT 2


RESULT 478
AX687641/c
LOCUS       AX687641                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 373 from Patent EP1281758.
ACCESSION   AX687641
VERSION     AX687641.1  GI:29410337
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 373 05-FEB-2003;
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            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      4 c      6 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        626 ACCAGCTCCAGGAGCT 641
              | ||||||||||| ||
Db         16 AGCAGCTCCAGGATCT 1


RESULT 479
AX687648/c
LOCUS       AX687648                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 380 from Patent EP1281758.
ACCESSION   AX687648
VERSION     AX687648.1  GI:29410344
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 380 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      9 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        627 CCAGCTCCAGGAGCTC 642
              ||||| |||| |||||
Db         17 CCAGCACCAGCAGCTC 2


RESULT 480
AX687649/c
LOCUS       AX687649                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 381 from Patent EP1281758.
ACCESSION   AX687649
VERSION     AX687649.1  GI:29410345
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 381 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      3 c      8 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        627 CCAGCTCCAGGAGCTC 642
              ||||| |||| |||||
Db         16 CCAGCACCAGCAGCTC 1


RESULT 481
AX690654/c
LOCUS       AX690654                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 3386 from Patent EP1281758.
ACCESSION   AX690654
VERSION     AX690654.1  GI:29413535
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 3386 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      3 c      7 g      5 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        628 CAGCTCCAGGAGCTCT 643
              |||| |||| ||||||
Db         17 CAGCACCAGCAGCTCT 2


RESULT 482
AX690656/c
LOCUS       AX690656                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 3388 from Patent EP1281758.
ACCESSION   AX690656
VERSION     AX690656.1  GI:29413537
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 3388 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      3 c      8 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        627 CCAGCTCCAGGAGCTC 642
              ||||| |||| |||||
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Db         16 CCAGCACCAGCAGCTC 1


RESULT 483
AX690685
LOCUS       AX690685                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 3417 from Patent EP1281758.
ACCESSION   AX690685
VERSION     AX690685.1  GI:29413566
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 3417 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      5 c      5 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        520 AACCTGCCGGAGGAGC 535
              | |||||| |||||||
Db          2 ATCCTGCCTGAGGAGC 17


RESULT 484
AX690686
LOCUS       AX690686                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 3418 from Patent EP1281758.
ACCESSION   AX690686
VERSION     AX690686.1  GI:29413567
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 3418 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      5 c      5 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        520 AACCTGCCGGAGGAGC 535
              | |||||| |||||||
Db          1 ATCCTGCCTGAGGAGC 16


RESULT 485
AX692527
LOCUS       AX692527                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5259 from Patent EP1281758.
ACCESSION   AX692527
VERSION     AX692527.1  GI:29415485
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5259 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      0 c      1 g     15 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTGGA 1159
              ||||||| ||||| ||
Db          2 TTTTTTTTTTTTTTGA 17


RESULT 486
AX692528
LOCUS       AX692528                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5260 from Patent EP1281758.
ACCESSION   AX692528
VERSION     AX692528.1  GI:29415486
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5260 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      0 c      2 g     14 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTGGA 1159
              ||||||| ||||| ||
Db          1 TTTTTTTTTTTTTTGA 16


RESULT 487
AX692661/c
LOCUS       AX692661                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5393 from Patent EP1281758.
ACCESSION   AX692661
VERSION     AX692661.1  GI:29415619
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5393 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      8 c      2 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        762 GTGGCGGGTGGATGTA 777
              ||||||||||  ||||
Db         17 GTGGCGGGTGCTTGTA 2


RESULT 488
AX692663/c
LOCUS       AX692663                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5395 from Patent EP1281758.
ACCESSION   AX692663
VERSION     AX692663.1  GI:29415621
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5395 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        6 a      9 c      2 g      0 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        761 GGTGGCGGGTGGATGT 776
              ||||||||||  |||
Db         16 GGTGGCGGGTGCTTGT 1


RESULT 489
AX722347
LOCUS       AX722347                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 34 from Patent WO03025176.
ACCESSION   AX722347
VERSION     AX722347.1  GI:30422848
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 34 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
BASE COUNT        5 a      5 c      3 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         63 ATTACCCACATAGGAT 78
              ||  ||||||||||||
Db          2 ATCTCCCACATAGGAT 17


RESULT 490
AX722414
LOCUS       AX722414                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 101 from Patent WO03025176.
ACCESSION   AX722414
VERSION     AX722414.1  GI:30422915
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 101 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
BASE COUNT        4 a      2 c      3 g      8 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1174 AACATGTTTCTATAGG 1189
              | |||  ||||||||||
Db          2 ATCATTTTTCTATAGG 17


RESULT 491
AX722491/c
LOCUS       AX722491                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 178 from Patent WO03025176.
ACCESSION   AX722491
VERSION     AX722491.1  GI:30422992
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 178 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
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BASE COUNT        7 a      3 c      3 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        855 ATACCGCTTTGAGGTC 870
              |||| |||||||| ||
Db         16 ATACTGCTTTGAGATC 1


RESULT 492
AX722931
LOCUS       AX722931                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 618 from Patent WO03025176.
ACCESSION   AX722931
VERSION     AX722931.1  GI:30423432
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 618 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
BASE COUNT        3 a      4 c      4 g      6 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1069 ATCAGGCAGGCTCTTC 1084
              |||||  |||||||||
Db          2 ATCAGTTAGGCTCTTC 17


RESULT 493
AX725749/c
LOCUS       AX725749                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3436 from Patent WO03025176.
ACCESSION   AX725749
VERSION     AX725749.1  GI:30505092
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 3436 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
BASE COUNT        3 a      5 c      2 g      7 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        919 AAGGAGATGGCAGATC 934
              ||| ||||| ||||||
Db         16 AAGAAGATGTCAGATC 1


RESULT 494
AX727907/c
LOCUS       AX727907                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 5594 from Patent WO03025176.
ACCESSION   AX727907
VERSION     AX727907.1  GI:30507250
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 5594 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
BASE COUNT        2 a      7 c      2 g      6 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        919 AAGGAGATGGCAGATC 934
              |||| || ||||||||
Db         16 AAGGTGAAGGCAGATC 1


RESULT 495
AX729823
LOCUS       AX729823                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 1457 from Patent WO03025175.
ACCESSION   AX729823
VERSION     AX729823.1  GI:30509166
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 1457 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      3 c      1 g     11 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1139 ATGCCTTTTTTTCTTT 1154
              || |||||||| |||
Db          2 ATCCCTTTTTTTATTT 17
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RESULT 496
AX729852/c
LOCUS       AX729852                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 1486 from Patent WO03025175.
ACCESSION   AX729852
VERSION     AX729852.1  GI:30509195
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 1486 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      6 c      4 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GGCAGTTGAGGTGGAT 21
              |||| ||||| |||||
Db         17 GGCACTTGAGCTGGAT 2


RESULT 497
AX730009
LOCUS       AX730009                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 1643 from Patent WO03025175.
ACCESSION   AX730009
VERSION     AX730009.1  GI:30509352
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 1643 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        6 a      2 c      5 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        429 GAGCACGTTCAGAAAG 444
              || || ||||||||||
Db          1 GATCATGTTCAGAAAG 16


RESULT 498
AX731190
LOCUS       AX731190                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 2824 from Patent WO03025175.
ACCESSION   AX731190
VERSION     AX731190.1  GI:30510533
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 2824 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        8 a      2 c      5 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        273 GATCAAAGAGGAAGCA 288
              |||| |||||||||| |
Db          1 GATCCAAGAGGAAGAA 16


RESULT 499
AX731637
LOCUS       AX731637                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3271 from Patent WO03025175.
ACCESSION   AX731637
VERSION     AX731637.1  GI:30510980
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 3271 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      7 c      4 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        164 GATCCTCAAGGTCTCG 179
              ||||| || |||||||
Db          1 GATCCCCACGGTCTCG 16


RESULT 500
AX731808/c
LOCUS       AX731808                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3442 from Patent WO03025175.
ACCESSION   AX731808
VERSION     AX731808.1  GI:30511151
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 3442 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        6 a      2 c      4 g      5 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        983 CAGTCCCATTCAGATC 998
              |||| ||||| |||||
Db         16 CAGTTCCATTAAGATC 1


RESULT 501
AX732100/c
LOCUS       AX732100                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3734 from Patent WO03025175.
ACCESSION   AX732100
VERSION     AX732100.1  GI:30511443
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 3734 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      5 c      6 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1066 CCCATCAGGCAGGCTC 1081
              ||||||||| ||| ||
Db         16 CCCATCAGGGAGGATC 1


RESULT 502
AX733260/c
LOCUS       AX733260                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 4894 from Patent WO03025175.
ACCESSION   AX733260
VERSION     AX733260.1  GI:30512603
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 4894 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        7 a      3 c      3 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        855 ATACCGCTTTGAGGTC 870
              |||| |||||||| ||
Db         16 ATACTGCTTTGAGATC 1


RESULT 503
AX733554
LOCUS       AX733554                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 5188 from Patent WO03025175.
ACCESSION   AX733554
VERSION     AX733554.1  GI:30512897
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 5188 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      3 c      1 g     11 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1139 ATGCCTTTTTTTCTTT 1154
              ||  ||||||||||||
Db         2 ATCACTTTTTTTCTTT 17


RESULT 504
AX733723
LOCUS       AX733723                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 5357 from Patent WO03025175.
ACCESSION   AX733723
VERSION     AX733723.1  GI:30513066
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 5357 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
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     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      2 c      5 g      6 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        435 GTTCAGAAAGTTGCTG 450
              | ||||| ||||||||
Db          1 GATCAGATAGTTGCTG 16


RESULT 505
BD067612
LOCUS       BD067612                 17 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors.
ACCESSION   BD067612
VERSION     BD067612.1  GI:22613215
KEYWORDS    JP 2001511003-A/452.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Akhtar,S., Fell,P. and Mcswiggen,J.A.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors
  JOURNAL   Patent: JP 2001511003-A 452 07-AUG-2001;
            RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT     OS   Unidentified
            PN   JP 2001511003-A/452
            PD   07-AUG-2001
            PF   14-JAN-1998 JP 1998532913
            PR   31-JAN-1997 US    60/036476,04-DEC-1997 US    08/985162 PI
            SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
            C12N9/00,C07K14/71
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                 related to
            CC   levels of epidermal growth factor receptors
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="unidentified"
                      /mol_type="genomic RNA"
                      /db_xref="taxon:32644"
BASE COUNT        3 a      8 c      3 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        574 CAGCAGGCCCTCCGTC 589
              ||||||| ||||| ||
Db          1 CAGCAGGTCCTCCATC 16


RESULT 506
BD104458
LOCUS       BD104458                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD104458
VERSION     BD104458.1  GI:22650032
KEYWORDS    WO 0192572-A/562.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 562 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/562
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
BASE COUNT        1 a      7 c      6 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        803 GCTCCCTGCAGCCGAG 818
              ||| ||||| ||||||
Db          1 GCTGCCTGCCGCCGAG 16


RESULT 507
BD104949
LOCUS       BD104949                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD104949
VERSION     BD104949.1  GI:22650523
KEYWORDS    WO 0192572-A/1053.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 1053 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/1053
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
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BASE COUNT        4 a      4 c      7 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        531 GGAGCAGCTGGGTGCC 546
              |||||||||| | |||
Db          1 GGAGCAGCTGAGAGCC 16


RESULT 508
BD105040
LOCUS       BD105040                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD105040
VERSION     BD105040.1  GI:22650614
KEYWORDS    WO 0192572-A/1144.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 1144 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/1144
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
BASE COUNT        5 a      8 c      3 g      1 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        195 CCACCCGGACGCCGAC 210
              ||||| ||||||| ||
Db          2 CCACCAGGACGCCTAC 17


RESULT 509
BD105056
LOCUS       BD105056                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD105056
VERSION     BD105056.1  GI:22650630
KEYWORDS    WO 0192572-A/1160.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 1160 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/1160
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
BASE COUNT        4 a      4 c      7 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        531 GGAGCAGCTGGGTGCC 546
              |||||||||| | |||
Db          1 GGAGCAGCTGAGAGCC 16


RESULT 510
BD105105
LOCUS       BD105105                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD105105
VERSION     BD105105.1  GI:22650679
KEYWORDS    WO 0192572-A/1209.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 1209 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/1209
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
BASE COUNT        5 a      4 c      6 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy        346 CACAGTGGCCGAGTGA 361
              || | ||||||||||
Db          2 CAGACTGGCCGAGTGA 17


RESULT 511
I52679
LOCUS       I52679                    17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 420 from patent US 5646042.
ACCESSION   I52679
VERSION     I52679.1  GI:2473880
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 420 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        1 a      8 c      3 g      5 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        795 CCTGGCTCGCTCCCTG 810
              |||||||| || ||||
Db          2 CCTGGCTCCCTACCTG 17


RESULT 512
I54290
LOCUS       I54290                    17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 2031 from patent US 5646042.
ACCESSION   I54290
VERSION     I54290.1  GI:2475493
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 2031 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        6 a      0 c      3 g      8 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1095 TGAACGTAATTATGTA 1110
              |||| || ||||||||
Db          1 TGAAAGTTATTATGTA 16


RESULT 513
A07991
LOCUS       A07991                    18 bp    DNA     linear   PAT 01-SEP-1993
DEFINITION  Oligonucleotide W.
ACCESSION   A07991
VERSION     A07991.1  GI:411542
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Browne,M.J., Dodd,I. and Robinson,J.H.
  TITLE     Novel compounds
  JOURNAL   Patent: EP 0370711-A 39 30-MAY-1990;
            BEECHAM GROUP PLC
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        3 a      3 c      6 g      6 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1180 TTTCTATAGGTGAGTG 1195
              | ||| ||||||||||
Db          3 TCTCTCTAGGTGAGTG 18


RESULT 514
A42230
LOCUS       A42230                    18 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 18 from Patent EP0635574.
ACCESSION   A42230
VERSION     A42230.1  GI:2297722
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Selten,G.C., Van,G.R. and Swinkels,B.W.
  TITLE     Selection marker gene free recombinant strains, a method for
            obtaining them and the use of these strains
  JOURNAL   Patent: EP 0635574-A 18 25-JAN-1995;
            GIST BROCADES NV (NL)
COMMENT     Other publication CN 1098743 950215
            Other publication JP 7147971 950613
            Other publication BR 9402912 950411
            Other publication FI 943485 950124
            Other publication CA 2128589 950124
            Other publication AU 6862894 950202.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
                     /clone="AB3781"
BASE COUNT        3 a      6 c      6 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        368 TGGGGGCCCAGCTTCC 383
              | |||||||||| |||
Db          3 TTGGGGCCCAGCGTCC 18


RESULT 515
A44527/c
LOCUS       A44527                    18 bp    DNA     linear   PAT 07-MAR-1997
DEFINITION  Sequence 3 from Patent WO9513395.
ACCESSION   A44527
VERSION     A44527.1  GI:2299345
KEYWORDS    .
SOURCE      Staphylococcus aureus
  ORGANISM  Staphylococcus aureus
            Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Springer,W. and Endermann,R.
  TITLE     SPECIFIC GENE PROBES AND METHODS FOR QUANTITATIVE DETECTION OF
            METHICILLIN-RESISTANT STAPHYLOCOCCI
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  JOURNAL   Patent: WO 9513395-A 3 18-MAY-1995;
            BAYER AG (DE)
COMMENT     Other publication DE 4338119 950511.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Staphylococcus aureus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:1280"
BASE COUNT        7 a      1 c      4 g      6 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        321 ATACCTGCATCATCCT 336
              ||| |||||||||| |
Db         18 ATAACTGCATCATCTT 3


RESULT 516
A63090
LOCUS       A63090                  18 bp    DNA     linear   PAT 12-MAR-1998
DEFINITION  Sequence 17 from Patent WO9720197.
ACCESSION   A63090
VERSION     A63090.1  GI:3716954
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Arguello,R., Avakian,H. and Madrigal,A.
  TITLE     METHOD FOR IDENTIFYING AN UNKNOWN ALLELE
  JOURNAL   Patent: WO 9720197-A 17 05-JUN-1997;
            ANTHONY NOLAN BONE MARROW TRUS (GB)
COMMENT     Other publication AU 7703796 19970619.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        5 a      4 c      7 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        531 GGAGCAGCTGGGTGCC 546
              |||||||||| | |||
Db          1 GGAGCAGCTGAGAGCC 16


RESULT 517
AR039073
LOCUS       AR039073                18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 39 from patent US 5807730.
ACCESSION   AR039073
VERSION     AR039073.1  GI:5958436
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Ito,K., Yamaki,T., Arii,T., Tsuruoka,M. and Nakamura,T.
  TITLE     Nitrile hydratase
  JOURNAL   Patent: US 5807730-A 39 15-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        4 a      5 c      5 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        879 CAAGTTCCAGGAGCTG 894
              || | ||||||||||
Db          3 CACGATCCAGGAGCTG 18


RESULT 518
AR039074
LOCUS       AR039074                18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 40 from patent US 5807730.
ACCESSION   AR039074
VERSION     AR039074.1  GI:5958437
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Ito,K., Yamaki,T., Arii,T., Tsuruoka,M. and Nakamura,T.
  TITLE     Nitrile hydratase
  JOURNAL   Patent: US 5807730-A 40 15-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        3 a      5 c      6 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        879 CAAGTTCCAGGAGCTG 894
              || | ||||||||||
Db          3 CACGGTCCAGGAGCTG 18


RESULT 519
AR040123
LOCUS       AR040123                18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 971 from patent US 5807743.
ACCESSION   AR040123
VERSION     AR040123.1  GI:5959486
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Stinchcomb,D.T. and McSwiggen,J.A.
  TITLE     Interleukin-2 receptor gamma-chain ribozymes
  JOURNAL   Patent: US 5807743-A 971 15-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        3 a      7 c      4 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        625 GACCAGCTCCAGGAGC 640
              | |||||||||||| |
Db          3 GTCCAGCTCCAGGACC 18


RESULT 520
AR052013/c
LOCUS       AR052013                18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 35 from patent US 5830755.
ACCESSION   AR052013
VERSION     AR052013.1  GI:5975377
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
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  AUTHORS   Nishimura,M. and Rosenberg,S.A.
  TITLE     T-cell receptors and their use in therapeutic and diagnostic
            methods
  JOURNAL   Patent: US 5830755-A 35 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        4 a      6 c      6 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        728 AGGGGGCCTGGCTGCC 743
              ||||| |||| |||||
Db         16 AGGGGTCCTGTCTGCC 1


RESULT 521
AR071253
LOCUS       AR071253                 18 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 39 from patent US 5910432.
ACCESSION   AR071253
VERSION     AR071253.1  GI:7222141
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Ito,K., Yamaki,T., Arii,T., Tsuruoka,M. and Nakamura,T.
  TITLE     Nitrile hydratase
  JOURNAL   Patent: US 5910432-A 39 08-JUN-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        4 a      5 c      5 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        879 CAAGTTCCAGGAGCTG 894
              || | ||||||||||
Db          3 CACGATCCAGGAGCTG 18


RESULT 522
AR071254
LOCUS       AR071254                 18 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 40 from patent US 5910432.
ACCESSION   AR071254
VERSION     AR071254.1  GI:7222142
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Ito,K., Yamaki,T., Arii,T., Tsuruoka,M. and Nakamura,T.
  TITLE     Nitrile hydratase
  JOURNAL   Patent: US 5910432-A 40 08-JUN-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        3 a      5 c      6 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        879 CAAGTTCCAGGAGCTG 894
              || | ||||||||||
Db          3 CACGGTCCAGGAGCTG 18


RESULT 523
AR076320
LOCUS       AR076320                 18 bp    DNA     linear   PAT 30-AUG-2000
DEFINITION  Sequence 34 from patent US 5958771.
ACCESSION   AR076320
VERSION     AR076320.1  GI:10003066
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Bennett,C.Frank., Ackermann,E.J. and Cowsert,L.M.
  TITLE     Antisense modulation of cellular inhibitor of Apoptosis-2
            expression
  JOURNAL   Patent: US 5958771-A 34 28-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        1 a      6 c      4 g      7 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        257 ACCTCCTGGGCTGGCT 272
              | ||||||||||| ||
Db          3 ATCTCCTGGGCTGTCT 18


RESULT 524
AR124253
LOCUS       AR124253                 18 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 28 from patent US 6171859.
ACCESSION   AR124253
VERSION     AR124253.1  GI:14109614
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Herrnstadt,C. and Parker,W.Davis.
  TITLE     Method of targeting conjugate molecules to mitochondria
  JOURNAL   Patent: US 6171859-A 28 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        3 a      9 c      3 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        590 TGCCCCCCACCAGCCT 605
              ||||| |||||| |||
Db          1 TGCCCGCCACCATCCT 16


RESULT 525
AR130093
LOCUS       AR130093                 18 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 85 from patent US 6187586.
ACCESSION   AR130093
VERSION     AR130093.1  GI:14117990
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Monia,B.P., Cowsert,L.M. and Roth,R.A.
  TITLE     Antisense modulation of AKT-3 expression
  JOURNAL   Patent: US 6187586-A 85 13-FEB-2001;
FEATURES             Location/Qualifiers
```

```
     source          1. .18
                     /organism="unknown"
BASE COUNT        5 a      5 c      4 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        375 CCAGCTTCCTCCAGAG 390
              |||| || ||||||||
Db          2 CCAGTTTACTCCAGAG 17


RESULT 526
AR187556
LOCUS       AR187556                  18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 3044 from patent US 6346398.
ACCESSION   AR187556
VERSION     AR187556.1  GI:20233521
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 3044 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        2 a      4 c      6 g      6 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1311 GTAGCCAGGTGCTTTT 1326
              | |||||| |||||||
Db          1 GGAGCCAGCTGCTTTT 16


RESULT 527
AR192890
LOCUS       AR192890                  18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 8378 from patent US 6346398.
ACCESSION   AR192890
VERSION     AR192890.1  GI:20238855
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 8378 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        2 a      5 c      6 g      5 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1311 GTAGCCAGGTGCTTTT 1326
              | |||||| |||||||
Db          1 GGAGCCAGCTGCTTTT 16


RESULT 528
AR196144/c
LOCUS       AR196144                  18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 609 from patent US 6350934.
ACCESSION   AR196144
VERSION     AR196144.1  GI:20245581
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
            Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
  TITLE     Nucleic acid encoding delta-9 desaturase
  JOURNAL   Patent: US 6350934-A 609 26-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        4 a      6 c      5 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        884 TCCAGGAGCTGCGGTA 899
              |||| ||||||||| |
Db         16 TCCATGAGCTGCGGGA 1


RESULT 529
AR196164
LOCUS       AR196164                  18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 629 from patent US 6350934.
ACCESSION   AR196164
VERSION     AR196164.1  GI:20245601
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
            Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
  TITLE     Nucleic acid encoding delta-9 desaturase
  JOURNAL   Patent: US 6350934-A 629 26-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        2 a      7 c      5 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        220 CGAGCTCCTCAGCCTC 235
              || ||| |||||||||
Db          2 CGTGCTGCTCAGCCTC 17


RESULT 530
AR266202
LOCUS       AR266202                  18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 14 from patent US 6492173.
ACCESSION   AR266202
VERSION     AR266202.1  GI:29695048
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of cyclin D2 expression
  JOURNAL   Patent: US 6492173-A 14 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
```

```
BASE COUNT        2 a      0 c      4 g     12 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1145 TTTTTTCTTTTTGGAA 1160
              ||||| |||||||||
Db          3 TTTTTGTTTTTTGGAA 18


RESULT 531
AR268667
LOCUS       AR268667                  18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 17 from patent US 6500614.
ACCESSION   AR268667
VERSION     AR268667.1  GI:29699282
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Arguello,R., Avakian,H. and Madrigal,A.
  TITLE     Method for identifying an unknown allele
  JOURNAL   Patent: US 6500614-A 17 31-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        5 a      4 c      7 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        531 GGAGCAGCTGGGTGCC 546
              |||||||||| | |||
Db          1 GGAGCAGCTGAGAGCC 16


RESULT 532
AR295769
LOCUS       AR295769                  18 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 7504 from patent US 6537751.
ACCESSION   AR295769
VERSION     AR295769.1  GI:31683053
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 7504 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        4 a      4 c      4 g      6 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        850 TCAGCATACCGCTTTG 865
              |||||||| ||||| |
Db          3 TCAGCATAACGCTTGG 18


RESULT 533
AR299440
LOCUS       AR299440                  18 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 11175 from patent US 6537751.
ACCESSION   AR299440
VERSION     AR299440.1  GI:31686724
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 11175 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
BASE COUNT        8 a      5 c      4 g      1 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        955 AGACTGCAGGACTGAC 970
              | || ||||||||||
Db          3 ACACAGCAGGACTGAC 18


RESULT 534
AX014691
LOCUS       AX014691                  18 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 28 from Patent WO9953091.
ACCESSION   AX014691
VERSION     AX014691.1  GI:10040965
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Holinski-Feder,E., Grimm,L., Ueffing,M. and Meitinger,T.
  TITLE     Dna coding for gdnf, parts of said dna and gdnf variants
  JOURNAL   Patent: WO 9953091-A 28 21-OCT-1999;
            HOLINSKI FEDER ELKE (DE); GRIMM LENA (DE); UEFFING MARIUS (DE);
            LUDWIG MAXIMILIANS UNI MUENCHE (DE); MEITINGER THOMAS (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        4 a      5 c      7 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        714 TGTGGCCCAGCAGCAG 729
              ||||| |||||| |||
Db          3 TGTGGACCAGCACCAG 18


RESULT 535
AX023724
LOCUS       AX023724                  18 bp    DNA     linear   PAT 15-SEP-2000
DEFINITION  Sequence 66 from Patent WO0017371.
ACCESSION   AX023724
VERSION     AX023724.1  GI:10184084
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Binley,K.M. and Naylor,S.
  TITLE     Polynucleotide constructs and uses thereof
  JOURNAL   Patent: WO 0017371-A 66 30-MAR-2000;
            BINLEY KATIE MARY (GB) ; NAYLOR STUART (GB) ; OXFORD BIOMEDICA LTD
            (GB)
FEATURES             Location/Qualifiers
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```
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
BASE COUNT        3 a      4 c      8 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1235 TGGTGCTGGACGTGGC 1250
              | |||| |||||||||
Db          2 TCGTGCAGGACGTGGC 17


RESULT 536
AX023725/c
LOCUS       AX023725                 18 bp    DNA     linear   PAT 15-SEP-2000
DEFINITION  Sequence 67 from Patent WO0017371.
ACCESSION   AX023725
VERSION     AX023725.1  GI:10184085
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Binley,K.M. and Naylor,S.
  TITLE     Polynucleotide constructs and uses thereof
  JOURNAL   Patent: WO 0017371-A 67 30-MAR-2000;
            BINLEY KATIE MARY (GB) ; NAYLOR STUART (GB) ; OXFORD BIOMEDICA LTD
            (GB)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
BASE COUNT        3 a      8 c      4 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1235 TGGTGCTGGACGTGGC 1250
              | |||| |||||||||
Db         17 TCGTGCAGGACGTGGC 2


RESULT 537
AX084272/c
LOCUS       AX084272                 18 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 66 from Patent WO0110902.
ACCESSION   AX084272
VERSION     AX084272.1  GI:13185775
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Shimkets,R.A. and Fernandes,E.
  TITLE     Nucleic acids and secreted polypeptides encoded thereby
  JOURNAL   Patent: WO 0110902-A 66 15-FEB-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="PCR PRIMER"
BASE COUNT        4 a      5 c      7 g      2 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1292 TTGCTCAGCCTGGCCC 1307
              |||||||||| || ||
Db         18 TTGCTCAGCCCGGTCC 3


RESULT 538
AX084275
LOCUS       AX084275                 18 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 69 from Patent WO0110902.
ACCESSION   AX084275
VERSION     AX084275.1  GI:13185778
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Shimkets,R.A. and Fernandes,E.
  TITLE     Nucleic acids and secreted polypeptides encoded thereby
  JOURNAL   Patent: WO 0110902-A 69 15-FEB-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="PCR PRIMER"
BASE COUNT        2 a      7 c      5 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1292 TTGCTCAGCCTGGCCC 1307
              |||||||||| || ||
Db          1 TTGCTCAGCCCGGTCC 16


RESULT 539
AX132990/c
LOCUS       AX132990                 18 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 4208 from Patent WO0130362.
ACCESSION   AX132990
VERSION     AX132990.1  GI:14139300
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 4208 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /note="Hammerhead ribozyme recognition site for cdc 2
                     kinase"
BASE COUNT        4 a      3 c      5 g      6 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        600 CAGCCTGAAGCCTGAC 615
              || ||||||| |||||
Db         18 CATCCTGAAGACTGAC 3
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RESULT 540
AX132991/c
LOCUS       AX132991                 18 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 4209 from Patent WO0130362.
ACCESSION   AX132991
VERSION     AX132991.1  GI:14139301
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 4209 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /note="Hammerhead ribozyme recognition site for cdc 2
                     kinase"
BASE COUNT        3 a      3 c      6 g      6 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        600 CAGCCTGAAGCCTGAC 615
              || ||||||| |||||
Db         16 CATCCTGAAGACTGAC 1


RESULT 541
AX133349
LOCUS       AX133349                 18 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 6 from Patent EP1111050.
ACCESSION   AX133349
VERSION     AX133349.1  GI:14139639
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Althaus,H. and Hauser,H.P.
  TITLE     Human procalcitonin, its production and use
  JOURNAL   Patent: EP 1111050-A 6 27-JUN-2001;
            Dade Behring Marburg GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
                     /note="Primer, nicht genomische DNA"
BASE COUNT        3 a      2 c      6 g      7 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        833 TGAAGCTTTCAGATGG 848
              ||||||||| || |||
Db          2 TGAAGCTTTTAGTTGG 17


RESULT 542
AX287718
LOCUS       AX287718                 18 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 104 from Patent WO0179481.
ACCESSION   AX287718
VERSION     AX287718.1  GI:17049474
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ladner,R.C., Cohen,E.H., Nastri,H.G., Rookey,K.L. and Hoet,R.
  TITLE     Novel methods of constructing libraries of genetic packages that
            collectively display the members of a diverse family of peptides,
            polypeptides or proteins
  JOURNAL   Patent: WO 0179481-A 104 25-OCT-2001;
            Dyax Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
BASE COUNT        3 a      7 c      3 g      5 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        804 CTCCCTGCAGCCGAGC 819
              |||||||||| || |
Db          3 CTCCCTGCAGCTGAAC 18


RESULT 543
AX300817/c
LOCUS       AX300817                 18 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 19 from Patent WO0185993.
ACCESSION   AX300817
VERSION     AX300817.1  GI:17382097
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cooper,D.N., Procter,A.M., Gregory,J.D. and Millar,D.S.
  TITLE     Method for detecting growth hormone variations in humans, the
            variations and their uses
  JOURNAL   Patent: WO 0185993-A 19 15-NOV-2001;
            University of Wales College of Medicine (GB)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      7 c      4 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1255 TGAGGCCAGGTTGAGG 1270
              ||||| ||| ||||||
Db         16 TGAGGTCAGCTTGAGG 1


RESULT 544
AX326982/c
LOCUS       AX326982                 18 bp    DNA     linear   PAT 07-JAN-2002
DEFINITION  Sequence 178 from Patent WO0178894.
ACCESSION   AX326982
VERSION     AX326982.1  GI:18097693
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
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REFERENCE   1
  AUTHORS   Keith,T.
  TITLE     Novel human gene relating to respiratory diseases, obesity, and
            inflammatory bowel disease
  JOURNAL   Patent: WO 0178894-A 178 25-OCT-2001;
            Genome Therapeutics Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT        2 a      7 c      3 g      6 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        725 AGCAGGGGGCCTGGCT 740
              ||||| |||| |||||
Db         16 AGCAGAGGGCATGGCT 1


RESULT 545
AX395464
LOCUS       AX395464                  18 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 36 from Patent WO0208433.
ACCESSION   AX395464
VERSION     AX395464.1  GI:21066426
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Tilton,G.B., Shockey,J.M. and Browse,J.A.
  TITLE     Acyl coenzyme a thioesterases
  JOURNAL   Patent: WO 0208433-A 36 31-JAN-2002;
            Tilton, Gregory B. (US) ; Shockey, Jay M. (US) ; Browse, John A.
            (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic"
BASE COUNT        6 a      7 c      2 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        643 TGCATCCCCCAAGACC 658
              || || ||||||||||
Db          2 TGAATTCCCCAAGACC 17


RESULT 546
AX468611
LOCUS       AX468611                  18 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 6 from Patent WO0240710.
ACCESSION   AX468611
VERSION     AX468611.1  GI:21901409
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Olek,A., Piepenbrock,C. and Berlin,K.
  TITLE     Method for detecting methylation states for a toxicological
            diagnostic
  JOURNAL   Patent: WO 0240710-A 6 23-MAY-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="chemically treated genomic DNA (Homo sapiens)"
BASE COUNT        2 a      1 c      4 g     11 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTGGA 1159
              |||||||| |||| ||
Db          2 TTTTTTTCGTTTTAGA 17


RESULT 547
AX657870
LOCUS       AX657870                  18 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 115 from Patent WO02103042.
ACCESSION   AX657870
VERSION     AX657870.1  GI:29160566
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Distler,J., Model,F. and Adorjan,P.
  TITLE     Method and nucleic acids for the differentiation of prostate tumors
  JOURNAL   Patent: WO 02103042-A 115 27-DEC-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="TGFA detection oligomer"
BASE COUNT        2 a      1 c      4 g     11 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTGGA 1159
              |||||||| |||| ||
Db          2 TTTTTTTCGTTTTAGA 17


RESULT 548
BD016293
LOCUS       BD016293                  18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Human procalcitonin and production and utlization thereof.
ACCESSION   BD016293
VERSION     BD016293.1  GI:22557431
KEYWORDS    JP 2001224388-A/6.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Althaus,H. and Hauser,H.P.
  TITLE     Human procalcitonin and production and utlization thereof
  JOURNAL   Patent: JP 2001224388-A 6 21-AUG-2001;
            DADE BEHRING MARBURG GMBH
COMMENT     OS   Unknown
            PN   JP 2001224388-A/6
            PD   21-AUG-2001
            PF   21-DEC-2000 JP 2000389161
            PR   22-DEC-1999 DE   19962434:8,03-APR-2000 DE   10016278:9 PR
            08-JUN-2000 DE   10027954:6
            PI   HARALD ALTHAUS,HANS PETER HAUSER
            PC   C12N15/09,A61K9/08,A61K38/23,A61K39/395,A61K47/28,A61K47/42,
            PC   A61P3/14,
            PC   A61P5/22,A61P35/04,C07K14/585,C07K16/26,C12N1/15,C12N1/19, PC
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            C12N1/21,
            PC   C12N5/10,C12P21/02,C12P21/08//C07J9/00,C12N15/00,A61K37/30, PC
              C12N5/00
            CC   Description of Unknown Organism: Primer, non genomic DNA FH
            Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unknown'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        3 a      2 c      6 g      7 t

  Query Match              0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        833 TGAAGCTTTCAGATGG 848
              ||||||||| || |||
Db          2 TGAAGCTTTTAGTTGG 17


RESULT 549
BD087944
LOCUS       BD087944                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD087944
VERSION     BD087944.1  GI:22633554
KEYWORDS    JP 2001321190-A/188.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 188 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/188
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                   Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        4 a      1 c     11 g      2 t

  Query Match              0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        936 GGAGAAGAGGTGTGAG 951
              |||| || ||||||||
Db          2 GGAGCAGGGGTGTGAG 17


RESULT 550
BD089627
LOCUS       BD089627                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD089627
VERSION     BD089627.1  GI:22635237
KEYWORDS    JP 2001321190-A/1871.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 1871 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/1871
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                   Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        6 a      7 c      3 g      2 t

  Query Match              0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        554 CAGGCATGCACACACT 569
              |||||||||||  |||
Db          2 CAGGCATGCACCAACT 17


RESULT 551
BD104004
LOCUS       BD104004                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD104004
VERSION     BD104004.1  GI:22649578
KEYWORDS    WO 0192572-A/108.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 108 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/108
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
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                     /db_xref="taxon:32630"
BASE COUNT        2 a      7 c      6 g      3 t

  Query Match              0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        803 GCTCCCTGCAGCCGAG 818
              ||| ||||| ||||||
Db          1 GCTGCCTGCCGCCGAG 16


RESULT 552
BD104016/c
LOCUS       BD104016                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD104016
VERSION     BD104016.1  GI:22649590
KEYWORDS    WO 0192572-A/120.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 120 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/120
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        4 a      5 c      8 g      1 t

  Query Match              0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        143 CGCTCGGCTCCGCTCC 158
              ||||||| ||| ||||
Db         18 CGCTCGGGTCCTCTCC 3


RESULT 553
BD104054
LOCUS       BD104054                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD104054
VERSION     BD104054.1  GI:22649628
KEYWORDS    WO 0192572-A/158.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 158 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/158
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        3 a      2 c      6 g      7 t

  Query Match              0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1182 TCTATAGGTGAGTGTT 1197
              ||||  ||||||||||
Db          1 TCTACGGGTGAGTGTT 16


RESULT 554
BD104475/c
LOCUS       BD104475                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD104475
VERSION     BD104475.1  GI:22650049
KEYWORDS    WO 0192572-A/579.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 579 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/579
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        4 a      5 c      8 g      1 t

  Query Match              0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
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  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        143 CGCTCGGCTCCGCTCC 158
              ||||||| ||| ||||
Db         18 CGCTCGGGTCCTCTCC 3


RESULT 555
BD104493
LOCUS       BD104493                  18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD104493
VERSION     BD104493.1  GI:22650067
KEYWORDS    WO 0192572-A/597.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 597 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/597
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        3 a      3 c      6 g      6 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1182 TCTATAGGTGAGTGTT 1197
              ||||  ||||||||||
Db          3 TCTACGGGTGAGTGTT 18


RESULT 556
BD104494
LOCUS       BD104494                  18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD104494
VERSION     BD104494.1  GI:22650068
KEYWORDS    WO 0192572-A/598.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 598 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/598
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        3 a      2 c      7 g      6 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1182 TCTATAGGTGAGTGTT 1197
              ||||  ||||||||||
Db          3 TCTAGGGGTGAGTGTT 18


RESULT 557
BD107307/c
LOCUS       BD107307                  18 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Reelin protein CR-50 epitope domain.
ACCESSION   BD107307
VERSION     BD107307.1  GI:23202125
KEYWORDS    JP 2002017361-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Mikoshiba,K. and Tate,N.
  TITLE     Reelin protein CR-50 epitope domain
  JOURNAL   Patent: JP 2002017361-A 10 22-JAN-2002;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH
COMMENT     OS   Artificial Sequence
            PN   JP 2002017361-A/10
            PD   22-JAN-2002
            PF   04-JUL-2000 JP 2000202801
            PI   KATSUHIKO MIKOSHIBA,NAOKO TATE
            PC   C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P25/00,C07K14/47,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10,C12P21/02,G01N33/15,G01N33/50, PC
            G01N33/50,
            PC   G01N33/53//(C12N15/09,C12R1:91),(C12N1/21,C12R1:19),C12N15/00,
            PC   A61K37/02,
            PC   C12N5/00,(C12N15/00,C12R1:91)
            CC   synthetic primer for PCR
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        4 a      5 c      6 g      3 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1019 GATGGTGCCAAAGTGC 1034
              |||||||||| | |||
Db         18 GATGGTGCCACACTGC 3
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```
RESULT 558
BD136724/c
LOCUS       BD136724                 18 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Best's macular dystrophy gene.
ACCESSION   BD136724
VERSION     BD136724.1  GI:23231669
KEYWORDS    JP 2002504559-A/6.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Petrukhin,K., Caskey,T.C., Metzker,M. and Wadelius,C.
  TITLE     Best's macular dystrophy gene
  JOURNAL   Patent: JP 2002504559-A 6 12-FEB-2002;
            MERCK & CO INC,CLAES WADELIUS
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002504559-A/6
            PD   12-FEB-2002
            PF   22-FEB-1999 JP 2000533447
            PR   25-FEB-1998 US    60/075941,18-DEC-1998 US    60/112926 PI
            KONSTANTIN PETRUKHIN,THOMAS C CASKEY,MICHAEL METZKER,CLAES  PI
            WADELIUS
            PC   C07K16/18,C07K14/47,C12N5/10,C12N15/09,C12P19/34,C12Q1/68// PC
              C12P21/08,
            PC   C12N5/00,C12N15/00
            CC   Best's macular dystrophy gene
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      6 c      3 g      8 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        269 GGCTGATCAAAGAGGA 284
              | ||||  |||||||||
Db         18 GCCTGAACAAAGAGGA 3


RESULT 559
E14123
LOCUS       E14123                   18 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  PCR primer for producing mutated Pseudonocardia nitrilehydratase.
ACCESSION   E14123
VERSION     E14123.1  GI:5708806
KEYWORDS    JP 1997275978-A/37.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Ito,K., Yamaki,T., Arii,T., Tsuruoka,M. and Nakamura,T.
  TITLE     NEW NITRILE-HYDRATASE
  JOURNAL   Patent: JP 1997275978-A 37 28-OCT-1997;
            MITSUI TOATSU CHEM INC
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997275978-A/37
            PD   28-OCT-1997
            PF   29-JAN-1997 JP 1997015295
            PR   14-FEB-1996 JP 96P    27004
            PI   ITO KIYOSHI, YAMAKI TOSHIBUMI, ARII TERUO, TSURUOKA MIYUKI, PI
              NAKAMURA TAKESHI
            PC   C12N9/88,C12N1/21,C12N15/09,(C12N9/88,C12R1:19),(C12N1/21, PC
             C12R1:19),
            PC   (C12N15/09,C12R1:01);
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .18
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        4 a      5 c      5 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        879 CAAGTTCCAGGAGCTG 894
              || | ||||||||||||
Db          3 CACGATCCAGGAGCTG 18


RESULT 560
E14124
LOCUS       E14124                   18 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  PCR primer for producing mutated Pseudonocardia nitrilehydratase.
ACCESSION   E14124
VERSION     E14124.1  GI:5708807
KEYWORDS    JP 1997275978-A/38.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Ito,K., Yamaki,T., Arii,T., Tsuruoka,M. and Nakamura,T.
  TITLE     NEW NITRILE-HYDRATASE
  JOURNAL   Patent: JP 1997275978-A 38 28-OCT-1997;
            MITSUI TOATSU CHEM INC
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997275978-A/38
            PD   28-OCT-1997
            PF   29-JAN-1997 JP 1997015295
            PR   14-FEB-1996 JP 96P    27004
            PI   ITO KIYOSHI, YAMAKI TOSHIBUMI, ARII TERUO, TSURUOKA MIYUKI, PI
              NAKAMURA TAKESHI
            PC   C12N9/88,C12N1/21,C12N15/09,(C12N9/88,C12R1:19),(C12N1/21, PC
             C12R1:19),
            PC   (C12N15/09,C12R1:01);
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .18
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        3 a      5 c      6 g      4 t

  Query Match             0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        879 CAAGTTCCAGGAGCTG 894
              || | ||||||||||||
Db          3 CACGGTCCAGGAGCTG 18
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RESULT 561
E32457
LOCUS       E32457                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32457
VERSION     E32457.1  GI:13018693
KEYWORDS    JP 2000037190-A/17.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 17 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/17
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
BASE COUNT        1 a      0 c      2 g     15 t

  Query Match              0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTGGA 1159
              ||||||| ||||| ||
Db          3 TTTTTTTTTTTTTTGA 18


RESULT 562
I27416
LOCUS       I27416                    18 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 52 from patent US 5565323.
ACCESSION   I27416
VERSION     I27416.1  GI:1818192
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Parker,W.Davis. and Herrnstadt,C.
  TITLE     Cytochrome oxidase mutations aiding diagnosis of sporadic
            alzheimer's disease
  JOURNAL   Patent: US 5565323-A 52 15-OCT-1996;
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unknown"
BASE COUNT        3 a      9 c      3 g      3 t

  Query Match              0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        590 TGCCCCCCACCAGCCT 605
              ||||| |||||| |||
Db          1 TGCCCGCCACCATCCT 16


RESULT 563
I27449/c
LOCUS       I27449                    18 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 85 from patent US 5565323.
ACCESSION   I27449
VERSION     I27449.1  GI:1818225
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Parker,W.Davis. and Herrnstadt,C.
  TITLE     Cytochrome oxidase mutations aiding diagnosis of sporadic
            alzheimer's disease
  JOURNAL   Patent: US 5565323-A 85 15-OCT-1996;
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unknown"
BASE COUNT        3 a      3 c      9 g      3 t

  Query Match              0.9%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3e+02;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        590 TGCCCCCCACCAGCCT 605
              ||||| |||||| |||
Db         18 TGCCCGCCACCATCCT 3


RESULT 564
A88281/c
LOCUS       A88281                    14 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 429 from Patent WO9833904.
ACCESSION   A88281
VERSION     A88281.1  GI:6736851
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 429 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES              Location/Qualifiers
     source           1. .14
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
BASE COUNT       10 a      2 c      1 g      1 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.3e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1112 TTTTCTGTTTAATT 1125
              |||||||||||  ||
Db         14 TTTTCTGTTTAGTT 1


RESULT 565
A90248/c
LOCUS       A90248                    14 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 429 from Patent EP0856579.
ACCESSION   A90248
VERSION     A90248.1  GI:6738762
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
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REFERENCE   1  (bases 1 to 14)
  AUTHORS   Brysch,W.D. and Schlingensiepen,K.D.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: EP 0856579-A 429 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT       10 a      2 c      1 g      1 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.3e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1112 TTTTCTGTTTAATT 1125
              ||||||||||| ||
Db         14 TTTTCTGTTTAGTT 1


RESULT 566
AR174022
LOCUS       AR174022                 14 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 12 from patent US 6306624.
ACCESSION   AR174022
VERSION     AR174022.1  GI:17914342
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
  TITLE     Retinoid metabolizing protein
  JOURNAL   Patent: US 6306624-A 12 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
BASE COUNT       0 a      0 c      2 g     12 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.3e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1145 TTTTTTCTTTTTGG 1158
              |||||| |||||||
Db          1 TTTTTTTTTTTTGG 14


RESULT 567
AX016298
LOCUS       AX016298                 14 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from Patent WO9949046.
ACCESSION   AX016298
VERSION     AX016298.1  GI:10041861
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Roberts,J.A., Wyatt,P. and Whitelaw,C.
  TITLE     Signal transduction protein involved in plant dehiscence
  JOURNAL   Patent: WO 9949046-A 1 30-SEP-1999;
            ROBERTS JEREMY ALAN (GB); BIOGEMMA UK LTD (GB); WYATT PAUL (GB);
            WHITELAW CATHERINE (GB)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="oligo dT anchor primer 7"
BASE COUNT       0 a      0 c      2 g     12 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.3e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1145 TTTTTTCTTTTTGG 1158
              |||||| |||||||
Db          1 TTTTTTTTTTTTGG 14


RESULT 568
AX642208
LOCUS       AX642208                 14 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 26 from Patent WO02061082.
ACCESSION   AX642208
VERSION     AX642208.1  GI:28474656
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Day,R.
  TITLE     Zis-sr nucleic acid and amino acid sequences involved in the
            regulated secretory pathway and/or the regulation of the
            neuroendocrine phenotype (nep)
  JOURNAL   Patent: WO 02061082-A 26 08-AUG-2002;
            Universite de Sherbrooke (CA)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
BASE COUNT       0 a      0 c      2 g     12 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.3e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1145 TTTTTTCTTTTTGG 1158
              |||||| |||||||
Db          1 TTTTTTTTTTTTGG 14


RESULT 569
AX659630
LOCUS       AX659630                 14 bp    DNA     linear   PAT 03-APR-2003
DEFINITION  Sequence 24 from Patent WO02103014.
ACCESSION   AX659630
VERSION     AX659630.1  GI:29161812
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Al-Mahmood,S.
  TITLE     Antisense oligonucleotides which can inhibit the formation of
            capillary tubes by endothelial cells
  JOURNAL   Patent: WO 02103014-A 24 27-DEC-2002;
            Al-Mahmood, Salman (FR)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide anti-sens"
BASE COUNT       0 a      0 c      2 g     12 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.3e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1145 TTTTTTCTTTTTGG 1158
              |||||| |||||||
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Db          1 TTTTTTTTTTTTGG 14


RESULT 570
BD065794/c
LOCUS       BD065794                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD065794
VERSION     BD065794.1  GI:22611397
KEYWORDS    JP 2001511000-A/429.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 429 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/429
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
                  Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Unknown'.
FEATURES              Location/Qualifiers
     source           1. .14
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
BASE COUNT       10 a      2 c      1 g      1 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.3e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1112 TTTTCTGTTTAATT 1125
              ||||||||||| ||
Db         14 TTTTCTGTTTAGTT 1


RESULT 571
BD069002
LOCUS       BD069002                  14 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors.
ACCESSION   BD069002
VERSION     BD069002.1  GI:22614605
KEYWORDS    JP 2001511003-A/1842.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Akhtar,S., Fell,P. and Mcswiggen,J.A.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors
  JOURNAL   Patent: JP 2001511003-A 1842 07-AUG-2001;
            RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT     OS   Unidentified
            PN   JP 2001511003-A/1842
            PD   07-AUG-2001
            PF   14-JAN-1998 JP 1998532913
            PR   31-JAN-1997 US    60/036476,04-DEC-1997 US    08/985162 PI
            SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
            C12N9/00,C07K14/71
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                  related to
            CC   levels of epidermal growth factor receptors
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .14
                      /organism="unidentified"
                      /mol_type="genomic RNA"
                      /db_xref="taxon:32644"
BASE COUNT       2 a      8 c      3 g      1 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.3e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1050 CGACAGCCCTGGCC 1063
              |||||||||| ||
Db          1 CGACAGCCCTGCCC 14


RESULT 572
BD073884
LOCUS       BD073884                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Isolation of novel aging factor gene P23.
ACCESSION   BD073884
VERSION     BD073884.1  GI:22619487
KEYWORDS    JP 2001512698-A/9.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Suishelm,K., Hosier,S. and Kubbies,M.
  TITLE     Isolation of novel aging factor gene P23
  JOURNAL   Patent: JP 2001512698-A 9 28-AUG-2001;
            UNIVERSITY OF WASHINGTON
COMMENT     OS   Unidentified
            PN   JP 2001512698-A/9
            PD   28-AUG-2001
            PF   05-AUG-1998 JP 2000506375
            PR   08-AUG-1997 US    08/908873
            PI   KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
            C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N15/09, PC
            C12P21/02,
            PC   C12P21/08,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Isolation of novel aging factor gene P23
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .14
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
BASE COUNT       0 a      0 c      2 g     12 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.3e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1145 TTTTTTCTTTTTGG 1158
              |||||| |||||||
Db          1 TTTTTTTTTTTTGG 14


RESULT 573
BD084126
LOCUS       BD084126                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Polymorphisms and new genes in the region of the human
            hemochromatosis gene.
ACCESSION   BD084126
VERSION     BD084126.1  GI:22629736
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KEYWORDS    JP 2001525663-A/14.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Polymorphisms and new genes in the region of the human
            hemochromatosis gene
  JOURNAL   Patent: JP 2001525663-A 14 11-DEC-2001;
            PROGENTIOR INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001525663-A/14
            PD   11-DEC-2001
            PF   30-SEP-1997 JP 1998516815
            PR   01-OCT-1996 US    08/724394,07-MAY-1997 US    08/852495 PI
            JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
            WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
            C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC   Polymorphisms
            and new genes in the region of the human CC   hemochromatosis gene
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Homo sapiens (human)'.
FEATURES            Location/Qualifiers
     source         1. .14
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
BASE COUNT       0 a      1 c      0 g     13 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.3e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
              ||||||||  |||||
Db          1 CTTTTTTTTTTTTT 14


RESULT 574
BD176797/c
LOCUS       BD176797                  14 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression.
ACCESSION   BD176797
VERSION     BD176797.1  GI:29122509
KEYWORDS    WO 02074951-A/44.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
  TITLE     Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression
  JOURNAL   Patent: WO 02074951-A 44 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
            KUNITAKA HIROSE,JUN SAKAI
COMMENT     OS   Artificial Sequence
            PN   WO 02074951-A/44
            PD   26-SEP-2002
            PF   13-MAR-2002 WO 2002JP002338
            PR   15-MAR-2001 JP 01P   073959
            PI   MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
            C12N15/09,C12Q1/68
            CC   Synthetic DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .14
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"
BASE COUNT      13 a      0 c      1 g      0 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.3e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
              ||||||||  |||||
Db          14 CTTTTTTTTTTTTT 1


RESULT 575
BD176803
LOCUS       BD176803                  14 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression.
ACCESSION   BD176803
VERSION     BD176803.1  GI:29122515
KEYWORDS    WO 02074951-A/50.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
  TITLE     Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression
  JOURNAL   Patent: WO 02074951-A 50 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
            KUNITAKA HIROSE,JUN SAKAI
COMMENT     OS   Artificial Sequence
            PN   WO 02074951-A/50
            PD   26-SEP-2002
            PF   13-MAR-2002 WO 2002JP002338
            PR   15-MAR-2001 JP 01P   073959
            PI   MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
            C12N15/09,C12Q1/68
            CC   Synthetic DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .14
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"
BASE COUNT       0 a      0 c      1 g     13 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.3e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTG 1157
              |||||||  ||||||
Db          1 TTTTTTTTTTTTTG 14


RESULT 576
A88282/c
LOCUS       A88282                    15 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 430 from Patent WO9833904.
ACCESSION   A88282
VERSION     A88282.1  GI:6736852
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 430 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES            Location/Qualifiers
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     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT       11 a      2 c      1 g      1 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 2.6e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1112 TTTTCTGTTTAATT 1125
              ||||||||||| ||
Db         15 TTTTCTGTTTAGTT 2


RESULT 577
A90249/c
LOCUS       A90249                    15 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 430 from Patent EP0856579.
ACCESSION   A90249
VERSION     A90249.1  GI:6738763
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Brysch,W.D. and Schlingensiepen,K.D.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: EP 0856579-A 430 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT       11 a      2 c      1 g      1 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 2.6e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1112 TTTTCTGTTTAATT 1125
              ||||||||||| ||
Db         15 TTTTCTGTTTAGTT 2


RESULT 578
AR084518/c
LOCUS       AR084518                  15 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 7 from patent US 5981185.
ACCESSION   AR084518
VERSION     AR084518.1  GI:10011289
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 7 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
BASE COUNT       14 a      1 c      0 g      0 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 2.6e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTG 1157
              ||||||| ||||||
Db         15 TTTTTTTTTTTTTG 2


RESULT 579
AR231294
LOCUS       AR231294                  15 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 31 from patent US 6451968.
ACCESSION   AR231294
VERSION     AR231294.1  GI:27272225
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
            Coull,J.M., Kiely,J. and Griffith,M.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6451968-A 31 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
BASE COUNT        0 a      2 c      0 g     13 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 2.6e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1142 CCTTTTTTTCTTTT 1155
              | ||||||||||||
Db          2 CTTTTTTTTCTTTT 15


RESULT 580
AX635278/c
LOCUS       AX635278                  15 bp    mRNA    linear   PAT 21-FEB-2003
DEFINITION  Sequence 2417 from Patent EP1260586.
ACCESSION   AX635278
VERSION     AX635278.1  GI:28470892
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 2417 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="mRNA"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      3 c      5 g      5 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 2.6e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        628 CAGCTCCAGGAGCT 641
              |||||||| |||||
Db         15 CAGCTCCAAGAGCT 2


RESULT 581
AX721645/c
LOCUS       AX721645                  15 bp    DNA     linear   PAT 07-MAY-2003
DEFINITION  Sequence 24 from Patent EP1298221.
ACCESSION   AX721645
VERSION     AX721645.1  GI:30422178
KEYWORDS    .
```

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SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van der Kuyl,A.C. and Cornelissen,M.
  TITLE     Means and methods for treatment evaluation
  JOURNAL   Patent: EP 1298221-A 24 02-APR-2003;
            PrimaGen Holding B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Tag with increased expression in SAGE libraries KS3
                     and KS4"
BASE COUNT        2 a      4 c      6 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 2.6e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        462 CAGCAGCCTGCAGG 475
              ||||||||||||| |
Db         14 CAGCAGCCTGCATG 1


RESULT 582
AX742553/c
LOCUS       AX742553                 15 bp    DNA     linear   PAT 12-MAY-2003
DEFINITION  Sequence 356 from Patent EP1302550.
ACCESSION   AX742553
VERSION     AX742553.1  GI:30576521
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lin,C.Y., Lin,R.W., You,C.M., Huang,H.H., Lee,B.H., Lee,H.H.,
            Lin,Y.J., Fan,C.C., Hsu,H.C., Shih,C.W., Yeh,C.H., Kao,Y.F.,
            Pan,C.L. and Chan,P.
  TITLE     Method and detector for identifying subtypes of human papilloma
            viruses
  JOURNAL   Patent: EP 1302550-A 356 16-APR-2003;
            King Car Food Industrial Co., Ltd. (TW)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide for Identifying HPV 61"
BASE COUNT        2 a      9 c      1 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 2.6e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        767 GGGTGGATGTAGCA 780
              ||| ||||||||||
Db         15 GGGGGGATGTAGCA 2


RESULT 583
BD005891/c
LOCUS       BD005891                 15 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Novel probes for the detection of Mycobacteria.
ACCESSION   BD005891
VERSION     BD005891.1  GI:18634262
KEYWORDS    JP 2001501825-A/102.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Stender,H., Lund,K. and Mollerup,T.A.
  TITLE     Novel probes for the detection of Mycobacteria
  JOURNAL   Patent: JP 2001501825-A 102 13-FEB-2001;
            DAKO AS
COMMENT     OS   Unidentified
            PN   JP 2001501825-A/102
            PD   13-FEB-2001
            PF   03-OCT-1997 JP 1998517095
            PR   04-OCT-1996 DK      1096/96,18-OCT-1996 DK      1156/96 PR
            05-MAY-1997 DK      0512/97
            PI   HENRIK STENDER,KAARE LUND,TINA ANDRESEN MOLLERUP PC
            C12Q1/68,C07K14/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      7 c      5 g      2 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 2.6e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        885 CCAGGAGCTGCGGT 898
              |||||||| |||||
Db         14 CCAGGAGCCGCGGT 1


RESULT 584
BD065795/c
LOCUS       BD065795                 15 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD065795
VERSION     BD065795.1  GI:22611398
KEYWORDS    JP 2001511000-A/430.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 430 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/430
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
                  Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Unknown'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT       11 a      2 c      1 g      1 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 2.6e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1112 TTTTCTGTTTAATT 1125
              |||||||||| ||
Db         15 TTTTCTGTTTAGTT 2
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RESULT 585
BD133913
LOCUS       BD133913                 15 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel oligonucleotide, vitronectin aptamer, anticancer agent and
            method of analyzing vitronectin.
ACCESSION   BD133913
VERSION     BD133913.1  GI:23228858
KEYWORDS    JP 2002058491-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Ishikawa,Y., Wada,T. and Ando,T.
  TITLE     Novel oligonucleotide, vitronectin aptamer, anticancer agent and
            method of analyzing vitronectin
  JOURNAL   Patent: JP 2002058491-A 3 26-FEB-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002058491-A/3
            PD   26-FEB-2002
            PF   22-AUG-2000 JP 2000251583
            PI   YOSHIAKI ISHIKAWA,TSUTOMU WADA,TAKAO ANDO
            PC   C12N15/09,C07H21/00,C12Q1/68,G01N33/53,G01N33/566//A61K31/712,
            PC   A61P35/00,
            PC   C12N15/00
            CC   This is a vitronectin aptamer
            FH   Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
BASE COUNT        2 a      5 c      6 g      2 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 2.6e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        628 CAGCTCCAGGAGCT 641
              ||||||| ||||||
Db          1 CAGCTCCGGGAGCT 14


RESULT 586
BD133913/c
LOCUS       BD133913                 15 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel oligonucleotide, vitronectin aptamer, anticancer agent and
            method of analyzing vitronectin.
ACCESSION   BD133913
VERSION     BD133913.1  GI:23228858
KEYWORDS    JP 2002058491-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Ishikawa,Y., Wada,T. and Ando,T.
  TITLE     Novel oligonucleotide, vitronectin aptamer, anticancer agent and
            method of analyzing vitronectin
  JOURNAL   Patent: JP 2002058491-A 3 26-FEB-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002058491-A/3
            PD   26-FEB-2002
            PF   22-AUG-2000 JP 2000251583
            PI   YOSHIAKI ISHIKAWA,TSUTOMU WADA,TAKAO ANDO
            PC   C12N15/09,C07H21/00,C12Q1/68,G01N33/53,G01N33/566//A61K31/712,
            PC   A61P35/00,
            PC   C12N15/00
            CC   This is a vitronectin aptamer
            FH   Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
BASE COUNT        2 a      5 c      6 g      2 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 2.6e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        628 CAGCTCCAGGAGCT 641
              ||||||| ||||||
Db         15 CAGCTCCCGGAGCT 2


RESULT 587
I38985/c
LOCUS       I38985                   15 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 23 from patent US 5616488.
ACCESSION   I38985
VERSION     I38985.1  GI:2083465
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
  TITLE     IL-5 targeted ribozymes
  JOURNAL   Patent: US 5616488-A 23 01-APR-1997;
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="unknown"
BASE COUNT        2 a      3 c      5 g      5 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 2.6e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        628 CAGCTCCAGGAGCT 641
              |||||||| |||||
Db         15 CAGCTCCAAGAGCT 2


RESULT 588
A88280/c
LOCUS       A88280                   16 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 428 from Patent WO9833904.
ACCESSION   A88280
VERSION     A88280.1  GI:6736850
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 428 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
BASE COUNT       11 a      2 c      2 g      1 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 16;
  Best Local Similarity   92.9%;  Pred. No. 2.9e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1112 TTTTCTGTTTAATT 1125
```

```
                    ||||||||||| ||
Db         15 TTTTCTGTTTAGTT 2


RESULT 589
A90247/c
LOCUS       A90247                    16 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 428 from Patent EP0856579.
ACCESSION   A90247
VERSION     A90247.1  GI:6738761
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Brysch,W.D. and Schlingensiepen,K.D.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: EP 0856579-A 428 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT       11 a      2 c      2 g      1 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 16;
  Best Local Similarity   92.9%;  Pred. No. 2.9e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1112 TTTTCTGTTTAATT 1125
                ||||||||||| ||
Db         15 TTTTCTGTTTAGTT 2


RESULT 590
AR002257
LOCUS       AR002257                  16 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 6 from patent US 5741643.
ACCESSION   AR002257
VERSION     AR002257.1  GI:3963811
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps
  JOURNAL   Patent: US 5741643-A 6 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        1 a      1 c      0 g     14 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 16;
  Best Local Similarity   92.9%;  Pred. No. 2.9e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
                ||||||||| |||||
Db          2 CTTTTTTTTTTTTT 15


RESULT 591
AR045207
LOCUS       AR045207                  16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 6 from patent US 5817795.
ACCESSION   AR045207
VERSION     AR045207.1  GI:5966672
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps having diagnostic and therapeutic
            applications
  JOURNAL   Patent: US 5817795-A 6 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        1 a      1 c      0 g     14 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 16;
  Best Local Similarity   92.9%;  Pred. No. 2.9e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
                ||||||||| |||||
Db          2 CTTTTTTTTTTTTT 15


RESULT 592
AR051238
LOCUS       AR051238                  16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 6 from patent US 5830658.
ACCESSION   AR051238
VERSION     AR051238.1  GI:5974602
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
            macromolecular structures
  JOURNAL   Patent: US 5830658-A 6 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        1 a      1 c      0 g     14 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 16;
  Best Local Similarity   92.9%;  Pred. No. 2.9e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
                ||||||||| |||||
Db          2 CTTTTTTTTTTTTT 15


RESULT 593
AR069284/c
LOCUS       AR069284                  16 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 23 from patent US 5891631.
ACCESSION   AR069284
VERSION     AR069284.1  GI:7220172
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Goldstein,J.L., Brown,M.S., Briggs,M.R. and Wang,X.
  TITLE     Methods relating tosterol regulatory element binding proteins
  JOURNAL   Patent: US 5891631-A 23 06-APR-1999;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        3 a      9 c      1 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 16;
  Best Local Similarity   92.9%;  Pred. No. 2.9e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        471 GCAGGGGGAGGACT 484
                ||||||||||||| |
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Db          16 GCAGGGGGAGGAGT 3


RESULT 594
AX067884
LOCUS       AX067884                 16 bp    DNA     linear   PAT 19-JAN-2001
DEFINITION  Sequence 25 from Patent WO0077205.
ACCESSION   AX067884
VERSION     AX067884.1  GI:12329741
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Barber,G.N., Saunders,L. and Perkins,D.
  TITLE     Human nuclear factors associated with dsrna (nfar)
  JOURNAL   Patent: WO 0077205-A 25 21-DEC-2000;
            Barber, Glen N. (US) ; Saunders, Laura (US) ; Perkins, Darren (US)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      4 c      7 g      4 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 16;
  Best Local Similarity   92.9%;  Pred. No. 2.9e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1259 GCCAGGTTGAGGCC 1272
              ||||||||| ||||
Db          2 GCCAGGTTGGGGCC 15


RESULT 595
AX282047/c
LOCUS       AX282047                 16 bp    DNA     linear   PAT 02-NOV-2001
DEFINITION  Sequence 179 from Patent WO0177392.
ACCESSION   AX282047
VERSION     AX282047.1  GI:16609298
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Ashby,M.
  TITLE     Methods for the survey and genetic analysis of populations
  JOURNAL   Patent: WO 0177392-A 179 18-OCT-2001;
            Ashby, Matthew (US)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
                     /note="Uncultured Acidobacterium Sub.Div-1"
BASE COUNT        1 a      6 c      5 g      4 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 16;
  Best Local Similarity   92.9%;  Pred. No. 2.9e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        890 AGCTGCGGTACAGC 903
              |||||||| |||||
Db         16 AGCTGCGGCACAGC 3


RESULT 596
BD065793/c
LOCUS       BD065793                 16 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD065793
VERSION     BD065793.1  GI:22611396
KEYWORDS    JP 2001511000-A/428.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 428 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/428
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
                 Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Unknown'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT       11 a      2 c      2 g      1 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 16;
  Best Local Similarity   92.9%;  Pred. No. 2.9e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1112 TTTTCTGTTTAATT 1125
              ||||||||||| ||
Db         15 TTTTCTGTTTAGTT 2


RESULT 597
I16032
LOCUS       I16032                   16 bp    DNA     linear   PAT 03-APR-1996
DEFINITION  Sequence 6 from patent US 5473060.
ACCESSION   I16032
VERSION     I16032.1  GI:1250940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps having diagnostic applications
  JOURNAL   Patent: US 5473060-A 6 05-DEC-1995;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        1 a      1 c      0 g     14 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 16;
  Best Local Similarity   92.9%;  Pred. No. 2.9e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
              |||||||| |||||
Db          2 CTTTTTTTTTTTTT 15


RESULT 598
I18842/c
LOCUS       I18842                   16 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 23 from patent US 5498696.
ACCESSION   I18842
VERSION     I18842.1  GI:1599197
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Briggs,M.R., Brown,M.S., Goldstein,J.L. and Wang,X.
  TITLE     Sterol regulatory element binding proteins and their use in
            screening assays
  JOURNAL   Patent: US 5498696-A 23 12-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        3 a      9 c      1 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 16;
  Best Local Similarity   92.9%;  Pred. No. 2.9e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        471 GCAGGGGGAGGACT 484
              ||||||||||||| |
Db         16 GCAGGGGGAGGAGT 3


RESULT 599
I22296/c
LOCUS       I22296                   16 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 23 from patent US 5527690.
ACCESSION   I22296
VERSION     I22296.1  GI:1602650
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Goldstein,J.L., Brown,M.S., Briggs,M.R. and Wang,X.
  TITLE     Methods and compositions relating to sterol regulatory element
            binding proteins
  JOURNAL   Patent: US 5527690-A 23 18-JUN-1996;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        3 a      9 c      1 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 16;
  Best Local Similarity   92.9%;  Pred. No. 2.9e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        471 GCAGGGGGAGGACT 484
              ||||||||||||| |
Db         16 GCAGGGGGAGGAGT 3


RESULT 600
I28367
LOCUS       I28367                   16 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 6 from patent US 5571677.
ACCESSION   I28367
VERSION     I28367.1  GI:1819143
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
            macromomolecular structures
  JOURNAL   Patent: US 5571677-A 6 05-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        1 a      1 c      0 g     14 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 16;
  Best Local Similarity   92.9%;  Pred. No. 2.9e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
              |||||||| |||||
Db          2 CTTTTTTTTTTTTT 15


RESULT 601
I47692/c
LOCUS       I47692                   16 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 4 from patent US 5639873.
ACCESSION   I47692
VERSION     I47692.1  GI:2471657
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Barascut,J.-L. and Imbach,J.-L.
  TITLE     Oligothionucleotides
  JOURNAL   Patent: US 5639873-A 4 17-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT       12 a      4 c      0 g      0 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 16;
  Best Local Similarity   92.9%;  Pred. No. 2.9e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1145 TTTTTTCTTTTTGG 1158
              |||||| |||||||
Db         14 TTTTTTTTTTTTGG 1


RESULT 602
A89326
LOCUS       A89326                   17 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 1474 from Patent WO9833904.
ACCESSION   A89326
VERSION     A89326.1  GI:6737896
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 1474 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      4 c      3 g      8 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        445 TTGCTGAAGTTTGT 458
              ||||||||||||| |
Db          3 TTGCTGAAGTTTCT 16


RESULT 603
AR045545/c
LOCUS       AR045545                 17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 338 from patent US 5817796.
ACCESSION   AR045545
VERSION     AR045545.1  GI:5967010
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL   Patent: US 5817796-A 338 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        3 a      9 c      2 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GGCAGGCAGTTGAG 15
              |||||| |||||||
Db         15 GGCAGGGAGTTGAG 2


RESULT 604
AR047254
LOCUS       AR047254                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2047 from patent US 5817796.
ACCESSION   AR047254
VERSION     AR047254.1  GI:5968719
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL   Patent: US 5817796-A 2047 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        8 a      0 c      2 g      7 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1118 GTTTAATTGAAAAA 1131
              |||| |||||||||
Db          4 GTTTTATTGAAAAA 17


RESULT 605
AR047256
LOCUS       AR047256                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2049 from patent US 5817796.
ACCESSION   AR047256
VERSION     AR047256.1  GI:5968721
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL   Patent: US 5817796-A 2049 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        8 a      0 c      2 g      7 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1118 GTTTAATTGAAAAA 1131
              |||| |||||||||
Db          2 GTTTTATTGAAAAA 15


RESULT 606
AR064971
LOCUS       AR064971                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 9 from patent US 5849482.
ACCESSION   AR064971
VERSION     AR064971.1  GI:5995187
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Meyer,R.B. Jr., Gamper,H.B., Kutyavin,I.V., Gall,A.A., Petrie,C.R.,
            Tabone,J.C. and Hurst,G.D.
  TITLE     Crosslinking oligonucleotides
  JOURNAL   Patent: US 5849482-A 9 15-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        0 a      1 c      5 g      9 t      2 others

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   81.2%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1147 TTTTCTTTTTGGAAGT 1162
              |||||||||:||  ||
Db          1 TTTTCTTTTYGGGGGT 16


RESULT 607
AR168853
LOCUS       AR168853                  17 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 79 from patent US 6288042.
ACCESSION   AR168853
VERSION     AR168853.1  GI:17904990
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Rando,R.F., Ojwaug,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
  TITLE     Anti-viral guanosine-rich tetrad forming oligonucleotides
  JOURNAL   Patent: US 6288042-A 79 11-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        0 a      1 c     12 g      4 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        762 GTGGCGGGTGGATG 775
              |||||||||||  ||
Db          1 GTGGCGGGTGGGTG 14


RESULT 608
AR186768
LOCUS       AR186768                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2256 from patent US 6346398.
ACCESSION   AR186768
VERSION     AR186768.1  GI:20232733
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
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  JOURNAL   Patent: US 6346398-A 2256 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        8 a      2 c      3 g      4 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1155 TTGGAAGTAAAGCA 1168
              |||||| |||||||
Db          1 TTGGAACTAAAGCA 14


RESULT 609
AR187059
LOCUS       AR187059                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2547 from patent US 6346398.
ACCESSION   AR187059
VERSION     AR187059.1  GI:20233024
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2547 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        1 a      2 c      0 g     14 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
              |||||||| |||||
Db          4 CTTTTTTTTTTTT 17


RESULT 610
AR187060
LOCUS       AR187060                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2548 from patent US 6346398.
ACCESSION   AR187060
VERSION     AR187060.1  GI:20233025
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2548 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        1 a      1 c      0 g     15 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
              |||||||| |||||
Db          3 CTTTTTTTTTTTT 16


RESULT 611
AR187061
LOCUS       AR187061                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2549 from patent US 6346398.
ACCESSION   AR187061
VERSION     AR187061.1  GI:20233026
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2549 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        1 a      1 c      0 g     15 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
              |||||||| |||||
Db          2 CTTTTTTTTTTTT 15


RESULT 612
AR187062
LOCUS       AR187062                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2550 from patent US 6346398.
ACCESSION   AR187062
VERSION     AR187062.1  GI:20233027
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2550 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        0 a      1 c      0 g     16 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
              |||||||| |||||
Db          1 CTTTTTTTTTTTT 14


RESULT 613
AR190520/c
LOCUS       AR190520                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 6008 from patent US 6346398.
ACCESSION   AR190520
VERSION     AR190520.1  GI:20236485
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 6008 12-FEB-2002;
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FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        1 a      1 c      8 g      7 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         23 AAACCAAACCCAGC 36
              ||||||||||| ||
Db         15 AAACCAAACCCTGC 2


RESULT 614
AR190521/c
LOCUS       AR190521                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 6009 from patent US 6346398.
ACCESSION   AR190521
VERSION     AR190521.1  GI:20236486
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 6009 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        1 a      1 c      8 g      7 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         23 AAACCAAACCCAGC 36
              ||||||||||| ||
Db         14 AAACCAAACCCTGC 1


RESULT 615
AR195674/c
LOCUS       AR195674                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 139 from patent US 6350934.
ACCESSION   AR195674
VERSION     AR195674.1  GI:20245111
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
            Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
  TITLE     Nucleic acid encoding delta-9 desaturase
  JOURNAL   Patent: US 6350934-A 139 26-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        4 a      5 c      5 g      3 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        884 TCCAGGAGCTGCGG 897
              |||| |||||||||
Db         14 TCCATGAGCTGCGG 1


RESULT 616
AR200322
LOCUS       AR200322                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 79 from patent US 6355785.
ACCESSION   AR200322
VERSION     AR200322.1  GI:20250396
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Rando,R.F., Fennewald,S., Zendegui,J.G., Ojwang,J.O., Hogan,M.E.,
            Pommier,Y. and Mazumder,A.
  TITLE     Guanosine-rich oligonucleotide integrase inhibitors
  JOURNAL   Patent: US 6355785-A 79 12-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        0 a      1 c     12 g      4 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        762 GTGGCGGGTGGATG 775
              ||||||||||| ||
Db          1 GTGGCGGGTGGGTG 14


RESULT 617
AR256849
LOCUS       AR256849                  17 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 3 from patent US 6485916.
ACCESSION   AR256849
VERSION     AR256849.1  GI:27306475
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Muramatsu,T., Fujita,T., Kiyama,M., Irie,T. and Okano,K.
  TITLE     Preparation method of nucleic acid sample for rare expressed genes
            and analyzing method using the prepared nucleic acid samples
            thereby
  JOURNAL   Patent: US 6485916-A 3 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        0 a      0 c      2 g     15 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTG 1157
              ||||||| ||||||
Db          4 TTTTTTTTTTTTTG 17


RESULT 618
AR262453
LOCUS       AR262453                  17 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 79 from patent US 6323185.
ACCESSION   AR262453
VERSION     AR262453.1  GI:28073884
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Rando,R.F., Fennewald,S., Zendegui,J.G., Ojwang,J.O. and Hogan,M.E.
  TITLE     Anti-viral guanosine-rich oligonucleotides and method of treating
            HIV
  JOURNAL   Patent: US 6323185-A 79 27-NOV-2001;
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FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        0 a      1 c     12 g      4 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        762 GTGGCGGGTGGATG 775
              ||||||||||| ||
Db          1 GTGGCGGGTGGGTG 14


RESULT 619
AR266626
LOCUS       AR266626                 17 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 64 from patent US 6495319.
ACCESSION   AR266626
VERSION     AR266626.1  GI:29695690
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 64 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        0 a      0 c      2 g     15 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTG 1157
              ||||||| ||||||
Db          4 TTTTTTTTTTTTTG 17


RESULT 620
AR286037
LOCUS       AR286037                 17 bp    RNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 409 from patent US 6528640.
ACCESSION   AR286037
VERSION     AR286037.1  GI:29723633
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
            Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
  TITLE     Synthetic ribonucleic acids with RNAse activity
  JOURNAL   Patent: US 6528640-A 409 04-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        5 a      3 c      7 g      2 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        477 GGAGGACTGCCGAG 490
              |||||| |||||||
Db          1 GGAGGAATGCCGAG 14


RESULT 621
AR286049
LOCUS       AR286049                 17 bp    RNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 421 from patent US 6528640.
ACCESSION   AR286049
VERSION     AR286049.1  GI:29723645
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
            Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
  TITLE     Synthetic ribonucleic acids with RNAse activity
  JOURNAL   Patent: US 6528640-A 421 04-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        3 a      9 c      2 g      3 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1297 CAGCCTGGCCCCAT 1310
              |||||| |||||||
Db          2 CAGCCTTGCCCCAT 15


RESULT 622
AR286185
LOCUS       AR286185                 17 bp    RNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 557 from patent US 6528640.
ACCESSION   AR286185
VERSION     AR286185.1  GI:29723781
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
            Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
  TITLE     Synthetic ribonucleic acids with RNAse activity
  JOURNAL   Patent: US 6528640-A 557 04-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        1 a      2 c      3 g     11 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1112 TTTTCTGTTTAATT 1125
              |||||||||| ||
Db          3 TTTTCTGTTTAGTT 16


RESULT 623
AR286443/c
LOCUS       AR286443                 17 bp    RNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 815 from patent US 6528640.
ACCESSION   AR286443
VERSION     AR286443.1  GI:29724039
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
            Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
  TITLE     Synthetic ribonucleic acids with RNAse activity
  JOURNAL   Patent: US 6528640-A 815 04-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .17
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                     /organism="unknown"
BASE COUNT        2 a      3 c     10 g      2 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        867 GGTCCCCACAGCCA 880
              ||||||||| ||||
Db         17 GGTCCCCACCGCCA 4


RESULT 624
AX217812/c
LOCUS       AX217812                  17 bp    mRNA    linear   PAT 07-SEP-2001
DEFINITION  Sequence 3254 from Patent WO0159103.
ACCESSION   AX217812
VERSION     AX217812.1  GI:15527873
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 3254 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
BASE COUNT        8 a      5 c      1 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1180 TTTCTATAGGTGAG 1193
              ||||||| ||||||
Db         17 TTTCTATTGGTGAG 4


RESULT 625
AX217813/c
LOCUS       AX217813                  17 bp    mRNA    linear   PAT 07-SEP-2001
DEFINITION  Sequence 3255 from Patent WO0159103.
ACCESSION   AX217813
VERSION     AX217813.1  GI:15527874
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 3255 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
BASE COUNT        8 a      5 c      1 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1180 TTTCTATAGGTGAG 1193
              ||||||| ||||||
Db         16 TTTCTATTGGTGAG 3


RESULT 626
AX217865/c
LOCUS       AX217865                  17 bp    mRNA    linear   PAT 07-SEP-2001
DEFINITION  Sequence 3307 from Patent WO0159103.
ACCESSION   AX217865
VERSION     AX217865.1  GI:15527926
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 3307 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
BASE COUNT        3 a      3 c      2 g      9 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        439 AGAAAGTTGCTGAA 452
              |||||||||| ||
Db         16 AGAAAGTTGCTCAA 3


RESULT 627
AX218175/c
LOCUS       AX218175                  17 bp    mRNA    linear   PAT 07-SEP-2001
DEFINITION  Sequence 3617 from Patent WO0159103.
ACCESSION   AX218175
VERSION     AX218175.1  GI:15528236
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 3617 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
BASE COUNT        8 a      5 c      1 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1180 TTTCTATAGGTGAG 1193
              ||||||| ||||||
Db         15 TTTCTATTGGTGAG 2
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RESULT 628
AX262900/c
LOCUS       AX262900                  17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 291 from Patent WO0173002.
ACCESSION   AX262900
VERSION     AX262900.1  GI:16511699
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 291 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      3 c      6 g      6 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        511 GTCAGCGCCAACCT 524
              ||||| ||||||||
Db         14 GTCAGAGCCAACCT 1


RESULT 629
AX262901
LOCUS       AX262901                  17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 292 from Patent WO0173002.
ACCESSION   AX262901
VERSION     AX262901.1  GI:16511700
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 292 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        6 a      6 c      3 g      2 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        511 GTCAGCGCCAACCT 524
              ||||| ||||||||
Db          4 GTCAGAGCCAACCT 17


RESULT 630
AX422449/c
LOCUS       AX422449                  17 bp    mRNA    linear   PAT 18-JUN-2002
DEFINITION  Sequence 785 from Patent WO0188124.
ACCESSION   AX422449
VERSION     AX422449.1  GI:21525831
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 785 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      8 c      2 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        824 TGATGCAGCTGAAG 837
              |||||||||| ||
Db         15 TGATGCAGCTGGAG 2


RESULT 631
AX422575
LOCUS       AX422575                  17 bp    mRNA    linear   PAT 18-JUN-2002
DEFINITION  Sequence 911 from Patent WO0188124.
ACCESSION   AX422575
VERSION     AX422575.1  GI:21525957
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 911 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      9 c      3 g      2 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        591 GCCCCCCACCAGCC 604
              || ||||||||||||
Db          4 GCTCCCCACCAGCC 17


RESULT 632
AX422576
LOCUS       AX422576                  17 bp    mRNA    linear   PAT 18-JUN-2002
DEFINITION  Sequence 912 from Patent WO0188124.
ACCESSION   AX422576
VERSION     AX422576.1  GI:21525958
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
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  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 912 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      9 c      3 g      1 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        591 GCCCCCCACCAGCC 604
              || ||||||||||||
Db          3 GCTCCCCACCAGCC 16


RESULT 633
AX422577
LOCUS       AX422577                 17 bp    mRNA    linear   PAT 18-JUN-2002
DEFINITION  Sequence 913 from Patent WO0188124.
ACCESSION   AX422577
VERSION     AX422577.1  GI:21525959
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 913 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      9 c      3 g      2 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        591 GCCCCCCACCAGCC 604
              || ||||||||||||
Db          2 GCTCCCCACCAGCC 15


RESULT 634
AX422896/c
LOCUS       AX422896                 17 bp    mRNA    linear   PAT 18-JUN-2002
DEFINITION  Sequence 1232 from Patent WO0188124.
ACCESSION   AX422896
VERSION     AX422896.1  GI:21526278
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 1232 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      8 c      2 g      4 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        824 TGATGCAGCTGAAG 837
              |||||||||| ||
Db         14 TGATGCAGCTGGAG 1


RESULT 635
AX423383
LOCUS       AX423383                 17 bp    mRNA    linear   PAT 18-JUN-2002
DEFINITION  Sequence 1719 from Patent WO0188124.
ACCESSION   AX423383
VERSION     AX423383.1  GI:21526765
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 1719 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        6 a      5 c      2 g      4 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         22 TAAACCAAACCCAG 35
              || ||||||||||||
Db          1 TATACCAAACCCAG 14


RESULT 636
AX499079
LOCUS       AX499079                 17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 386 from Patent EP1229046.
ACCESSION   AX499079
VERSION     AX499079.1  GI:23381372
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 386 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      4 c      7 g      1 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy        523 CTGCCGGAGGAGCA 536
              ||||||||||||| |
Db          1 CTGCCGGAGGAGGA 14


RESULT 637
AX530984/c
LOCUS       AX530984                 17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 493 from Patent EP1239051.
ACCESSION   AX530984
VERSION     AX530984.1  GI:25253755
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 493 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      4 c      8 g      1 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        632 TCCAGGAGCTCTGC 645
              ||| ||||||||||
Db         17 TCCCGGAGCTCTGC 4


RESULT 638
AX530988/c
LOCUS       AX530988                 17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 497 from Patent EP1239051.
ACCESSION   AX530988
VERSION     AX530988.1  GI:25253763
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 497 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      4 c      8 g      1 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        631 CTCCAGGAGCTCTG 644
              |||| |||||||||
Db         14 CTCCCGGAGCTCTG 1


RESULT 639
AX532255/c
LOCUS       AX532255                 17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 1764 from Patent EP1239051.
ACCESSION   AX532255
VERSION     AX532255.1  GI:25256295
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 1764 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      2 c      7 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        908 CCCTGGTCCTAAAG 921
              |||| |||||||||
Db         17 CCCTTGTCCTAAAG 4


RESULT 640
AX532256/c
LOCUS       AX532256                 17 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 1765 from Patent EP1239051.
ACCESSION   AX532256
VERSION     AX532256.1  GI:25256297
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M.
  TITLE     Human posh-like protein 1
  JOURNAL   Patent: EP 1239051-A 1765 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      2 c      6 g      4 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        908 CCCTGGTCCTAAAG 921
              |||| |||||||||
Db         16 CCCTTGTCCTAAAG 3


RESULT 641
AX546102
LOCUS       AX546102                 17 bp    DNA     linear   PAT 26-NOV-2002
DEFINITION  Sequence 1615 from Patent EP1243660.
ACCESSION   AX546102
VERSION     AX546102.1  GI:25811313
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
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  AUTHORS   Zhang,J., Gu,Y. and Nguyen,C.T.
  TITLE     Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
  JOURNAL   Patent: EP 1243660-A 1615 25-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      4 c      8 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        302 CTGTGGGGGCTGCA 315
              ||||||||||  |||
Db          4 CTGTGGGGGCAGCA 17


RESULT 642
AX546103
LOCUS       AX546103                  17 bp    DNA     linear   PAT 26-NOV-2002
DEFINITION  Sequence 1616 from Patent EP1243660.
ACCESSION   AX546103
VERSION     AX546103.1  GI:25811314
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J., Gu,Y. and Nguyen,C.T.
  TITLE     Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
  JOURNAL   Patent: EP 1243660-A 1616 25-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      4 c      7 g      4 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        302 CTGTGGGGGCTGCA 315
              ||||||||||  |||
Db          3 CTGTGGGGGCAGCA 16


RESULT 643
AX546104
LOCUS       AX546104                  17 bp    DNA     linear   PAT 26-NOV-2002
DEFINITION  Sequence 1617 from Patent EP1243660.
ACCESSION   AX546104
VERSION     AX546104.1  GI:25811315
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J., Gu,Y. and Nguyen,C.T.
  TITLE     Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
  JOURNAL   Patent: EP 1243660-A 1617 25-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      3 c      8 g      4 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        302 CTGTGGGGGCTGCA 315
              ||||||||||  |||
Db          2 CTGTGGGGGCAGCA 15


RESULT 644
AX546105
LOCUS       AX546105                  17 bp    DNA     linear   PAT 26-NOV-2002
DEFINITION  Sequence 1618 from Patent EP1243660.
ACCESSION   AX546105
VERSION     AX546105.1  GI:25811316
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J., Gu,Y. and Nguyen,C.T.
  TITLE     Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
  JOURNAL   Patent: EP 1243660-A 1618 25-SEP-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      3 c      9 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        302 CTGTGGGGGCTGCA 315
              ||||||||||  |||
Db          1 CTGTGGGGGCAGCA 14


RESULT 645
AX580294
LOCUS       AX580294                  17 bp    mRNA    linear   PAT 10-JAN-2003
DEFINITION  Sequence 2132 from Patent WO0211674.
ACCESSION   AX580294
VERSION     AX580294.1  GI:27649496
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
            and Grupe,A.
  TITLE     Method and reagent for the inhibition of calcium activated chloride
            channel-1 (clca-1)
  JOURNAL   Patent: WO 0211674-A 2132 14-FEB-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
            Thompson, James (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
BASE COUNT        7 a      6 c      2 g      2 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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```
Qy        647 TCCCCCAAGACCTG 660
              ||| ||||||||||
Db          1 TCCACCAAGACCTG 14


RESULT 646
AX615236/c
LOCUS       AX615236                 17 bp    DNA     linear   PAT 20-FEB-2003
DEFINITION  Sequence 43 from Patent EP1262488.
ACCESSION   AX615236
VERSION     AX615236.1  GI:28446135
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y. and Nguyen,C.T.
  TITLE     Human lccl-domain containing protein
  JOURNAL   Patent: EP 1262488-A 43 04-DEC-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT       14 a      1 c      2 g      0 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTG 1157
              ||||||||||| ||
Db         17 TTTTTTTCTTTCTG 4


RESULT 647
AX615237/c
LOCUS       AX615237                 17 bp    DNA     linear   PAT 20-FEB-2003
DEFINITION  Sequence 44 from Patent EP1262488.
ACCESSION   AX615237
VERSION     AX615237.1  GI:28446136
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y. and Nguyen,C.T.
  TITLE     Human lccl-domain containing protein
  JOURNAL   Patent: EP 1262488-A 44 04-DEC-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT       13 a      2 c      2 g      0 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTG 1157
              ||||||||||| ||
Db         16 TTTTTTTCTTTCTG 3


RESULT 648
AX615238/c
LOCUS       AX615238                 17 bp    DNA     linear   PAT 20-FEB-2003
DEFINITION  Sequence 45 from Patent EP1262488.
ACCESSION   AX615238
VERSION     AX615238.1  GI:28446137
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y. and Nguyen,C.T.
  TITLE     Human lccl-domain containing protein
  JOURNAL   Patent: EP 1262488-A 45 04-DEC-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT       12 a      2 c      2 g      1 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTG 1157
              ||||||||||| ||
Db         15 TTTTTTTCTTTCTG 2


RESULT 649
AX615239/c
LOCUS       AX615239                 17 bp    DNA     linear   PAT 20-FEB-2003
DEFINITION  Sequence 46 from Patent EP1262488.
ACCESSION   AX615239
VERSION     AX615239.1  GI:28446138
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y. and Nguyen,C.T.
  TITLE     Human lccl-domain containing protein
  JOURNAL   Patent: EP 1262488-A 46 04-DEC-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT       11 a      2 c      3 g      1 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTG 1157
              ||||||||||| ||
Db         14 TTTTTTTCTTTCTG 1


RESULT 650
AX615893/c
LOCUS       AX615893                 17 bp    DNA     linear   PAT 20-FEB-2003
DEFINITION  Sequence 700 from Patent EP1262488.
ACCESSION   AX615893
VERSION     AX615893.1  GI:28446939
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y. and Nguyen,C.T.
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  TITLE     Human lccl-domain containing protein
  JOURNAL   Patent: EP 1262488-A 700 04-DEC-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      6 c      4 g      4 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        527 CGGAGGAGCAGCTG 540
              | ||||||||||||
Db         17 CTGAGGAGCAGCTG 4


RESULT 651
AX615894/c
LOCUS       AX615894                 17 bp    DNA     linear   PAT 20-FEB-2003
DEFINITION  Sequence 701 from Patent EP1262488.
ACCESSION   AX615894
VERSION     AX615894.1  GI:28446940
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y. and Nguyen,C.T.
  TITLE     Human lccl-domain containing protein
  JOURNAL   Patent: EP 1262488-A 701 04-DEC-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      7 c      4 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        527 CGGAGGAGCAGCTG 540
              | ||||||||||||
Db         16 CTGAGGAGCAGCTG 3


RESULT 652
AX648752/c
LOCUS       AX648752                 17 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 592 from Patent EP1273660.
ACCESSION   AX648752
VERSION     AX648752.1  GI:29151570
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y.
  TITLE     Human sodium-hydrogen exchanger like protein 1
  JOURNAL   Patent: EP 1273660-A 592 08-JAN-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      6 c      4 g      4 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        921 GGAGATGGCAGATC 934
              |||||||||||  ||
Db         17 GGAGATGGCAGTTC 4


RESULT 653
AX648756/c
LOCUS       AX648756                 17 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 596 from Patent EP1273660.
ACCESSION   AX648756
VERSION     AX648756.1  GI:29151574
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y.
  TITLE     Human sodium-hydrogen exchanger like protein 1
  JOURNAL   Patent: EP 1273660-A 596 08-JAN-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      7 c      2 g      4 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        920 AGGAGATGGCAGAT 933
              |||||||||||| |
Db         14 AGGAGATGGCAGTT 1


RESULT 654
AX672063/c
LOCUS       AX672063                 17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 508 from Patent WO03004526.
ACCESSION   AX672063
VERSION     AX672063.1  GI:29330411
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 508 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        6 a      6 c      4 g      1 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        539 TGGGTGCCCTGCTG 552
              |||||| |||||||
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Db         17 TGGGTGTCCTGCTG 4


RESULT 655
AX672221
LOCUS       AX672221                  17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 666 from Patent WO03004526.
ACCESSION   AX672221
VERSION     AX672221.1  GI:29330569
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 666 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      2 c      4 g      6 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        329 ATCATCCTGGTGAT 342
              ||||| ||||||||
Db          2 ATCATACTGGTGAT 15


RESULT 656
AX672590/c
LOCUS       AX672590                  17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 1035 from Patent WO03004526.
ACCESSION   AX672590
VERSION     AX672590.1  GI:29330938
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 1035 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        6 a      6 c      2 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        294 AATGTCTGCTGTGG 307
              ||||| ||||||||
Db         17 AATGTGTGCTGTGG 4


RESULT 657
AX672718/c
LOCUS       AX672718                  17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 1163 from Patent WO03004526.
ACCESSION   AX672718
VERSION     AX672718.1  GI:29331066
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 1163 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      8 c      5 g      1 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        540 GGGTGCCCTGCTGG 553
              |||||||| |||||
Db         17 GGGTGCCCGGCTGG 4


RESULT 658
AX672921/c
LOCUS       AX672921                  17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 1366 from Patent WO03004526.
ACCESSION   AX672921
VERSION     AX672921.1  GI:29331269
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 1366 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      8 c      2 g      4 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        529 GAGGAGCAGCTGGG 542
              ||||||||| ||||
Db         17 GAGGAGCAGTTGGG 4


RESULT 659
AX673606
LOCUS       AX673606                  17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 2051 from Patent WO03004526.
ACCESSION   AX673606
VERSION     AX673606.1  GI:29331954
KEYWORDS    .
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 2051 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      3 c      1 g     12 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
              | ||||||||||||
Db          4 CCTTTTTTCTTTTT 17


RESULT 660
AX673696
LOCUS       AX673696                 17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 2141 from Patent WO03004526.
ACCESSION   AX673696
VERSION     AX673696.1  GI:29332044
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 2141 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      3 c      6 g      5 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        857 ACCGCTTTGAGGTC 870
              | ||||||||||||
Db          2 ATCGCTTTGAGGTC 15


RESULT 661
AX674202
LOCUS       AX674202                 17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 2647 from Patent WO03004526.
ACCESSION   AX674202
VERSION     AX674202.1  GI:29332550
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 2647 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      1 c      7 g      6 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        448 CTGAAGTTTGTGGT 461
              |||||||||| |||
Db          4 CTGAAGTTTGGGGT 17


RESULT 662
AX674701
LOCUS       AX674701                 17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 3146 from Patent WO03004526.
ACCESSION   AX674701
VERSION     AX674701.1  GI:29333049
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 3146 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      3 c      7 g      4 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        669 CTTGGCCAGCGTGG 682
              ||||| ||||||||
Db          4 CTTGGACAGCGTGG 17


RESULT 663
AX674715
LOCUS       AX674715                 17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 3160 from Patent WO03004526.
ACCESSION   AX674715
VERSION     AX674715.1  GI:29333063
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 3160 16-JAN-2003;
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Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 2 a 4 c 4 g 7 t

Query Match 0.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1330 GATCTTGTGTTTCA 1343
||||||||||| |||
Db 1 GATCTTGTGTCTCA 14

RESULT 664
AX687638/c
LOCUS AX687638 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 370 from Patent EP1281758.
ACCESSION AX687638
VERSION AX687638.1 GI:29410334
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 370 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 4 a 4 c 6 g 3 t

Query Match 0.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 628 CAGCTCCAGGAGCT 641
|||||||||||| ||
Db 17 CAGCTCCAGGATCT 4

RESULT 665
AX687639/c
LOCUS AX687639 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 371 from Patent EP1281758.
ACCESSION AX687639
VERSION AX687639.1 GI:29410335
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 371 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 3 a 5 c 6 g 3 t

Query Match 0.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 628 CAGCTCCAGGAGCT 641
|||||||||||| ||
Db 16 CAGCTCCAGGATCT 3

RESULT 666
AX690687
LOCUS AX690687 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 3419 from Patent EP1281758.
ACCESSION AX690687
VERSION AX690687.1 GI:29413568
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 3419 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 2 a 6 c 5 g 4 t

Query Match 0.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 522 CCTGCCGGAGGAGC 535
|||||| |||||||
Db 2 CCTGCCTGAGGAGC 15

RESULT 667
AX690688
LOCUS AX690688 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 3420 from Patent EP1281758.
ACCESSION AX690688
VERSION AX690688.1 GI:29413595
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 3420 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 2 a 7 c 5 g 3 t

Query Match 0.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 522 CCTGCCGGAGGAGC 535
|||||| |||||||

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Db          1 CCTGCCTGAGGAGC 14


RESULT 668
AX692522
LOCUS       AX692522                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5254 from Patent EP1281758.
ACCESSION   AX692522
VERSION     AX692522.1  GI:29415480
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5254 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      1 c      0 g     15 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
              ||||||||  |||||
Db          4 CTTTTTTTTTTTTT 17


RESULT 669
AX692523
LOCUS       AX692523                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5255 from Patent EP1281758.
ACCESSION   AX692523
VERSION     AX692523.1  GI:29415481
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5255 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      1 c      0 g     16 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
              ||||||||  |||||
Db          3 CTTTTTTTTTTTTT 16


RESULT 670
AX692524
LOCUS       AX692524                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5256 from Patent EP1281758.
ACCESSION   AX692524
VERSION     AX692524.1  GI:29415482
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5256 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      1 c      0 g     16 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
              ||||||||  |||||
Db          2 CTTTTTTTTTTTTT 15


RESULT 671
AX692525
LOCUS       AX692525                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5257 from Patent EP1281758.
ACCESSION   AX692525
VERSION     AX692525.1  GI:29415483
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5257 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      1 c      0 g     16 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
              ||||||||  |||||
Db          1 CTTTTTTTTTTTTT 14


RESULT 672
AX692526
LOCUS       AX692526                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5258 from Patent EP1281758.
ACCESSION   AX692526
VERSION     AX692526.1  GI:29415484
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5258 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        0 a      0 c      1 g     16 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTG 1157
              ||||||| ||||||
Db          4 TTTTTTTTTTTTTG 17


RESULT 673
AX692529
LOCUS       AX692529                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5261 from Patent EP1281758.
ACCESSION   AX692529
VERSION     AX692529.1  GI:29415487
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5261 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      0 c      2 g     13 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTG 1157
              ||||||| ||||||
Db          1 TTTTTTTTTTTTTG 14


RESULT 674
AX693202/c
LOCUS       AX693202                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5934 from Patent EP1281758.
ACCESSION   AX693202
VERSION     AX693202.1  GI:29416166
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5934 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      3 c      9 g      1 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        572 TCCAGCAGGCCCTC 585
              |||||| |||||||
Db         17 TCCAGCTGGCCCTC 4


RESULT 675
AX693206/c
LOCUS       AX693206                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5938 from Patent EP1281758.
ACCESSION   AX693206
VERSION     AX693206.1  GI:29416170
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5938 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      5 c      7 g      2 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        571 CTCCAGCAGGCCCT 584
              ||||||| ||||||
Db         14 CTCCAGCTGGCCCT 1


RESULT 676
AX722562
LOCUS       AX722562                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 249 from Patent WO03025176.
ACCESSION   AX722562
VERSION     AX722562.1  GI:30423063
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 249 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
BASE COUNT        4 a      4 c      5 g      4 t
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  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        550 CTGGCAGGCATGCA 563
              |||||| |||||||
Db          4 CTGGCATGCATGCA 17


RESULT 677
AX722630/c
LOCUS       AX722630                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 317 from Patent WO03025176.
ACCESSION   AX722630
VERSION     AX722630.1  GI:30423131
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 317 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
BASE COUNT        6 a      3 c      2 g      6 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1320 TGCTTTTGTAGATC 1333
              ||| ||||||||||
Db         14 TGCATTTGTAGATC 1


RESULT 678
AX723850
LOCUS       AX723850                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 1537 from Patent WO03025176.
ACCESSION   AX723850
VERSION     AX723850.1  GI:30503193
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 1537 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
BASE COUNT        1 a      2 c      1 g     13 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1142 CCTTTTTTTCTTTT 1155
              ||||||||| ||||
Db          4 CCTTTTTTTTTTTT 17


RESULT 679
AX724112
LOCUS       AX724112                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 1799 from Patent WO03025176.
ACCESSION   AX724112
VERSION     AX724112.1  GI:30503455
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 1799 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
BASE COUNT        1 a      9 c      2 g      5 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        582 CCTCCGTCTGCCCC 595
              ||||| ||||||||
Db          4 CCTCCTTCTGCCCC 17


RESULT 680
AX725587/c
LOCUS       AX725587                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3274 from Patent WO03025176.
ACCESSION   AX725587
VERSION     AX725587.1  GI:30504930
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 3274 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
BASE COUNT        3 a      5 c      4 g      5 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1005 GGACAGGCACCTGA 1018
              ||||||||| ||||
Db         16 GGACAGGCATCTGA 3


RESULT 681
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AX725730/c
LOCUS       AX725730                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3417 from Patent WO03025176.
ACCESSION   AX725730
VERSION     AX725730.1  GI:30505073
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 3417 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
BASE COUNT        2 a      6 c      5 g      4 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        229 CAGCCTCAGGCATC 242
              ||||||||||  |||
Db         14 CAGCCTCAGGGATC 1


RESULT 682
AX725917
LOCUS       AX725917                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3604 from Patent WO03025176.
ACCESSION   AX725917
VERSION     AX725917.1  GI:30505260
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 3604 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
BASE COUNT        5 a      5 c      4 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        122 TCCACACGGGACAG 135
              |||||||  ||||||
Db          3 TCCACACTGGACAG 16


RESULT 683
AX727828/c
LOCUS       AX727828                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 5515 from Patent WO03025176.
ACCESSION   AX727828
VERSION     AX727828.1  GI:30507171
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 5515 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
BASE COUNT        4 a      6 c      2 g      5 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        921 GGAGATGGCAGATC 934
              |||||||| |||||
Db         14 GGAGATGGAAGATC 1


RESULT 684
AX729364
LOCUS       AX729364                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 998 from Patent WO03025175.
ACCESSION   AX729364
VERSION     AX729364.1  GI:30508707
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 998 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        6 a      2 c      6 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        271 CTGATCAAAGAGGA 284
              ||| ||||||||||
Db          4 CTGGTCAAAGAGGA 17


RESULT 685
AX729843
LOCUS       AX729843                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 1477 from Patent WO03025175.
ACCESSION   AX729843
VERSION     AX729843.1  GI:30509186
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 1477 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      3 c      3 g      6 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1330 GATCTTGTGTTTCA 1343
              ||||||||||  |||
Db          1 GATCTTGTGTATCA 14


RESULT 686
AX729912/c
LOCUS       AX729912                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 1546 from Patent WO03025175.
ACCESSION   AX729912
VERSION     AX729912.1  GI:30509255
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 1546 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a     11 c      2 g      2 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        761 GGTGGCGGGTGGAT 774
              ||  ||||||||||||
Db         15 GGAGGCGGGTGGAT 2


RESULT 687
AX729998
LOCUS       AX729998                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 1632 from Patent WO03025175.
ACCESSION   AX729998
VERSION     AX729998.1  GI:30509341
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 1632 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        6 a      1 c      7 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        273 GATCAAAGAGGAAG 286
              |||||  ||||||||
Db          1 GATCAGAGAGGAAG 14


RESULT 688
AX730052/c
LOCUS       AX730052                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 1686 from Patent WO03025175.
ACCESSION   AX730052
VERSION     AX730052.1  GI:30509395
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 1686 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      4 c      8 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        627 CCAGCTCCAGGAGC 640
              ||||||||||||  |
Db         14 CCAGCTCCAGGATC 1


RESULT 689
AX731309
LOCUS       AX731309                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 2943 from Patent WO03025175.
ACCESSION   AX731309
VERSION     AX731309.1  GI:30510652
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 2943 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 4 a 2 c 3 g 8 t

Query Match 0.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1101 TAATTATGTAGTTT 1114
| ||||||||||||
Db 3 TCATTATGTAGTTT 16

RESULT 690
AX731411/c
LOCUS AX731411 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3045 from Patent WO03025175.
ACCESSION AX731411
VERSION AX731411.1 GI:30510754
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 3045 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 5 a 5 c 3 g 4 t

Query Match 0.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 451 AAGTTTGTGGTCAG 464
|||||||||| |||
Db 17 AAGTTTGTGGCCAG 4

RESULT 691
AX731447/c
LOCUS AX731447 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3081 from Patent WO03025175.
ACCESSION AX731447
VERSION AX731447.1 GI:30510790
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 3081 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 4 a 5 c 2 g 6 t

Query Match 0.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 921 GGAGATGGCAGATC 934
||||||| ||||||
Db 14 GGAGATGACAGATC 1

RESULT 692
AX731728/c
LOCUS AX731728 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3362 from Patent WO03025175.
ACCESSION AX731728
VERSION AX731728.1 GI:30511071
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 3362 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 4 a 4 c 3 g 6 t

Query Match 0.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 268 TGGCTGATCAAAGA 281
||||||| ||||||
Db 16 TGGCTGAACAAAGA 3

RESULT 693
AX732671/c
LOCUS AX732671 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4305 from Patent WO03025175.
ACCESSION AX732671
VERSION AX732671.1 GI:30512014
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 4305 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 6 a 6 c 4 g 1 t

Query Match 0.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 539 TGGGTGCCCTGCTG 552
|||||| |||||||

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Db         17 TGGGTGTCCTGCTG 4


RESULT 694
AX734182/c
LOCUS       AX734182                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 5816 from Patent WO03025175.
ACCESSION   AX734182
VERSION     AX734182.1  GI:30513525
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 5816 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      8 c      2 g      4 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        529 GAGGAGCAGCTGGG 542
              ||||||||| ||||
Db         17 GAGGAGCAGTTGGG 4


RESULT 695
AX734441/c
LOCUS       AX734441                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 31 from Patent WO03025177.
ACCESSION   AX734441
VERSION     AX734441.1  GI:30513718
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 31 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      6 c      4 g      2 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1291 GTTGCTCAGCCTGG 1304
              ||||||||| ||||
Db         17 GTTGCTCAGGCTGG 4


RESULT 696
AX734896
LOCUS       AX734896                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 486 from Patent WO03025177.
ACCESSION   AX734896
VERSION     AX734896.1  GI:30514173
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 486 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      3 c      8 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1251 CATGTGAGGCCAGG 1264
              | ||||||||||||
Db         4 CGTGTGAGGCCAGG 17


RESULT 697
AX735539
LOCUS       AX735539                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 1129 from Patent WO03025177.
ACCESSION   AX735539
VERSION     AX735539.1  GI:30514816
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 1129 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        7 a      3 c      5 g      2 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        273 GATCAAAGAGGAAG 286
              |||| |||||||||
Db         1 GATCCAAGAGGAAG 14


RESULT 698
AX735762
LOCUS       AX735762                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 1352 from Patent WO03025177.
ACCESSION   AX735762
VERSION     AX735762.1  GI:30515039
KEYWORDS    .
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 1352 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      4 c      6 g      3 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1251 CATGTGAGGCCAGG 1264
              ||||||||| |||||
Db          4 CATGTGAGCCCAGG 17


RESULT 699
AX736077/c
LOCUS       AX736077                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 1667 from Patent WO03025177.
ACCESSION   AX736077
VERSION     AX736077.1  GI:30515354
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 1667 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a     10 c      2 g      2 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        761 GGTGGCGGGTGGAT 774
              || ||||||||||||
Db         15 GGAGGCGGGTGGAT 2


RESULT 700
AX737750
LOCUS       AX737750                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3340 from Patent WO03025177.
ACCESSION   AX737750
VERSION     AX737750.1  GI:30517038
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 3340 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      2 c      3 g      7 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1150 TCTTTTTGGAAGTA 1163
              |||||||||| ||
Db          3 TCTTTTTGGAAATA 16


RESULT 701
AX738070/c
LOCUS       AX738070                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3660 from Patent WO03025177.
ACCESSION   AX738070
VERSION     AX738070.1  GI:30517358
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 3660 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        7 a      4 c      4 g      2 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1320 TGCTTTTGTAGATC 1333
              |||| |||||||||
Db         14 TGCTCTTGTAGATC 1


RESULT 702
AX738493
LOCUS       AX738493                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 4083 from Patent WO03025177.
ACCESSION   AX738493
VERSION     AX738493.1  GI:30517781
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 4083 27-MAR-2003;
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          Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        1 a      1 c      1 g     14 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
              ||||||||| |||||
Db          4 CTTTTTTTTTTTTT 17


RESULT 703
AX738516
LOCUS       AX738516                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 4106 from Patent WO03025177.
ACCESSION   AX738516
VERSION     AX738516.1  GI:30517804
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 4106 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        3 a      8 c      2 g      4 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1201 CCTTCACACCTCCC 1214
              ||||||||| |||||
Db          4 CCTTCACAGCTCCC 17


RESULT 704
AX739654/c
LOCUS       AX739654                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 5244 from Patent WO03025177.
ACCESSION   AX739654
VERSION     AX739654.1  GI:30518951
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 5244 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT       14 a      1 c      1 g      1 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTG 1157
              ||||||| ||||||
Db         17 TTTTTTTTTTTTTG 4


RESULT 705
AX739841
LOCUS       AX739841                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 5431 from Patent WO03025177.
ACCESSION   AX739841
VERSION     AX739841.1  GI:30519138
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 5431 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
BASE COUNT        3 a      3 c      7 g      4 t

  Query Match             0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        669 CTTGGCCAGCGTGG 682
              ||||| ||||||||
Db          4 CTTGGACAGCGTGG 17


RESULT 706
BD011732
LOCUS       BD011732                  17 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  795, a novel gene related to pollen allergy.
ACCESSION   BD011732
VERSION     BD011732.1  GI:22091921
KEYWORDS    WO 0065050-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     795, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0065050-A 4 02-NOV-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0065050-A/4
            PD   02-NOV-2000
            PF   26-APR-2000 WO 2000JP002734
            PR   27-APR-1999 JP 99P   120494
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
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            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC
            A61P37/00
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
BASE COUNT        0 a      0 c      2 g     15 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTG 1157
              ||||||| ||||||
Db          4 TTTTTTTTTTTTTG 17


RESULT 707
BD066839
LOCUS       BD066839                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD066839
VERSION     BD066839.1  GI:22612442
KEYWORDS    JP 2001511000-A/1474.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 1474 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/1474
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
                  Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unknown'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
BASE COUNT        2 a      4 c      3 g      8 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        445 TTGCTGAAGTTTGT 458
              ||||||||||||| |
Db          3 TTGCTGAAGTTTCT 16


RESULT 708
BD067278
LOCUS       BD067278                 17 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors.
ACCESSION   BD067278
VERSION     BD067278.1  GI:22612881
KEYWORDS    JP 2001511003-A/118.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Akhtar,S., Fell,P. and Mcswiggen,J.A.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors
  JOURNAL   Patent: JP 2001511003-A 118 07-AUG-2001;
            RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT     OS   Unidentified
            PN   JP 2001511003-A/118
            PD   07-AUG-2001
            PF   14-JAN-1998 JP 1998532913
            PR   31-JAN-1997 US    60/036476,04-DEC-1997 US    08/985162 PI
            SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
            C12N9/00,C07K14/71
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                  related to
            CC   levels of epidermal growth factor receptors
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="unidentified"
                      /mol_type="genomic RNA"
                      /db_xref="taxon:32644"
BASE COUNT        3 a      3 c      5 g      6 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1099 CGTAATTATGTAGT 1112
              |||||||||||  ||
Db          3 CGTAATTATGTGGT 16


RESULT 709
BD067279
LOCUS       BD067279                 17 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors.
ACCESSION   BD067279
VERSION     BD067279.1  GI:22612882
KEYWORDS    JP 2001511003-A/119.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Akhtar,S., Fell,P. and Mcswiggen,J.A.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors
  JOURNAL   Patent: JP 2001511003-A 119 07-AUG-2001;
            RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT     OS   Unidentified
            PN   JP 2001511003-A/119
            PD   07-AUG-2001
            PF   14-JAN-1998 JP 1998532913
            PR   31-JAN-1997 US    60/036476,04-DEC-1997 US    08/985162 PI
            SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
            C12N9/00,C07K14/71
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                  related to
            CC   levels of epidermal growth factor receptors
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
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     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"
BASE COUNT        4 a      2 c      5 g      6 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1099 CGTAATTATGTAGT 1112
              ||||||||||| ||
Db          2 CGTAATTATGTGGT 15


RESULT 710
BD091744
LOCUS       BD091744                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  441, a novel gene related to pollen allergy.
ACCESSION   BD091744
VERSION     BD091744.1  GI:22637355
KEYWORDS    WO 0073435-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
  TITLE     441, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073435-A 4 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
COMMENT     OS   Artificial Sequence
            PN   WO 0073435-A/4
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003190
            PR   27-MAY-1999 JP 99P   148783
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI
            PC   C12N15/10,C12Q1/68,G01N33/15,G01N33/50
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        0 a      0 c      2 g     15 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTG 1157
              ||||||| ||||||
Db          4 TTTTTTTTTTTTTG 17


RESULT 711
BD091752
LOCUS       BD091752                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  465, a novel gene related to pollen allergy.
ACCESSION   BD091752
VERSION     BD091752.1  GI:22637363
KEYWORDS    WO 0073439-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     465, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073439-A 4 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073439-A/4
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003191
            PR   27-MAY-1999 JP 99P   148784
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,A61P37/08,A61K39/36,A61K45/00 CC   Description
            of Artificial Sequence:Artificially Synthesized CC   Primer
            Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        0 a      0 c      2 g     15 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTG 1157
              ||||||| ||||||
Db          4 TTTTTTTTTTTTTG 17


RESULT 712
BD091775
LOCUS       BD091775                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  787, a novel gene related to pollen allergy.
ACCESSION   BD091775
VERSION     BD091775.1  GI:22637386
KEYWORDS    WO 0073440-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     787, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073440-A 4 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073440-A/4
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003192
            PR   27-MAY-1999 JP 99P   148785
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,C12N5/08,C12N5/06,C07K14/415 CC   Description of
            Artificial Sequence:Artificially Synthesized CC   Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
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BASE COUNT         0 a      0 c      2 g     15 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTG 1157
              ||||||| ||||||
Db          4 TTTTTTTTTTTTTG 17


RESULT 713
BD097336
LOCUS       BD097336                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for examination for allergosis.
ACCESSION   BD097336
VERSION     BD097336.1  GI:22642910
KEYWORDS    WO 0165259-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0165259-A 7 07-SEP-2001;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI,YUTAKA
            FUJIKI,KAZUO FUKAWA,OSAMU KUDO TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI
            OBAYASHI,KEIKO MATSUI, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0165259-A/7
            PD   07-SEP-2001
            PF   23-FEB-2001 WO 2001JP001372
            PR   02-MAR-2000 JP 00P    61832
            PI   TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI OBAYASHI,KEIKO MATSUI, PI
              HIROHISA SAITO
            PC   G01N33/53,C12Q1/68,C12N15/12,G01N33/15,A01K67/027,A61K39/395,
            PC   A61P37/08
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT         0 a      0 c      2 g     15 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTG 1157
              ||||||| ||||||
Db          4 TTTTTTTTTTTTTG 17


RESULT 714
BD142810
LOCUS       BD142810                 17 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Method of examining allergic disease.
ACCESSION   BD142810
VERSION     BD142810.1  GI:23237755
KEYWORDS    WO 0224903-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
            Tsujimoto,G. and Takahashi,E.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0224903-A 4 28-MAR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO,EIKI
            TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0224903-A/4
            PD   28-MAR-2002
            PF   21-SEP-2001 WO 2001JP008246
            PR   25-SEP-2000 JP 00P   291318
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO,EIKI TAKAHASHI
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC           primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT         0 a      0 c      2 g     15 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTG 1157
              ||||||| ||||||
Db          4 TTTTTTTTTTTTTG 17


RESULT 715
BD143836
LOCUS       BD143836                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD143836
VERSION     BD143836.1  GI:27849594
KEYWORDS    JP 2002095500-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Tsujimoto,K.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: JP 2002095500-A 4 02-APR-2002;
            GENOX RESEARCH INC,THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
COMMENT     OS   Artificial Sequence
            PN   JP 2002095500-A/4
            PD   02-APR-2002
            PF   25-SEP-2000 JP 2000291316
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   KOZO TSUJIMOTO
            PC
            C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC
             C07K14/47,
            PC   C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
            ,C12N15/09,C12P21/02,
            PC   C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00, PC
             C12N15/00
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            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        0 a      0 c      2 g     15 t

  Query Match              0.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTG 1157
              ||||||| ||||||
Db          4 TTTTTTTTTTTTTG 17


RESULT 716
BD167837
LOCUS       BD167837                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination of allergosis.
ACCESSION   BD167837
VERSION     BD167837.1  GI:27873649
KEYWORDS    WO 0233122-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
            and Takahashi,E.
  TITLE     Method for examination of allergosis
  JOURNAL   Patent: WO 0233122-A 4 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI
            HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
            SAITO,EIKI TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0233122-A/4
            PD   25-APR-2002
            PF   11-OCT-2001 WO 2001JP008937
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO,EIKI TAKAHASHI
            PC   C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC
             A61K39/395,
            PC   A01K67/027//C07K16/18,C12N5/10
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            CC            anchor
            CC   primer sequence
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            FT   source          1. .17
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FEATURES             Location/Qualifiers
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  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTG 1157
              ||||||| ||||||
Db          4 TTTTTTTTTTTTTG 17


RESULT 717
BD167909
LOCUS       BD167909                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD167909
VERSION     BD167909.1  GI:27873721
KEYWORDS    WO 0226962-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
            Saito,H.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0226962-A 8 04-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI,KAZUO MIYANAGA YUJI
            SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, TAKESHI
            NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0226962-A/8
            PD   04-APR-2002
            PF   21-SEP-2001 WO 2001JP008247
            PR   26-SEP-2000 JP 00P   293021
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
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            CC   sequence
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Qy       1144 TTTTTTTCTTTTTG 1157
              ||||||| ||||||
Db          4 TTTTTTTTTTTTTG 17


RESULT 718
BD168113
LOCUS       BD168113                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination for allergosis.
ACCESSION   BD168113
VERSION     BD168113.1  GI:27873925
KEYWORDS    WO 0233069-A/20.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Saito,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0233069-A 20 25-APR-2002;
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GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA,CHUHEI NOJIRI,NOBUO MATSUHASHI,KOJI NISHIZAWA, YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO

COMMENT OS Artificial Sequence
PN WO 0233069-A/20
PD 25-APR-2002
PF 28-SEP-2001 WO 2001JP008574
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09,C12N15/63,C12Q1/68,C12Q1/02,G01N33/53,C12N5/10, PC A61K39/395,
PC C07K14/47,C07K16/18//C12P21/02,C12P21/08
CC Description of Artificial Sequence:an artificially synthesized

CC anchor
CC primer sequence
FH Key Location/Qualifiers
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FT /organism='Artificial Sequence'.

FEATURES Location/Qualifiers
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BASE COUNT 0 a 0 c 2 g 15 t

Query Match 0.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1144 TTTTTTTCTTTTTG 1157
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Db 4 TTTTTTTTTTTTTG 17

RESULT 719
BD171179
LOCUS BD171179 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD171179
VERSION BD171179.1 GI:27876991
KEYWORDS WO 0250269-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and Tsujimoto,G.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0250269-A 4 27-JUN-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI,AKINORI OTA YOSHIKO MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, TAKESHI NAGASU, GOZO TSUJIMOTO

COMMENT OS Artificial Sequence
PN WO 0250269-A/4
PD 27-JUN-2002
PF 21-DEC-2001 WO 2001JP011286
PR 21-DEC-2000 JP 00P 389476
PI YOSHIKO MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, PI TAKESHI NAGASU,
PI GOZO TSUJIMOTO
PC C12N15/11,C07K16/18,A61K67/027,A61K31/711,A61K45/00,A61K48/00,
PC A61P37/08,
PC C12Q1/68,G01N33/50
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CC primer sequence
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FT /organism='Artificial Sequence'.

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/mol_type="genomic DNA"
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BASE COUNT 0 a 0 c 2 g 15 t

Query Match 0.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1144 TTTTTTTCTTTTTG 1157
||||||| ||||||
Db 4 TTTTTTTTTTTTTG 17

RESULT 720
E34260
LOCUS E34260 17 bp DNA linear PAT 31-JAN-2002
DEFINITION Pollinosis-associated gene.
ACCESSION E34260
VERSION E34260.1 GI:18624265
KEYWORDS JP 2000106879-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M., Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
TITLE Pollinosis-associated gene
JOURNAL Patent: JP 2000106879-A 4 18-APR-2000;
GENOX RESEARCH INC
COMMENT OS Artificial Sequence
PN JP 2000106879-A/4
PD 18-APR-2000
PF 06-OCT-1998 JP 1998284610
PR
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NING NO,
PI KAORU OGAWA
PC C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC

FH Key Location/Qualifiers
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FEATURES Location/Qualifiers
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BASE COUNT 0 a 0 c 2 g 15 t

Query Match 0.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1144 TTTTTTTCTTTTTG 1157
||||||| ||||||
Db 4 TTTTTTTTTTTTTG 17

RESULT 721
E59657
LOCUS E59657 17 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for preparing nucleic acid sample for analyzing minor gene, nucleic acid sample thus prepared and method for analyzing nucleic acid sample by using the same, and reagent kit and analysis service for using the same.
ACCESSION E59657
VERSION E59657.1 GI:13019451
KEYWORDS JP 2000037193-A/3.

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SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Takamichi,M., Tsuyoshi,F., Masaharu,K., Takashi,I. and Kazunori,O.
  TITLE     Method for preparing nucleic acid sample for analyzing minor gene,
            nucleic acid sample thus prepared and method for analyzing nucleic
            acid sample by using the same, and reagent kit and analysis service
            for using the same
  JOURNAL   Patent: JP 2000037193-A 3 08-FEB-2000;
            HITACHI LTD
COMMENT     OS   Unidentified
            PN   JP 2000037193-A/3
            PD   08-FEB-2000
            PF   19-MAY-1999 JP 1999138051
            PR
            PI   TAKAMICHI MATSUMURA,TSUYOSHI FUJITA,MASAHARU KIYAMA, PI
            TAKASHI IRIE,
            PI   KAZUNORI OKANO
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
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Qy       1144 TTTTTTTCTTTTTG 1157
              ||||||| ||||||
Db          4 TTTTTTTTTTTTTG 17


RESULT 722
I52597/c
LOCUS       I52597                   17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 338 from patent US 5646042.
ACCESSION   I52597
VERSION     I52597.1  GI:2473798
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 338 08-JUL-1997;
FEATURES              Location/Qualifiers
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  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db         15 GGCAGGGAGTTGAG 2


RESULT 723
I54306
LOCUS       I54306                   17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 2047 from patent US 5646042.
ACCESSION   I54306
VERSION     I54306.1  GI:2475509
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 2047 08-JUL-1997;
FEATURES              Location/Qualifiers
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                      /organism="unknown"
BASE COUNT        8 a      0 c      2 g      7 t

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  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1118 GTTTAATTGAAAAA 1131
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Db          4 GTTTTATTGAAAAA 17


RESULT 724
I54308
LOCUS       I54308                   17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 2049 from patent US 5646042.
ACCESSION   I54308
VERSION     I54308.1  GI:2475511
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 2049 08-JUL-1997;
FEATURES              Location/Qualifiers
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BASE COUNT        8 a      0 c      2 g      7 t

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  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1118 GTTTAATTGAAAAA 1131
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Db          2 GTTTTATTGAAAAA 15


RESULT 725
I57029/c
LOCUS       I57029                   17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 30 from patent US 5650553.
ACCESSION   I57029
VERSION     I57029.1  GI:2477442
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Ecker,J., Rothenberg,M., Lehman,A. and Roman,G.
  TITLE     Plant genes for sensitivity to ethylene and pathogens
  JOURNAL   Patent: US 5650553-A 30 22-JUL-1997;
FEATURES              Location/Qualifiers
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  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db         17 CCACCAAGACCTGG 4
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RESULT 726
AX404467/c
LOCUS AX404467 21 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 293 from Patent WO0224747.
ACCESSION AX404467
VERSION AX404467.1 GI:21437748
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Brinkmann,U. and Hoffmeyer,S.
TITLE Polymorphisms in human genes of cardiovascular regulators and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 0224747-A 293 28-MAR-2002;
Epidauros Biotechnologie AG (DE)
FEATURES Location/Qualifiers
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/note="artificial sequence"
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Best Local Similarity 92.9%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        802 CGCTCCCTGCAGCC 815
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Db         18 CTCTCCCTGCAGCC 5
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Job time : 25 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 8, 2004, 16:39:52 ; Search time 19 Seconds
(without alignments)
1.727 Million cell updates/sec

Title: us-09-904-568-3
Perfect score: 1355
Sequence: 1 gggcaggcagttgaggtgga.....gtgtttcaggcagggcccgg 1355

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 668 seqs, 12108 residues

Total number of hits satisfying chosen parameters: 1336

Minimum DB seq length: 12
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 750 summaries

Database : rng3.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	30	2.2	41	1	ABA03588	Human HS1 protein
	2	22	1.6	22	1	AAC67363	Alzheimer's diseas
	3	22	1.6	22	1	AAZ57266	Human mitochondria
c	4	20	1.5	20	1	AAC67508	Alzheimer's diseas
c	5	18.2	1.3	25	1	ABV92615	Human POSHL1 scann
c	6	18.2	1.3	25	1	ABV92616	Human POSHL1 scann
c	7	18.2	1.3	25	1	ABV92617	Human POSHL1 scann
c	8	17.8	1.3	21	1	AAF79922	PCR primer used to
c	9	17.8	1.3	25	1	ABV92613	Human POSHL1 scann
c	10	17.8	1.3	25	1	ABV92614	Human POSHL1 scann
	11	17.6	1.3	25	1	AAC95776	HLA DRB1 gene PCR
	12	17.6	1.3	25	1	AAC96237	16s rRNA gene PCR
c	13	17.2	1.3	22	1	ABT33591	NOV reverse PCR pr
	14	17.2	1.3	24	1	AAL45714	AML cancer cells d
	15	16.8	1.2	21	1	AAT46092	Primer for STS ass
c	16	16.8	1.2	21	1	AAZ26500	Human polymorphic
	17	16.8	1.2	21	1	AAV05879	Primer #10 for STS
	18	16.8	1.2	21	1	ABK94277	Endothelin convert
c	19	16.8	1.2	21	1	ABK94278	Endothelin convert
	20	16.4	1.2	18	1	AAV48107	Beta-globin fusion
	21	16.4	1.2	18	1	AAC67511	Alzheimer's diseas
	22	16.4	1.2	18	1	AAA94334	Human beta-globin
c	23	16.2	1.2	21	1	AAZ26499	Human polymorphic
c	24	16.2	1.2	21	1	AAC67429	Alzheimer's diseas
c	25	16.2	1.2	21	1	AAZ57277	Human mitochondria
c	26	16.2	1.2	23	1	AAQ64857	Ig gamma chain pro
	27	15.8	1.2	20	1	AAX22417	EP-897990 Seq ID 6
c	28	15.8	1.2	20	1	AAC68751	Human FUT3 antisen
	29	15.8	1.2	20	1	AAZ45870	PCR primer R1570RA
	30	15.8	1.2	20	1	AAZ60204	PCR primer F1570RA
	31	15.8	1.2	20	1	AAZ56049	PCR primer for bet
	32	15.8	1.2	20	1	AAH25407	Detection probe fo
c	33	15.8	1.2	20	1	ABS73911	Human cytohesin-1
	34	15.8	1.2	20	1	ABN83653	Human immunodefici
c	35	15.8	1.2	20	1	ABQ66447	Human cytohesin-1
	36	15.8	1.2	20	1	ABK51604	Human immunodefici
c	37	15.8	1.2	20	1	ABA04617	MOL2 forward PCR p
	38	15.8	1.2	21	1	AAV47652	Mouse focal adhesi
	39	15.8	1.2	21	1	AAV49607	Focal adhesion kin
c	40	15.8	1.2	21	1	AAZ76174	Human biallelic ma
c	41	15.8	1.2	21	1	AAA63852	PCR primer used to
c	42	15.8	1.2	21	1	AAA47627	Intronic primer (5
	43	15.8	1.2	21	1	AAL47730	Ras gene PCR prime
	44	15.8	1.2	21	1	ABK94275	Endothelin convert
c	45	15.8	1.2	21	1	ABK94276	Endothelin convert
	46	15.8	1.2	22	1	ABQ80130	Probe DBM0157P, id
	47	15.8	1.2	22	1	ABQ80159	Probe DBM0157P, id
c	48	15.4	1.1	18	1	ABK85826	Myotonic dystrophy
	49	15.4	1.1	18	1	AAI71035	Human tumour suppr
	50	15.4	1.1	20	1	AAT03278	Mycobacterium tube
c	51	15.4	1.1	20	1	AAZ77095	Human biallelic ma
	52	15.4	1.1	21	1	AAQ75612	Reverse transcript
c	53	15.4	1.1	21	1	AAT84695	KSHV DNA polymeras
c	54	15.4	1.1	21	1	AAT51587	KSHV DNA polymeras
c	55	15.4	1.1	21	1	AAH91924	Human inflammatory
	56	15.4	1.1	21	1	AAF96193	Human gene single
c	57	15.2	1.1	20	1	AAQ65816	Type II procollage
c	58	15.2	1.1	20	1	AAT39478	Steroidogenesis ac
	59	15.2	1.1	20	1	AAZ04965	PCR primer used to
c	60	15.2	1.1	20	1	AAX94626	PCR primer used to
c	61	15.2	1.1	20	1	AAX92281	PCR primer used to
	62	15.2	1.1	20	1	AAX33259	PEBP2 alpha A gene
	63	15.2	1.1	20	1	ABS74296	Human calcium chan
	64	15.2	1.1	20	1	ABS74306	Human calcium chan
	65	15.2	1.1	20	1	ABS76637	Novel metalloprote
c	66	15.2	1.1	20	1	ABS67685	Casein kinase-2 an
	67	15.2	1.1	20	1	ABK69390	Chimeric phosphoro
c	68	15.2	1.1	21	1	AAZ26599	Human polymorphic
c	69	15.2	1.1	21	1	AAC58095	Human PRO2038 hybr
c	70	15.2	1.1	21	1	AAA31011	Primer used to ass
c	71	15.2	1.1	21	1	AAA32137	Primer used to ass
	72	15.2	1.1	21	1	AAF75464	Codon-optimised HP
	73	15.2	1.1	21	1	ABK94273	Endothelin convert
c	74	15.2	1.1	21	1	ABK94274	Endothelin convert
	75	15	1.1	15	1	AAX31672	Tag sequence of a
	76	15	1.1	15	1	ABK32626	Human pancreatic c
c	77	15	1.1	17	1	ABK12664	Rat interleukin 11
c	78	15	1.1	18	1	AAF62379	LSR-leptin interac
	79	15	1.1	21	1	AAZ26122	Human polymorphic
	80	15	1.1	21	1	AAZ26123	Human polymorphic
	81	15	1.1	21	1	AAZ26124	Human polymorphic
c	82	15	1.1	21	1	ABK65504	Human single nucle
c	83	15	1.1	21	1	ABK65804	Human single nucle
c	84	14.8	1.1	18	1	AAX67028	Mouse B7 hairpin r
	85	14.8	1.1	18	1	AAD52710	Psammomys obesus A
	86	14.8	1.1	19	1	AAT96652	Mouse tub gene pri
	87	14.8	1.1	19	1	AAA94645	Mouse tub gene PCR
	88	14.8	1.1	19	1	AAA84761	Cyclin F ribozyme
	89	14.8	1.1	19	1	AAH59923	Cyclin F ribozyme
c	90	14.8	1.1	19	1	AAF91219	Human multi drug r
	91	14.8	1.1	19	1	AAF91221	Human multi drug r
c	92	14.8	1.1	20	1	AAQ52925	Herpes simplex vir
	93	14.8	1.1	20	1	AAZ02840	PCR primer used to
c	94	14.8	1.1	20	1	AAA70403	Plant beta-tubulin
c	95	14.8	1.1	20	1	AAC79519	Human p38beta anti
c	96	14.8	1.1	20	1	AAA72640	PCR primer SEQ ID
	97	14.8	1.1	20	1	AAA11329	Human TRPC7 gene e
c	98	14.8	1.1	20	1	AAA11141	Primer #2 for rat
c	99	14.8	1.1	20	1	AAS45551	Tumour-specific Ig
c	100	14.8	1.1	20	1	AAF92937	Wild type sequence
c	101	14.8	1.1	20	1	AAD17405	Human sFRP2 gene s
	102	14.8	1.1	20	1	AAD40654	Human hepsin antis
	103	14.8	1.1	20	1	AAD40836	Human hepsin antis
c	104	14.8	1.1	20	1	AAD41521	Nrf2 gene specific
	105	14.8	1.1	20	1	AAD36447	Mouse L66 intron 4
	106	14.8	1.1	20	1	ABA05916	Hepatitis B virus

c 107	14.8	1.1	20	1	AAS16509	Human Type II GnRH
c 108	14.8	1.1	20	1	ABI93685	Capture oligonucle
c 109	14.8	1.1	20	1	ABT34167	Human short hetero
c 110	14.8	1.1	20	1	ABX78118	Human p38-beta MAP
111	14.8	1.1	21	1	AAQ75627	Reverse transcript
112	14.8	1.1	21	1	AAV81770	Human SAD PCR prim
c 113	14.8	1.1	21	1	AAA59547	PCR primer used to
c 114	14.8	1.1	21	1	AAZ45243	Reverse PCR primer
c 115	14.8	1.1	21	1	AAI70244	Interleukin-1 rece
116	14.8	1.1	21	1	AAD19825	CmYLCV CmpC promot
c 117	14.8	1.1	21	1	AAD19826	CmYLCV CmpC promot
c 118	14.8	1.1	21	1	AAF85557	Human hNDS4-isofor
119	14.8	1.1	21	1	ABK15655	Anchored oligo-dt
120	14.4	1.1	17	1	AAQ51986	B-cell mRNA ribozy
121	14.4	1.1	17	1	AAA21347	Integrin alpha 6 s
122	14.4	1.1	17	1	AAA21348	Integrin alpha 6 s
c 123	14.4	1.1	17	1	AAA25575	Oestrogen receptor
124	14.4	1.1	17	1	ACA07666	NFKB sub-unit modu
125	14.4	1.1	17	1	ACA08919	NFKB sub-unit modu
c 126	14.4	1.1	18	1	AAA52540	Human MN promoter
127	14.4	1.1	18	1	ABL31110	Human HLA genotypi
c 128	14.4	1.1	18	1	ABK30214	CYP2D6 gene polymo
c 129	14.4	1.1	19	1	AAF91220	Human multi drug r
130	14.4	1.1	19	1	AAF91222	Human multi drug r
131	14.4	1.1	19	1	AAD34212	Erwinia rhapontici
c 132	14.4	1.1	19	1	ACA10200	Human NOVX DNA pro
c 133	14.4	1.1	19	1	ABX56454	Human NOV25a, NOV2
134	14.4	1.1	20	1	AAT41134	Human gene signatu
135	14.4	1.1	20	1	AAQ75560	Reverse transcript
136	14.4	1.1	20	1	AAV06457	Avian sex determin
c 137	14.4	1.1	20	1	AAT99084	Primer alphaEN-S2
c 138	14.4	1.1	20	1	AAZ37518	Human mdm2 phospho
c 139	14.4	1.1	20	1	AAZ09195	Oligonucleotide 7
140	14.4	1.1	20	1	AAX26904	Primer used for ST
c 141	14.4	1.1	20	1	AAA48521	Murine villin gene
c 142	14.4	1.1	20	1	AAA49259	Mouse villin gene
143	14.4	1.1	20	1	AAS45819	Mouse PARP-2 antis
c 144	14.4	1.1	20	1	AAS29287	Human mdm2 antisen
c 145	14.4	1.1	20	1	AAF80672	Human mdm2 phospho
c 146	14.4	1.1	20	1	ABT32305	Neuroblastoma-rela
c 147	14.4	1.1	20	1	ABZ76936	Bovine DGAT BAC-DN
c 148	14.4	1.1	20	1	ABZ77002	Bovine DGAT PCR pr
149	14.4	1.1	20	1	AAD51819	DNA fragment #1 us
150	14.2	1.0	19	1	AAD04572	Human insulinoma-a
c 151	14.2	1.0	19	1	ABT13587	Liver regeneration
152	14.2	1.0	20	1	AAQ82417	Chromosome 11 (loc
153	14.2	1.0	20	1	AAT17134	Primer for cGMP-ph
c 154	14.2	1.0	20	1	AAT92490	BRCA2 cancer susce
155	14.2	1.0	20	1	AAT73292	Primer 2 for pUC19
c 156	14.2	1.0	20	1	AAV57183	Human Notch-3 muta
c 157	14.2	1.0	20	1	AAV57102	Human Notch3 mutan
c 158	14.2	1.0	20	1	AAV38813	PCR primer used to
c 159	14.2	1.0	20	1	AAZ32721	Human chemokine re
160	14.2	1.0	20	1	AAZ03892	PCR primer used to
161	14.2	1.0	20	1	AAX29423	Rat JNK1-specific
c 162	14.2	1.0	20	1	AAZ71860	Human biallelic ma
c 163	14.2	1.0	20	1	AAZ77262	Human biallelic ma
c 164	14.2	1.0	20	1	AAC93165	Human STAT3 phosph
c 165	14.2	1.0	20	1	AAC93217	Human STAT3 phosph
166	14.2	1.0	20	1	AAC62966	JNK antisense olig
c 167	14.2	1.0	20	1	AAA99073	Putative suppresso
168	14.2	1.0	20	1	AAA99178	Bovine cytochrome
169	14.2	1.0	20	1	AAA99182	Bovine cytochrome
170	14.2	1.0	20	1	AAA72160	Humanised anti-Fas
171	14.2	1.0	20	1	AAA11598	Humanised HFE7A de
c 172	14.2	1.0	20	1	AAA40718	Mouse fibrinogen-l
c 173	14.2	1.0	20	1	AAA35414	Myrtaceae microsat
c 174	14.2	1.0	20	1	AAZ40588	NPTII gene forward
c 175	14.2	1.0	20	1	AAI66616	Rat leukotriene B4
c 176	14.2	1.0	20	1	AAS08740	Human PD-ABC form
c 177	14.2	1.0	20	1	AAS08831	Human PD-ABC form
178	14.2	1.0	20	1	AAH57078	Human oestrogen re
c 179	14.2	1.0	20	1	AAH57086	Human oestrogen re
c 180	14.2	1.0	20	1	AAF62896	Human PEPCK-cytoso
181	14.2	1.0	20	1	AAA91053	PCR primer for Hum
182	14.2	1.0	20	1	AAH89204	Human polymorphic
183	14.2	1.0	20	1	ABQ81623	CYP2E1 sense prime
184	14.2	1.0	20	1	AAL49010	Murine IL-13 codin
c 185	14.2	1.0	20	1	AAL47998	Human homeodomain-
c 186	14.2	1.0	20	1	AAD37217	Human MEKK4 antise
187	14.2	1.0	20	1	ABK15887	HES-1 (hairy-enhan
188	14.2	1.0	20	1	ABL45977	Humanised anti-Fas
189	14.2	1.0	20	1	ABL48720	Humanised anti-Fas
190	14.2	1.0	20	1	AAS97928	Murine SAC1 gene-s
c 191	14.2	1.0	20	1	AAS96782	Human STAT3 antise
c 192	14.2	1.0	20	1	AAS96834	Human STAT3 antise
193	14.2	1.0	20	1	ABI96234	Capture oligonucle
194	14.2	1.0	20	1	AAD52224	Human IFNGR1 antis
c 195	14.2	1.0	20	1	AAD52321	Human IFNGR2 antis
c 196	14.2	1.0	20	1	ABX33984	Human interleukin
c 197	14.2	1.0	20	1	ABX34251	Antisense oligonuc
198	14	1.0	17	1	AAQ20005	Oligonucleotide #1
199	14	1.0	17	1	AAA21349	Integrin alpha 6 s
200	14	1.0	17	1	AAA21350	Integrin alpha 6 s
201	14	1.0	17	1	ACA06319	NFKB sub-unit modu
202	14	1.0	18	1	AAQ20007	Oligonucleotide #3
203	14	1.0	19	1	AAV70248	Human HMGI-C exon
204	14	1.0	19	1	AAA82832	cdk4 ribozyme bind
205	14	1.0	19	1	AAA82833	cdk4 ribozyme bind
206	14	1.0	19	1	AAH57994	Cell-cycle depende
207	14	1.0	19	1	AAH57995	Cell-cycle depende
208	14	1.0	19	1	ABL55323	Human HMGI-C exon
209	14	1.0	20	1	AAQ86242	Reverse transcript
210	14	1.0	20	1	AAT10191	Alkaline endogluca
211	14	1.0	20	1	AAT64842	Fusarium oxysporum
c 212	14	1.0	20	1	AAZ72938	Human biallelic ma
213	14	1.0	20	1	AAA53330	Reverse PCR primer
c 214	14	1.0	20	1	AAF83877	Human NOVINTRA C D
c 215	14	1.0	20	1	AAC83988	PrP gene PrnD PCR
216	14	1.0	20	1	ABQ82751	AttacinD AMP gene
217	14	1.0	20	1	AAD46116	Drosophila melanog
218	14	1.0	20	1	ABT09862	K+beta M6 related
c 219	14	1.0	20	1	ABL59377	Primer based on a
c 220	14	1.0	20	1	ABQ74025	Human NOVINTRA C f
221	14	1.0	20	1	AAD39371	S2 gene amplifying
c 222	14	1.0	20	1	ABI93616	Capture oligonucle
223	14	1.0	20	1	ABI95663	Capture oligonucle
c 224	13.8	1.0	17	1	AAT88942	Bumper primer 2 fo
c 225	13.8	1.0	17	1	AAV97865	Human EGF-R target
c 226	13.8	1.0	17	1	AAV97237	Human EGF-R target
c 227	13.8	1.0	17	1	AAX30261	HIV gag bumper pri
228	13.8	1.0	17	1	AAF02208	Hammerhead ribozym
229	13.8	1.0	17	1	AAF02788	Hammerhead ribozym
c 230	13.8	1.0	17	1	AAF05406	Hammerhead ribozym
231	13.8	1.0	17	1	AAZ45525	Primer used to scr
c 232	13.8	1.0	17	1	ABA79028	Factor VIII mutati
233	13.8	1.0	17	1	ABA79029	Factor VIII mutati
234	13.8	1.0	17	1	AAF92872	Human ABC1 transcr
c 235	13.8	1.0	17	1	ABK03156	Human CD20 Inozyme
c 236	13.8	1.0	17	1	ABV90547	Human POSHL1 scann
c 237	13.8	1.0	17	1	ABV90548	Human POSHL1 scann
c 238	13.8	1.0	17	1	ABV90549	Human POSHL1 scann
c 239	13.8	1.0	17	1	ABV90550	Human POSHL1 scann
c 240	13.8	1.0	17	1	ABV90551	Human POSHL1 scann
c 241	13.8	1.0	17	1	ABV90553	Human POSHL1 scann
c 242	13.8	1.0	17	1	ABQ63635	Human KTOM1a porti
243	13.8	1.0	17	1	ABK56690	Human CLCA1 gene e
c 244	13.8	1.0	17	1	ABK57443	Human CLCA1 gene e
c 245	13.8	1.0	17	1	ABN01791	Human GDMLP-1 17-m
246	13.8	1.0	17	1	ABN06165	Human GDMLP-1 17-m
247	13.8	1.0	17	1	ABN06166	Human GDMLP-1 17-m
c 248	13.8	1.0	17	1	ABN08390	Human GDMLP-1 17-m
c 249	13.8	1.0	17	1	ABN08391	Human GDMLP-1 17-m
250	13.8	1.0	17	1	ABN10236	Human GDMLP-1 17-m
251	13.8	1.0	17	1	ABN10237	Human GDMLP-1 17-m
252	13.8	1.0	17	1	ABK18358	Human ERG hammerhe

c 253	13.8	1.0	17	1	ABK19019	Human ERG DNAzyme
c 254	13.8	1.0	17	1	ABK19334	Human ERG Amberzym
255	13.8	1.0	17	1	ABT35326	Tumour suppression
256	13.8	1.0	17	1	ABT35714	Tumour suppression
257	13.8	1.0	17	1	ACA06320	NFKB sub-unit modu
258	13.8	1.0	17	1	ABZ61741	Human H-Ras DNAzym
259	13.8	1.0	17	1	ABZ64935	Human HER2 DNAzyme
260	13.8	1.0	17	1	ABZ65512	Human HER2 DNAzyme
261	13.8	1.0	18	1	AAQ10847	Probe to N-termina
262	13.8	1.0	18	1	AAQ78449	TGF-beta gene phos
c 263	13.8	1.0	18	1	AAX67046	Mouse B7 hairpin r
264	13.8	1.0	18	1	AAX62708	Granule bound star
c 265	13.8	1.0	18	1	AAT87896	Lower primer for e
266	13.8	1.0	18	1	AAV57794	Human chromosome 1
c 267	13.8	1.0	18	1	AAV41332	Interleukin-9 (IL-
268	13.8	1.0	18	1	AAZ70371	Human biallelic ma
269	13.8	1.0	18	1	AAA09267	3' primer for rat
c 270	13.8	1.0	18	1	AAD19799	CmYLCV viral genom
c 271	13.8	1.0	18	1	AAS45542	Tumour-specific Ig
c 272	13.8	1.0	18	1	AAF62371	Zinc finger coding
273	13.8	1.0	18	1	AAF92873	Human ABC1 transcr
c 274	13.8	1.0	18	1	AAH47607	Human Her-3 mRNA i
275	13.8	1.0	18	1	ABX03799	DNA encoding secre
c 276	13.8	1.0	18	1	ABS52111	Human adipocyte C1
c 277	13.8	1.0	19	1	AAQ27299	pSPL1 primer DHA14
c 278	13.8	1.0	19	1	AAQ47696	Sequence of primer
c 279	13.8	1.0	19	1	AAX36444	Target sequence fo
c 280	13.8	1.0	19	1	AAT95586	Primer for SSCP an
c 281	13.8	1.0	19	1	AAT51286	Human AD4 gene PCR
282	13.8	1.0	19	1	AAV51978	Zea mays genome re
283	13.8	1.0	19	1	AAV51979	Zea mays genome re
c 284	13.8	1.0	19	1	AAV56488	Human DP2.5 APC pr
c 285	13.8	1.0	19	1	AAT96201	Primer for SSCP an
c 286	13.8	1.0	19	1	AAZ10311	Antisense oligonuc
c 287	13.8	1.0	19	1	AAX33236	Wheat viviparous 1
c 288	13.8	1.0	19	1	AAX05488	2' modified oligo
c 289	13.8	1.0	19	1	AAA93490	Human SRP19 gene e
290	13.8	1.0	19	1	AAA84760	Cyclin F ribozyme
c 291	13.8	1.0	19	1	AAA06830	Phosphorothioate o
292	13.8	1.0	19	1	AAA23478	Clone vc46_1 hybri
c 293	13.8	1.0	19	1	AAZ94157	Human PEMT2 PCR pr
c 294	13.8	1.0	19	1	AAZ48149	Oligonucleotide SE
c 295	13.8	1.0	19	1	AAS11124	Bacterial 16s RNA
296	13.8	1.0	19	1	AAH59922	Cyclin F ribozyme
c 297	13.8	1.0	19	1	ABS67159	DP1, SRP19, DP25 g
298	13.6	1.0	15	1	ABA81571	Human phospholipid
299	13.6	1.0	15	1	ABL91860	Human LIPG gene al
300	13.6	1.0	15	1	AAS94583	Human PLTP gene al
301	13.6	1.0	21	1	AAC67429	Alzheimer's diseas
302	13.6	1.0	21	1	AAZ57277	Human mitochondria
303	13.4	1.0	15	1	AAX18364	RT-PCR primer of t
304	13.4	1.0	15	1	AAF95031	Mutant capture oli
305	13.4	1.0	15	1	AAF45161	Antisense oligonuc
c 306	13.4	1.0	15	1	AAF46436	IGFBP2 oligonucleo
c 307	13.4	1.0	15	1	AAF46437	IGFBP2 oligonucleo
c 308	13.4	1.0	15	1	AAF46438	IGFBP2 oligonucleo
309	13.4	1.0	15	1	AAF46503	IGFBP2 oligonucleo
c 310	13.4	1.0	15	1	AAF49863	IGF-I oligonucleot
c 311	13.4	1.0	15	1	AAF49864	IGF-I oligonucleot
c 312	13.4	1.0	15	1	AAF51703	IGF-I oligonucleot
c 313	13.4	1.0	15	1	ABS97176	Human CYP4501A2 Ex
314	13.4	1.0	15	1	AAL48126	Human neuropeptide
315	13.4	1.0	17	1	AAT06918	Chromosomal locus
316	13.4	1.0	17	1	AAT64712	Primer E15 for map
317	13.4	1.0	17	1	AAA21346	Integrin alpha 6 s
c 318	13.4	1.0	17	1	AAC66363	PCR primer used to
319	13.4	1.0	17	1	AAF02209	Hammerhead ribozym
320	13.4	1.0	17	1	AAA36112	Human genomic SNP
c 321	13.4	1.0	17	1	AAA25574	Oestrogen receptor
322	13.4	1.0	17	1	ABA77189	Adenosine deaminas
c 323	13.4	1.0	17	1	ABA77190	Adenosine deaminas
324	13.4	1.0	17	1	ABA77193	Adenosine deaminas
c 325	13.4	1.0	17	1	ABA77194	Adenosine deaminas
326	13.4	1.0	17	1	ABA77197	Adenosine deaminas
c 327	13.4	1.0	17	1	ABA77198	Adenosine deaminas
c 328	13.4	1.0	17	1	ABA80972	LDLR mutation corr
329	13.4	1.0	17	1	ABA80973	LDLR mutation corr
330	13.4	1.0	17	1	AAF44454	Human PRO1245 reve
331	13.4	1.0	17	1	ABV73116	LGALS1 cDNA quanti
332	13.4	1.0	17	1	ABV79137	Human HTPL scannin
333	13.4	1.0	17	1	ABV79138	Human HTPL scannin
334	13.4	1.0	17	1	ABV79139	Human HTPL scannin
c 335	13.4	1.0	17	1	ABV89781	Human POSHL1 scann
c 336	13.4	1.0	17	1	ABV89782	Human POSHL1 scann
c 337	13.4	1.0	17	1	ABV89783	Human POSHL1 scann
c 338	13.4	1.0	17	1	ABV90552	Human POSHL1 scann
339	13.4	1.0	17	1	ABK40398	Reverse PCR primer
340	13.4	1.0	17	1	ABK56691	Human CLCA1 gene e
341	13.4	1.0	17	1	ABK18409	Human ERG hammerhe
342	13.4	1.0	17	1	ABK18410	Human ERG hammerhe
c 343	13.4	1.0	17	1	ABK19335	Human ERG Amberzym
344	13.4	1.0	17	1	ABT39230	Tumour suppression
c 345	13.4	1.0	17	1	ABT39985	Tumour suppression
346	13.4	1.0	17	1	ABX80463	Novel human secret
347	13.4	1.0	17	1	ABX80967	Human secreted/tra
348	13.4	1.0	17	1	ABX81350	Novel human secret
349	13.4	1.0	17	1	ABX90440	Human secreted/tra
350	13.4	1.0	17	1	ABX78051	Human PRO PCR prim
351	13.4	1.0	17	1	ABX79647	Human sectreted/tr
c 352	13.4	1.0	17	1	ABZ60185	Human K-Ras DNAzym
353	13.4	1.0	17	1	ABZ61172	Human K-Ras DNAzym
c 354	13.4	1.0	17	1	ABZ61566	Human H-Ras DNAzym
355	13.4	1.0	17	1	ABZ61903	Human H-Ras DNAzym
356	13.4	1.0	17	1	ABX64286	Human PRO DNA PCR
357	13.4	1.0	17	1	ABX17250	Human PRO probe #5
c 358	13.4	1.0	18	1	AAQ26549	Control probe #4 f
c 359	13.4	1.0	18	1	AAQ52841	Cytomegalovirus ta
360	13.4	1.0	18	1	AAX67098	Human B7-2 hairpin
361	13.4	1.0	18	1	AAV54171	Nucleotide sequenc
c 362	13.4	1.0	18	1	AAA48761	Human G-alpha-16 a
363	13.4	1.0	18	1	AAA10983	DNA sequence #4 us
c 364	13.4	1.0	18	1	AAA10986	Partial signalling
365	13.4	1.0	18	1	AAZ90641	Human adipose tiss
366	13.4	1.0	18	1	AAZ97002	Nucleotide sequenc
c 367	13.4	1.0	18	1	AAZ97005	Nucleotide sequenc
c 368	13.4	1.0	18	1	AAZ44140	Human EGR-1 DNA an
c 369	13.4	1.0	18	1	AAZ35905	Human sentrin phos
370	13.4	1.0	18	1	AAH75239	Human inducible NO
371	13.4	1.0	18	1	AAH55881	Human SCN1A PCR-SS
372	13.4	1.0	18	1	AAH25339	Antisense oligonuc
373	13.4	1.0	18	1	AAH25861	DNA array oligonuc
c 374	13.4	1.0	18	1	AAF62366	Zinc finger coding
375	13.4	1.0	18	1	AAF58213	Sequence determina
c 376	13.4	1.0	18	1	AAF58216	Sequence determina
c 377	13.4	1.0	18	1	ABZ10842	Haematopoietic cel
378	13.4	1.0	19	1	AAQ75547	Reverse transcript
379	13.4	1.0	19	1	AAX06004	Oligo used in cons
380	13.4	1.0	19	1	AAS45588	Human PARP-2 RT-PC
c 381	13.4	1.0	19	1	ABL88875	HIV-1 related bind
382	13.2	1.0	18	1	AAN92661	Probe to polymorph
383	13.2	1.0	18	1	AAQ54537	HLA-DP genotype de
c 384	13.2	1.0	18	1	AAQ89247	Hepatitis C virus
385	13.2	1.0	18	1	AAX75643	Mouse flt-1 VEGF r
386	13.2	1.0	18	1	AAX71704	Human KDR VEGF rec
387	13.2	1.0	18	1	AAX70233	Human flt1 VEGF re
388	13.2	1.0	18	1	AAT84310	Human VEGF-C gene
c 389	13.2	1.0	18	1	AAT80260	Oligo HCV91, targe
390	13.2	1.0	18	1	AAQ67556	Anti-metallothione
c 391	13.2	1.0	18	1	AAQ67557	Anti-metallothione
392	13.2	1.0	18	1	AAV16730	Oligonucleotide of
393	13.2	1.0	18	1	AAZ01197	PCR primer for PG1
c 394	13.2	1.0	18	1	AAX77049	PCR primer for the
c 395	13.2	1.0	18	1	AAX57940	PCR primer for G.
c 396	13.2	1.0	18	1	AAX03321	PCR primer PCR53 u
c 397	13.2	1.0	18	1	AAZ71683	Human biallelic ma
398	13.2	1.0	18	1	AAA92417	Oligonucleotide PC

	399	13.2	1.0	18	1	AAA55497	TRAF1 antisense ol
	400	13.2	1.0	18	1	AAA27086	Human NF-kappa-B p
c	401	13.2	1.0	18	1	AAA39029	Unknown bacterial
c	402	13.2	1.0	18	1	AAA15532	Human G-alpha-i3 a
c	403	13.2	1.0	18	1	AAA09715	G-alpha-i2 antisen
	404	13.2	1.0	18	1	AAZ91440	Human Ship-2 phosp
	405	13.2	1.0	18	1	AAZ65527	Immunosuppressant
c	406	13.2	1.0	18	1	AAI66785	PPAR-gamma mRNA am
	407	13.2	1.0	18	1	AAF89283	Sample member clus
	408	13.2	1.0	18	1	AAH75784	Human NOV 12 rever
	409	13.2	1.0	18	1	AAH51027	Human nGPCR9 PCR p
	410	13.2	1.0	18	1	AAF26667	Human Smad7 phosph
	411	13.2	1.0	18	1	ABQ82729	VEGFR-3 binding pe
	412	13.2	1.0	18	1	ABS70260	PCR primer, #6, us
c	413	13.2	1.0	18	1	ABS65844	Inhibitory oligonu
c	414	13.2	1.0	18	1	ABT06049	Human IgM heavy ch
c	415	13.2	1.0	18	1	ABK47739	Beta-actin reverse
c	416	13.2	1.0	18	1	ABK24039	B7-related protein
	417	13.2	1.0	18	1	ABL43688	Human chromosome 1
c	418	13.2	1.0	18	1	ABT21516	Multiplex group PC
c	419	13.2	1.0	18	1	ABT15904	B7-related PCR pri
	420	13.2	1.0	18	1	ABV77248	PCR primer for hum
c	421	13.2	1.0	18	1	ABQ84276	Beta-actin reverse
c	422	13.2	1.0	18	1	ABZ10445	Haematopoietic cel
c	423	13.2	1.0	18	1	ABZ10446	Haematopoietic cel
c	424	13.2	1.0	18	1	ABZ11019	Haematopoietic cel
c	425	13.2	1.0	18	1	ABZ11020	Haematopoietic cel
	426	13.2	1.0	18	1	ABZ11021	Haematopoietic cel
	427	13.2	1.0	18	1	ABZ11022	Haematopoietic cel
c	428	13	1.0	13	1	ABC89050	Oligonucleotide SE
	429	13	1.0	13	1	ABC89051	Oligonucleotide SE
c	430	13	1.0	13	1	ABC99986	Oligonucleotide SE
	431	13	1.0	13	1	ABC99987	Oligonucleotide SE
	432	13	1.0	13	1	ABF16196	Oligonucleotide SE
c	433	13	1.0	13	1	ABF16197	Oligonucleotide SE
c	434	13	1.0	13	1	ABH17590	Oligonucleotide SE
	435	13	1.0	13	1	ABH17591	Oligonucleotide SE
	436	13	1.0	13	1	ABH18096	Oligonucleotide SE
c	437	13	1.0	13	1	ABH18097	Oligonucleotide SE
	438	13	1.0	14	1	AAV92063	Human C-raf target
	439	13	1.0	15	1	AAT55016	Human relA hammerh
c	440	13	1.0	15	1	AAC73458	Reverse primer #97
c	441	13	1.0	15	1	ABA81582	Human phospholipid
c	442	13	1.0	15	1	AAF51701	IGF-I oligonucleot
c	443	13	1.0	15	1	AAF51702	IGF-I oligonucleot
	444	13	1.0	15	1	ABK98166	Triple helix formi
	445	13	1.0	15	1	ABK98185	Triple helix formi
c	446	13	1.0	15	1	ABK95944	Human LIPE gene po
	447	13	1.0	15	1	ABK81414	SCYA20 allele spec
	448	13	1.0	15	1	ABL52099	Human PER1 allele
c	449	13	1.0	15	1	ABK67885	Human ADH7 gene al
	450	13	1.0	15	1	ABA97405	Nucleotide sequenc
	451	13	1.0	15	1	ABK64023	Human BF gene alle
	452	13	1.0	15	1	AAS19628	ASO primer #7 to d
c	453	13	1.0	15	1	AAS98667	Colony stimulating
c	454	13	1.0	15	1	AAS94594	Human PLTP gene al
	455	13	1.0	15	1	ABL42625	Hairpin beacon tar
	456	13	1.0	16	1	AAQ20008	Oligonucleotide #4
	457	13	1.0	17	1	AAQ20006	Oligonucleotide #2
	458	13	1.0	17	1	AAQ33416	Polymorphic site r
	459	13	1.0	17	1	AAQ92208	p53 detection prob
	460	13	1.0	17	1	AAT95093	Probe for acid sph
c	461	13	1.0	17	1	AAV97224	Human EGF-R target
	462	13	1.0	17	1	ABV79135	Human HTPL scannin
	463	13	1.0	17	1	ABV79136	Human HTPL scannin
	464	13	1.0	17	1	AAD33183	LDLR cDNA amplifyi
c	465	13	1.0	18	1	AAT05895	Human IL-2 exon 3-
	466	13	1.0	18	1	AAZ31808	Human G-alpha-13 a
c	467	13	1.0	18	1	AAZ74428	Human biallelic ma
c	468	13	1.0	18	1	AAH26911	Fluorescent oligon
c	469	13	1.0	18	1	AAD15912	Y strand RNA oligo
c	470	13	1.0	18	1	ABK41151	Human obesity-asso
c	471	12.8	0.9	16	1	AAQ68252	Triple helix formi
c	472	12.8	0.9	16	1	AAQ80862	Purine-rich methyl
c	473	12.8	0.9	16	1	AAQ95859	Primer A (Group 11
	474	12.8	0.9	16	1	AAT43025	Juvenile glaucoma
	475	12.8	0.9	16	1	AAX18366	RT-PCR primer of t
c	476	12.8	0.9	16	1	AAC63258	Oligonucleotide #3
	477	12.8	0.9	16	1	AAC63300	Oligonucleotide #7
	478	12.8	0.9	16	1	AAA46382	PCR primer used fo
	479	12.8	0.9	16	1	AAF73460	HGF nucleic acid l
	480	12.8	0.9	16	1	ABL95939	Probe #23 for assa
	481	12.8	0.9	16	1	ABX94194	Human SCCA2 gene,
	482	12.8	0.9	16	1	ABX94515	23S rDNA helix 54
c	483	12.8	0.9	17	1	AAT53533	Rat ICAM hammerhea
c	484	12.8	0.9	17	1	AAT53757	Rat ICAM hammerhea
	485	12.8	0.9	17	1	AAT81190	Human c-myb hammer
	486	12.8	0.9	17	1	AAX75174	Mouse flt-1 VEGF r
c	487	12.8	0.9	17	1	AAX71624	Human KDR VEGF rec
	488	12.8	0.9	17	1	AAX63011	Delta-9 desaturase
	489	12.8	0.9	17	1	AAX62200	Granule bound star
	490	12.8	0.9	17	1	AAV97672	Human EGF-R target
	491	12.8	0.9	17	1	AAV94931	Mouse IL-2 recepto
	492	12.8	0.9	17	1	AAV94898	Mouse IL-2 recepto
	493	12.8	0.9	17	1	AAV39410	Humanised anti-HM1
	494	12.8	0.9	17	1	AAA20491	Integrin alpha 6 s
	495	12.8	0.9	17	1	AAX59454	Primer used in con
	496	12.8	0.9	17	1	AAF02787	Hammerhead ribozym
	497	12.8	0.9	17	1	AAF02789	Hammerhead ribozym
	498	12.8	0.9	17	1	AAF03345	Hammerhead ribozym
c	499	12.8	0.9	17	1	AAF05405	Hammerhead ribozym
c	500	12.8	0.9	17	1	AAF05437	Hammerhead ribozym
	501	12.8	0.9	17	1	AAF06984	Hammerhead ribozym
	502	12.8	0.9	17	1	AAF07122	Hammerhead ribozym
c	503	12.8	0.9	17	1	AAC70618	Single nucleotide
c	504	12.8	0.9	17	1	AAC70621	Single nucleotide
	505	12.8	0.9	17	1	AAA25453	Oestrogen receptor
	506	12.8	0.9	17	1	AAA25454	Oestrogen receptor
c	507	12.8	0.9	17	1	ABA80996	LDLR mutation corr
	508	12.8	0.9	17	1	ABA80997	LDLR mutation corr
	509	12.8	0.9	17	1	ABA81248	PSEN1 mutation cor
c	510	12.8	0.9	17	1	ABA81249	PSEN1 mutation cor
c	511	12.8	0.9	17	1	ABK03155	Human CD20 Inozyme
c	512	12.8	0.9	17	1	ABK03627	Human CD20 DNAzyme
c	513	12.8	0.9	17	1	ABV80570	Human HTPL scannin
c	514	12.8	0.9	17	1	ABV80571	Human HTPL scannin
	515	12.8	0.9	17	1	ABV82838	Human HTPL scannin
	516	12.8	0.9	17	1	ABV82839	Human HTPL scannin
	517	12.8	0.9	17	1	ABV89507	Human POSHL1 scann
	518	12.8	0.9	17	1	ABV89508	Human POSHL1 scann
	519	12.8	0.9	17	1	ABV90534	Human POSHL1 scann
	520	12.8	0.9	17	1	ABV90535	Human POSHL1 scann
c	521	12.8	0.9	17	1	ABV90546	Human POSHL1 scann
c	522	12.8	0.9	17	1	ABV90554	Human POSHL1 scann
c	523	12.8	0.9	17	1	ABV91053	Human POSHL1 scann
c	524	12.8	0.9	17	1	ABV91054	Human POSHL1 scann
c	525	12.8	0.9	17	1	ABQ63634	Human KTOM1a porti
c	526	12.8	0.9	17	1	ABQ63636	Human KTOM1a porti
	527	12.8	0.9	17	1	ABK55869	Human CLCA1 gene e
c	528	12.8	0.9	17	1	ABK56045	Human CLCA1 gene e
c	529	12.8	0.9	17	1	ABK56620	Human CLCA1 gene e
c	530	12.8	0.9	17	1	ABK56621	Human CLCA1 gene e
	531	12.8	0.9	17	1	ABK57130	Human CLCA1 gene e
c	532	12.8	0.9	17	1	ABK57404	Human CLCA1 gene e
c	533	12.8	0.9	17	1	ABN01790	Human GDMLP-1 17-m
c	534	12.8	0.9	17	1	ABN01792	Human GDMLP-1 17-m
	535	12.8	0.9	17	1	ABN01897	Human GDMLP-1 17-m
	536	12.8	0.9	17	1	ABN01898	Human GDMLP-1 17-m
	537	12.8	0.9	17	1	ABN06164	Human GDMLP-1 17-m
	538	12.8	0.9	17	1	ABN06167	Human GDMLP-1 17-m
	539	12.8	0.9	17	1	ABN06274	Human GDMLP-1 17-m
	540	12.8	0.9	17	1	ABN06275	Human GDMLP-1 17-m
	541	12.8	0.9	17	1	ABN06515	Human GDMLP-1 17-m
	542	12.8	0.9	17	1	ABN06516	Human GDMLP-1 17-m
c	543	12.8	0.9	17	1	ABN08389	Human GDMLP-1 17-m
c	544	12.8	0.9	17	1	ABN08392	Human GDMLP-1 17-m

c	545	12.8	0.9	17	1	ABN09587	Human GDMLP-1 17-m
c	546	12.8	0.9	17	1	ABN09588	Human GDMLP-1 17-m
	547	12.8	0.9	17	1	ABN10235	Human GDMLP-1 17-m
	548	12.8	0.9	17	1	ABN10238	Human GDMLP-1 17-m
	549	12.8	0.9	17	1	ABN10239	Human GDMLP-1 17-m
	550	12.8	0.9	17	1	ABN10240	Human GDMLP-1 17-m
c	551	12.8	0.9	17	1	ABN10735	Human GDMLP-1 17-m
c	552	12.8	0.9	17	1	ABN10736	Human GDMLP-1 17-m
c	553	12.8	0.9	17	1	ABN10737	Human GDMLP-1 17-m
c	554	12.8	0.9	17	1	ABN10738	Human GDMLP-1 17-m
	555	12.8	0.9	17	1	ABK17830	Human ERG hammerhe
	556	12.8	0.9	17	1	ABK18357	Human ERG hammerhe
	557	12.8	0.9	17	1	ABK18359	Human ERG hammerhe
c	558	12.8	0.9	17	1	ABK18805	Human ERG DNAzyme
	559	12.8	0.9	17	1	ABK19286	Human ERG Amberzym
c	560	12.8	0.9	17	1	ABK19333	Human ERG Amberzym
c	561	12.8	0.9	17	1	ABK25511	Male-sterile plant
	562	12.8	0.9	17	1	ABK25512	Male-sterile plant
c	563	12.8	0.9	17	1	ABK25527	Male-sterile plant
	564	12.8	0.9	17	1	ABK25528	Male-sterile plant
	565	12.8	0.9	17	1	ABL31073	Human HLA genotypi
	566	12.8	0.9	17	1	ABL31564	Human HLA genotypi
	567	12.8	0.9	17	1	ABL31655	Human HLA genotypi
	568	12.8	0.9	17	1	ABL31671	Human HLA genotypi
	569	12.8	0.9	17	1	ABL31720	Human HLA genotypi
	570	12.8	0.9	17	1	ABA01457	Streptococcus ther
	571	12.8	0.9	17	1	ABT35820	Tumour suppression
c	572	12.8	0.9	17	1	ABT35849	Tumour suppression
	573	12.8	0.9	17	1	ABT36006	Tumour suppression
	574	12.8	0.9	17	1	ABT37187	Tumour suppression
	575	12.8	0.9	17	1	ABT37634	Tumour suppression
c	576	12.8	0.9	17	1	ABT37805	Tumour suppression
c	577	12.8	0.9	17	1	ABT38097	Tumour suppression
c	578	12.8	0.9	17	1	ABT39257	Tumour suppression
	579	12.8	0.9	17	1	ABT39551	Tumour suppression
	580	12.8	0.9	17	1	ABT39720	Tumour suppression
	581	12.8	0.9	17	1	ACA06264	NFKB sub-unit modu
	582	12.8	0.9	17	1	ACA06326	NFKB sub-unit modu
c	583	12.8	0.9	17	1	ACA06585	NFKB sub-unit modu
	584	12.8	0.9	17	1	ACA06587	NFKB sub-unit modu
c	585	12.8	0.9	17	1	ACA06653	NFKB sub-unit modu
c	586	12.8	0.9	17	1	ACA06814	NFKB sub-unit modu
c	587	12.8	0.9	17	1	ACA06858	NFKB sub-unit modu
c	588	12.8	0.9	17	1	ACA06859	NFKB sub-unit modu
c	589	12.8	0.9	17	1	ACA07770	NFKB sub-unit modu
	590	12.8	0.9	17	1	ACA08920	NFKB sub-unit modu
c	591	12.8	0.9	17	1	ACC44610	Human CBFA1 type I
c	592	12.8	0.9	17	1	ABZ60572	Human K-Ras DNAzym
	593	12.8	0.9	17	1	ABZ61171	Human K-Ras DNAzym
c	594	12.8	0.9	17	1	ABZ61760	Human H-Ras DNAzym
c	595	12.8	0.9	17	1	ABZ61761	Human H-Ras DNAzym
	596	12.8	0.9	17	1	ABZ64859	Human HER2 DNAzyme
	597	12.8	0.9	17	1	ABZ64966	Human HER2 DNAzyme
	598	12.8	0.9	18	1	AAQ70348	Antisense oligonuc
c	599	12.8	0.9	18	1	AAQ86978	Primer 1 to amplif
c	600	12.8	0.9	18	1	AAT50704	Rabbit CETP hairpi
c	601	12.8	0.9	18	1	AAT28333	Multi-G oligonucle
	602	12.8	0.9	18	1	AAT30032	NER PCR primer ES1
	603	12.8	0.9	18	1	AAX75628	Mouse flt-1 VEGF r
	604	12.8	0.9	18	1	AAX70294	Human flt1 VEGF re
c	605	12.8	0.9	18	1	AAX62734	Granule bound star
	606	12.8	0.9	18	1	AAX62754	Granule bound star
	607	12.8	0.9	18	1	AAT94805	Human leukocyte an
	608	12.8	0.9	18	1	AAT76410	Human endothelin-1
	609	12.8	0.9	18	1	AAX10189	Human biallelic po
	610	12.8	0.9	18	1	AAV95056	Mouse IL-2 recepto
	611	12.8	0.9	18	1	AAV54165	Nucleotide sequenc
	612	12.8	0.9	18	1	AAV35391	HIV-1 gag protein
c	613	12.8	0.9	18	1	AAZ33132	Treponema pallidum
	614	12.8	0.9	18	1	AAZ41035	Cellular inhibitor
	615	12.8	0.9	18	1	AAZ22129	Human c-IAP-2 mRNA
c	616	12.8	0.9	18	1	AAZ21232	Human CG1CE PCR pr
	617	12.8	0.9	18	1	AAX54203	Human endothelin-1
	618	12.8	0.9	18	1	AAX54193	Human endothelin-1
c	619	12.8	0.9	18	1	AAX26160	Primer for cDNA sy
	620	12.8	0.9	18	1	AAV81061	De-immunised 708 V
	621	12.8	0.9	18	1	AAZ73148	Human biallelic ma
	622	12.8	0.9	18	1	AAZ76819	Human biallelic ma
	623	12.8	0.9	18	1	AAF19759	Human endothelin-1
	624	12.8	0.9	18	1	AAF19769	Human endothelin-1
c	625	12.8	0.9	18	1	AAA86618	Cdc 2 kinase hamme
c	626	12.8	0.9	18	1	AAA86619	Cdc 2 kinase hamme
c	627	12.8	0.9	18	1	AAA29110	Primer 1 for eosin
	628	12.8	0.9	18	1	AAA12057	Murine promoter OB
	629	12.8	0.9	18	1	AAA33637	Low adenosine anti
	630	12.8	0.9	18	1	AAA33647	Low adenosine anti
	631	12.8	0.9	18	1	AAZ90647	Human adipose tiss
c	632	12.8	0.9	18	1	AAH47994	Human inducible NO
c	633	12.8	0.9	18	1	AAH61784	Cdc 2 kinase hamme
c	634	12.8	0.9	18	1	AAH61785	Cdc 2 kinase hamme
c	635	12.8	0.9	18	1	AAF61243	C. glutamicum ATCC
	636	12.8	0.9	18	1	AAF79677	Human Akt-3 antise
c	637	12.8	0.9	18	1	AAF74480	Clone 21399247.0.1
	638	12.8	0.9	18	1	AAF74483	Clone 21399247.0.1
	639	12.8	0.9	18	1	AAF68906	COXII probe #12.
	640	12.8	0.9	18	1	AAH49174	Human procalcitoni
c	641	12.8	0.9	18	1	ABZ72206	Gene 216 SSCP sequ
	642	12.8	0.9	18	1	ABT11916	Neublastin DNA rel
	643	12.8	0.9	18	1	ABQ65394	Human gene methyla
	644	12.8	0.9	18	1	ABK11324	Arabidopsis Acyl c
c	645	12.8	0.9	18	1	ABL40174	Mouse reelin prote
c	646	12.8	0.9	18	1	ABA05859	Corynebacterium th
	647	12.8	0.9	18	1	ABL30619	Human HLA genotypi
c	648	12.8	0.9	18	1	ABL30631	Human HLA genotypi
	649	12.8	0.9	18	1	ABL30669	Human HLA genotypi
c	650	12.8	0.9	18	1	ABL31090	Human HLA genotypi
	651	12.8	0.9	18	1	ABL31108	Human HLA genotypi
	652	12.8	0.9	18	1	ABL31109	Human HLA genotypi
c	653	12.8	0.9	18	1	AAS18869	Growth hormone 1 g
	654	12.8	0.9	18	1	ABL43144	Human chromosome 1
	655	12.8	0.9	18	1	ABL44827	Human chromosome 1
	656	12.8	0.9	18	1	ACA60576	Antisense inhibiti
c	657	12.8	0.9	18	1	ABX75059	Human gene 216 pol
	658	12.8	0.9	18	1	AAD50969	DM20 primer, to de
c	659	12.8	0.9	18	1	ABZ56925	Vallinoid receptor
	660	12.8	0.9	18	1	ABQ83705	EPO B-A oligonucle
c	661	12.6	0.9	13	1	ABF87744	Oligonucleotide SE
	662	12.6	0.9	13	1	ABF87745	Oligonucleotide SE
	663	12.6	0.9	13	1	ABF93458	Oligonucleotide SE
c	664	12.6	0.9	13	1	ABF93459	Oligonucleotide SE
	665	12.6	0.9	13	1	ABH10200	Oligonucleotide SE
c	666	12.6	0.9	13	1	ABH10201	Oligonucleotide SE
	667	12.6	0.9	15	1	AAL44238	Human interleukin
	668	12.6	0.9	15	1	ABL36325	Human lysosomal ac
	669	12.6	0.9	16	1	AAD44145	Oligo-dT PCR prime
	670	12.6	0.9	18	1	AAX87332	Reverse transcript
c	671	12.4	0.9	18	1	ABT11916	Neublastin DNA rel
c	672	12.4	0.9	21	1	ABK94277	Endothelin convert
	673	12.4	0.9	21	1	ABK94278	Endothelin convert
c	674	12.2	0.9	18	1	AAX70294	Human flt1 VEGF re
	675	12.2	0.9	20	1	AAH57086	Human oestrogen re
c	676	12	0.9	20	1	AAA11329	Human TRPC7 gene e
	677	12	0.9	20	1	AAD37217	Human MEKK4 antise
c	678	12	0.9	21	1	AAL47730	Ras gene PCR prime
	679	11.8	0.9	18	1	ABS52111	Human adipocyte C1
	680	11.6	0.9	18	1	ABK85826	Myotonic dystrophy
	681	11.6	0.9	18	1	AAT87896	Lower primer for e
	682	11.6	0.9	18	1	AAV41332	Interleukin-9 (IL-
c	683	11.6	0.9	18	1	AAX75628	Mouse flt-1 VEGF r
	684	11.6	0.9	19	1	AAX33236	Wheat viviparous 1
c	685	11.4	0.8	17	1	ABV89507	Human POSHL1 scann
c	686	11.4	0.8	17	1	ABV89508	Human POSHL1 scann
	687	11.4	0.8	18	1	AAT80260	Oligo HCV91, targe
	688	11.4	0.8	18	1	ABS65844	Inhibitory oligonu
c	689	11.4	0.8	20	1	AAH89204	Human polymorphic
c	690	11.4	0.8	21	1	ABK94275	Endothelin convert

	691	11.4	0.8	21	1	ABK94276	Endothelin convert
c	692	11.4	0.8	21	1	AAF96193	Human gene single
c	693	11.2	0.8	17	1	ACA06326	NFKB sub-unit modu
	694	11.2	0.8	18	1	AAQ26549	Control probe #4 f
	695	11	0.8	17	1	ABZ61566	Human H-Ras DNAzym
c	696	11	0.8	20	1	AAX33259	PEBP2 alpha A gene
c	697	11	0.8	20	1	ABS74296	Human calcium chan
c	698	11	0.8	20	1	ABS74306	Human calcium chan
	699	11	0.8	20	1	AAI66616	Rat leukotriene B4
c	700	11	0.8	20	1	ABK15887	HES-1 (hairy-enhan
c	701	11	0.8	21	1	AAV47652	Mouse focal adhesi
c	702	11	0.8	21	1	AAV49607	Focal adhesion kin
c	703	10.8	0.8	17	1	ABL31720	Human HLA genotypi
	704	10.8	0.8	17	1	ACA07770	NFKB sub-unit modu
c	705	10.8	0.8	20	1	AAX26904	Primer used for ST
c	706	10.8	0.8	21	1	ABK94273	Endothelin convert
	707	10.8	0.8	21	1	ABK94274	Endothelin convert
	708	10.6	0.8	17	1	ABQ63635	Human KTOM1a porti
	709	10.6	0.8	17	1	ABV89781	Human POSHL1 scann
	710	10.6	0.8	18	1	AAZ35905	Human sentrin phos
c	711	10.6	0.8	18	1	AAH55881	Human SCN1A PCR-SS
c	712	10.6	0.8	18	1	AAV95056	Mouse IL-2 recepto
	713	10.6	0.8	19	1	AAF91219	Human multi drug r
c	714	10.6	0.8	19	1	AAF91221	Human multi drug r
	715	10.6	0.8	19	1	AAF91220	Human multi drug r
c	716	10.6	0.8	19	1	AAF91222	Human multi drug r
c	717	10.6	0.8	19	1	AAD04572	Human insulinoma-a
	718	10.6	0.8	19	1	AAZ94157	Human PEMT2 PCR pr
	719	10.6	0.8	20	1	AAS08740	Human PD-ABC form
	720	10.6	0.8	20	1	AAS08831	Human PD-ABC form
c	721	10.6	0.8	20	1	AAA91053	PCR primer for Hum
	722	10.6	0.8	21	1	AAA59547	PCR primer used to
	723	10.4	0.8	16	1	AAQ68252	Triple helix formi
	724	10.4	0.8	16	1	AAQ80862	Purine-rich methyl
c	725	10.4	0.8	16	1	ABX94194	Human SCCA2 gene,
c	726	10.4	0.8	17	1	ACA07666	NFKB sub-unit modu
c	727	10.4	0.8	17	1	ACA06320	NFKB sub-unit modu
c	728	10.4	0.8	17	1	ACA06587	NFKB sub-unit modu
c	729	10.4	0.8	17	1	ACA08920	NFKB sub-unit modu
	730	10.4	0.8	20	1	AAS45551	Tumour-specific Ig
	731	10.4	0.8	20	1	ABZ76936	Bovine DGAT BAC-DN
	732	10.4	0.8	20	1	ABZ77002	Bovine DGAT PCR pr
	733	10.4	0.8	20	1	AAZ71860	Human biallelic ma
	734	10.4	0.8	20	1	AAC93165	Human STAT3 phosph
	735	10.4	0.8	20	1	AAS96782	Human STAT3 antise
	736	10.4	0.8	21	1	AAT84695	KSHV DNA polymeras
	737	10.4	0.8	21	1	AAT51587	KSHV DNA polymeras
	738	10.4	0.8	23	1	AAQ64857	Ig gamma chain pro
c	739	10.2	0.8	15	1	AAF45161	Antisense oligonuc
	740	10.2	0.8	15	1	AAF49864	IGF-I oligonucleot
	741	10.2	0.8	17	1	ACA06585	NFKB sub-unit modu
	742	10.2	0.8	18	1	AAX67028	Mouse B7 hairpin r
c	743	10.2	0.8	18	1	AAV57794	Human chromosome 1
c	744	10.2	0.8	18	1	AAA27086	Human NF-kappa-B p
	745	10.2	0.8	18	1	AAQ86978	Primer 1 to amplif
c	746	10.2	0.8	18	1	AAV81061	De-immunised 708 V
c	747	10.2	0.8	19	1	AAV51978	Zea mays genome re
c	748	10.2	0.8	19	1	AAV51979	Zea mays genome re
	749	10.2	0.8	20	1	AAT39478	Steroidogenesis ac
	750	10.2	0.8	20	1	AAT99084	Primer alphaEN-S2

ALIGNMENTS

RESULT 1
ABA03588/c
ID ABA03588 standard; DNA; 41 BP.
XX
AC ABA03588;
XX
DT 04-MAR-2002 (first entry)
XX
DE Human HS1 protein 16 coding sequence probe #1.
XX
KW Human; HS1 protein 16; cancer; immune disease; dysplasia; phlogosis;
KW cytostatic; virucide; immunomodulator; antiinflammatory; haemostatic;
KW HIV infection; gene therapy; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200181382-A1.
XX
PD 01-NOV-2001.
XX
PF 23-APR-2001; 2001WO-CN00580.
XX
PR 27-APR-2000; 2000CN-0115496.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-026139/03.
XX
PT Human HS1 protein 16 and encoded polynucleotide, used in diagnosis and
PT treatment of malignant tumors, hemopathy, human immunodeficiency virus
PT infection, immunological diseases and inflammation -
XX
PS Example 6; Page 14; 38pp; Chinese.
XX
CC The present invention provides the protein and coding sequences of human
CC HS1 protein 16. The sequences can be used in the treatment of
CC haematogenic cancer, immune diseases, dysplasia, phlogosis and HIV
CC infection. The present sequence is a probe for the coding sequence of the
CC invention.
XX
SQ Sequence 41 BP; 9 A; 4 C; 11 G; 17 T; 0 other;

Query Match 2.2%; Score 30; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         77 ATGAATAATAGCAGTTCTACCGTACAACCC 106
              ||||||||||||||||||||||||||||||
Db         41 ATGAATAATAGCAGTTCTACCGTACAACCC 12
```

RESULT 2
AAC67363
ID AAC67363 standard; DNA; 22 BP.
XX
AC AAC67363;
XX
DT 14-FEB-2001 (first entry)
XX
DE Alzheimer's disease-linked mitochondrial SNP PCR primer #63.
XX
KW Human; mitochondrial genome; single nucleotide polymorphism; SNP;
KW Alzheimer's disease; mtDNA; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200063441-A2.
XX
PD 26-OCT-2000.
XX
PF 19-APR-2000; 2000WO-US10906.
XX
PR 20-APR-1999; 99US-0130447.
PR 22-OCT-1999; 99US-0160901.
XX
PA (MITO-) MITOKOR.
XX
PI Herrnstadt C, Davis RE;
XX

DR WPI; 2000-672748/65.
XX
PT Diagnosing a subject at the risk for or having Alzheimer's disease
PT comprises determining at least one single nucleotide polymorphism in
PT mitochondrial DNA associated with the disease in the sample from the
PT subject -
XX
PS Example 4; Page 38; 89pp; English.
XX
CC The present invention describes a novel method for determining the risk
CC of or diagnosing Alzheimer's disease using single nucleotide
CC polymorphisms (SNPs) present in an individual's mitochondrial DNA
CC (mtDNA). In additon, the SNPs identified can be used to identify agents
CC suitable for use in treating Alzheimer's disease. Sequences
CC AAC67301-C67610 are PCR primers used to demonstrate the method of the
CC invention.
XX
SQ Sequence 22 BP; 9 A; 5 C; 3 G; 5 T; 0 other;

Query Match 1.6%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 AGCTACGCAAAATCTTAGCATA 55
||||||||||||||||||||||
Db 1 AGCTACGCAAAATCTTAGCATA 22

RESULT 3
AAZ57266
ID AAZ57266 standard; DNA; 22 BP.
XX
AC AAZ57266;
XX
DT 30-MAR-2000 (first entry)
XX
DE Human mitochondrial DNA NADH dehydrogenase PCR primer SEQ ID NO:65.
XX
KW Human; mitochondrial DNA; extramitochondrial DNA; mtDNA; exmtDNA;
KW diagnosis; quantification; detection; dystonia; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; schizophrenia; stroke;
KW non-insulin dependent diabetes mellitus; mitochondrial encephalopathy;
KW lactic acidosis; myoclonic epilepsy ragged red fibre syndrome;
KW Leber's hereditary optic neuropathy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO9966075-A2.
XX
PD 23-DEC-1999.
XX
PF 14-JUN-1999; 99WO-US13426.
XX
PR 15-JUN-1998; 98US-0097889.
PR 15-JUN-1998; 98US-0098079.
PR 30-APR-1999; 99US-0302681.
XX
PA (MITO-) MITOKOR.
XX
PI Herrnstadt C, Ghosh SS, Clevenger W, Fahy ED, Davis RE;
XX
DR WPI; 2000-097754/08.
XX
PT Quantification of extramitochondrial DNA for diagnosis of, e.g.
PT Alzheimer's, Huntington's and Parkinson's disease -
XX
PS Disclosure; Page 32; 157pp; English.
XX
CC The present invention describes a method for the quantification of
CC extramitochondrial DNA (exmtDNA) by determining the ratio of a first
CC and second biological sample containing exmtDNA and mitochondrial DNA
CC (mtDNA) to determine the risk or presence of a disease associated with
CC altered mitochondrial function. The method can be used to determine
CC the risk of or presence of a disease associated with altered
CC mitochondrial function, especially Alzheimer's disease, Huntington's
CC disease, Parkinson's disease, dystonia, schizophrenia, non-insulin
CC dependent diabetes mellitus, mitochondrial encephalopathy, lactic
CC acidosis, stroke, myoclonic epilepsy ragged red fibre syndrome and
CC Leber's hereditary optic neuropathy. The method can also be used to
CC identify agents suitable for treating such diseases, in particular
CC Alzheimer's disease. AAZ57202 to AAZ57313 represent nucleotide sequences
CC used in the exemplification of the present invention. More specifically
CC AAZ57206 to AAZ57313 are PCR primers used in the detection of exmtDNA
CC and mtDNA.
XX
SQ Sequence 22 BP; 9 A; 5 C; 3 G; 5 T; 0 other;

Query Match 1.6%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 AGCTACGCAAAATCTTAGCATA 55
||||||||||||||||||||||
Db 1 AGCTACGCAAAATCTTAGCATA 22

RESULT 4
AAC67508/c
ID AAC67508 standard; DNA; 20 BP.
XX
AC AAC67508;
XX
DT 14-FEB-2001 (first entry)
XX
DE Alzheimer's disease-linked mitochondrial SNP PCR primer #208.
XX
KW Human; mitochondrial genome; single nucleotide polymorphism; SNP;
KW Alzheimer's disease; mtDNA; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200063441-A2.
XX
PD 26-OCT-2000.
XX
PF 19-APR-2000; 2000WO-US10906.
XX
PR 20-APR-1999; 99US-0130447.
PR 22-OCT-1999; 99US-0160901.
XX
PA (MITO-) MITOKOR.
XX
PI Herrnstadt C, Davis RE;
XX
DR WPI; 2000-672748/65.
XX
PT Diagnosing a subject at the risk for or having Alzheimer's disease
PT comprises determining at least one single nucleotide polymorphism in
PT mitochondrial DNA associated with the disease in the sample from the
PT subject -
XX
PS Example 9; Page 51; 89pp; English.
XX
CC The present invention describes a novel method for determining the risk
CC of or diagnosing Alzheimer's disease using single nucleotide
CC polymorphisms (SNPs) present in an individual's mitochondrial DNA
CC (mtDNA). In additon, the SNPs identified can be used to identify agents
CC suitable for use in treating Alzheimer's disease. Sequences
CC AAC67301-C67610 are PCR primers used to demonstrate the method of the
CC invention.
XX
SQ Sequence 20 BP; 4 A; 3 C; 6 G; 7 T; 0 other;

Query Match 1.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          33 CAGCTACGCAAAATCTTAGC 52
               ||||||||||||||||||||
Db          20 CAGCTACGCAAAATCTTAGC 1
```

RESULT 5
ABV92615/c
ID ABV92615 standard; DNA; 25 BP.
XX
AC ABV92615;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 3328.
XX
KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX
OS Homo sapiens.
XX
PN EP1239051-A2.
XX
PD 11-SEP-2002.
XX
PF 28-JAN-2002; 2002EP-0001165.
XX
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 23-MAY-2001; 2001US-0864761.
PR 10-OCT-2001; 2001US-0328205.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M;
XX
DR WPI; 2002-684061/74.
XX
PT Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,
PT POSHL-1, useful for treating disorders associated with decreased
PT expression or activity of human POSHL1 -
XX
PS Example 2; SEQ ID NO 3328; 60pp + Sequence Listing; English.
XX
CC The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention.
CC Note: The present sequence did not form part of the printed
CC specification, but is based on sequence information supplied to Derwent
CC by the European Patent Office.
XX
SQ Sequence 25 BP; 4 A; 12 C; 4 G; 5 T; 0 other;

```
  Query Match              1.3%;  Score 18.2;  DB 1;  Length 25;
  Best Local Similarity   87.0%;  Pred. No. 40;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         261 CCTGGGCTGGCTGATCAAAGAGG 283
               | |||||||| |||||| |||||
Db          25 CATGGGCTGGGTGATCACAGAGG 3
```

RESULT 6
ABV92616/c
ID ABV92616 standard; DNA; 25 BP.
XX
AC ABV92616;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 3329.
XX
KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX
OS Homo sapiens.
XX
PN EP1239051-A2.
XX
PD 11-SEP-2002.
XX
PF 28-JAN-2002; 2002EP-0001165.
XX
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 23-MAY-2001; 2001US-0864761.
PR 10-OCT-2001; 2001US-0328205.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M;
XX
DR WPI; 2002-684061/74.
XX
PT Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,
PT POSHL-1, useful for treating disorders associated with decreased
PT expression or activity of human POSHL1 -
XX
PS Example 2; SEQ ID NO 3329; 60pp + Sequence Listing; English.
XX
CC The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention.
CC Note: The present sequence did not form part of the printed

```
CC   specification, but is based on sequence information supplied to Derwent
CC   by the European Patent Office.
XX
SQ   Sequence 25 BP; 4 A; 11 C; 5 G; 5 T; 0 other;

  Query Match             1.3%;  Score 18.2;  DB 1;  Length 25;
  Best Local Similarity   87.0%;  Pred. No. 40;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        261 CCTGGGCTGGCTGATCAAAGAGG 283
              | ||||||||| |||||| |||||
Db         24 CATGGGCTGGGTGATCACAGAGG 2


RESULT 7
ABV92617/c
ID   ABV92617 standard; DNA; 25 BP.
XX
AC   ABV92617;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Human POSHL1 scanning oligonucleotide SEQ ID NO 3330.
XX
KW   Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW   Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW   gene therapy; transgenic; ss.
XX
OS   Homo sapiens.
XX
PN   EP1239051-A2.
XX
PD   11-SEP-2002.
XX
PF   28-JAN-2002; 2002EP-0001165.
XX
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00666.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   30-JAN-2001; 2001WO-US00670.
PR   23-MAY-2001; 2001US-0864761.
PR   10-OCT-2001; 2001US-0328205.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M;
XX
DR   WPI; 2002-684061/74.
XX
PT   Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,
PT   POSHL-1, useful for treating disorders associated with decreased
PT   expression or activity of human POSHL1 -
XX
PS   Example 2; SEQ ID NO 3330; 60pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated SH3 domain (POSH)-like signalling
CC   protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC   acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC   (S1) having 95% deviations, especially conservative substitutions or a
CC   fragment of the sequences comprising at least 8 contiguous amino acids.
CC   Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC   adaptor protein that interacts with Rho family small GTPases as well as
CC   downstream components of the signal transduction pathway. (I) is useful
CC   for identifying a specific binding partner. (I) and nucleic acids (II)
CC   encoding (I) are useful for diagnosing, monitoring disease and treating
CC   caused by altered expression of human POSHL1 including diagnosing and
CC   treating cancer, they useful in the development of vaccines and (II) is
CC   useful in gene therapy. (II) is useful for constructing microarrays which
CC   are useful for measuring and for surveying gene expression and creating
CC   transgenic non-human animals capable of producing the proteins. The
CC   present sequence is that of a scanning oligonucleotide useful in examples
CC   of the invention.
CC   Note: The present sequence did not form part of the printed
CC   specification, but is based on sequence information supplied to Derwent
CC   by the European Patent Office.
XX
SQ   Sequence 25 BP; 5 A; 10 C; 5 G; 5 T; 0 other;

  Query Match             1.3%;  Score 18.2;  DB 1;  Length 25;
  Best Local Similarity   87.0%;  Pred. No. 40;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        261 CCTGGGCTGGCTGATCAAAGAGG 283
              | ||||||||| |||||| |||||
Db         23 CATGGGCTGGGTGATCACAGAGG 1


RESULT 8
AAF79922/c
ID   AAF79922 standard; DNA; 21 BP.
XX
AC   AAF79922;
XX
DT   11-JUN-2001  (first entry)
XX
DE   PCR primer used to amplify human and murine GL50 cDNA sequences.
XX
KW   GL50; antigen; antigen presenting cell; T cell proliferation; tumour;
KW   graft-versus-host disease; autoimmune disease; allergy; viral infection;
KW   acquired immune deficiency syndrome; AIDS; vaccine; PCR primer; ss.
XX
OS   Homo sapiens.
OS   Mus musculus.
XX
PN   WO200121796-A2.
XX
PD   29-MAR-2001.
XX
PF   21-SEP-2000; 2000WO-US25892.
XX
PR   21-SEP-1999;   99US-0155043.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Ling V,  Dunussi-Joannopolulos K;
XX
DR   WPI; 2001-244938/25.
XX
PT   New isolated nucleic acid encoding a GL50 polypeptide for modulating a
PT   immune response and reducing the proliferation of a tumour cell -
XX
PS   Disclosure; Page 117; 195pp; English.
XX
CC   PCR primers AAF79922-27 were used to amplify sequences from the 3'
CC   end of cDNA encoding human and murine GL50 polypeptides. GL50
CC   molecules are antigens on the surface of antigen presenting cells,
CC   which costimulate T cell proliferation and bind to costimulatory
CC   receptor ligands on T cells. GL50 modulating agents are used to
CC   modulate an immune response in a subject. GL50 polypeptides are used
CC   to modulate T cell costimulation, and to reduce the proliferation of
CC   a tumour cell. Diseases that can be treated using GL50 molecules are
CC   graft-versus-host disease, autoimmune disease, allergies, acquired
CC   immune deficiency syndrome (AIDS), and viral infections.  The GL50
CC   molecules can be used in vaccines. GL50 polynucleotides can be used
CC   to locate gene regions associated with genetic disease, in tissue
CC   typing, and in forensic identification of a biological sample.
XX
SQ   Sequence 21 BP; 2 A; 11 C; 5 G; 3 T; 0 other;

  Query Match             1.3%;  Score 17.8;  DB 1;  Length 21;
  Best Local Similarity   90.5%;  Pred. No. 38;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy        944 GGTGTGAGCGCAGACTGCAGG 964
              |||| |||||||||||||| ||
Db         21 GGTGCGAGCGCAGACTGCGGG 1


RESULT 9
ABV92613/c
ID   ABV92613 standard; DNA; 25 BP.
XX
AC   ABV92613;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Human POSHL1 scanning oligonucleotide SEQ ID NO 3326.
XX
KW   Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW   Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW   gene therapy; transgenic; ss.
XX
OS   Homo sapiens.
XX
PN   EP1239051-A2.
XX
PD   11-SEP-2002.
XX
PF   28-JAN-2002; 2002EP-0001165.
XX
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00666.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   30-JAN-2001; 2001WO-US00670.
PR   23-MAY-2001; 2001US-0864761.
PR   10-OCT-2001; 2001US-0328205.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M;
XX
DR   WPI; 2002-684061/74.
XX
PT   Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,
PT   POSHL-1, useful for treating disorders associated with decreased
PT   expression or activity of human POSHL1 -
XX
PS   Example 2; SEQ ID NO 3326; 60pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated SH3 domain (POSH)-like signalling
CC   protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC   acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC   (S1) having 95% deviations, especially conservative substitutions or a
CC   fragment of the sequences comprising at least 8 contiguous amino acids.
CC   Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC   adaptor protein that interacts with Rho family small GTPases as well as
CC   downstream components of the signal transduction pathway. (I) is useful
CC   for identifying a specific binding partner. (I) and nucleic acids (II)
CC   encoding (I) are useful for diagnosing, monitoring disease and treating
CC   caused by altered expression of human POSHL1 including diagnosing and
CC   treating cancer, they useful in the development of vaccines and (II) is
CC   useful in gene therapy. (II) is useful for constructing microarrays which
CC   are useful for measuring and for surveying gene expression and creating
CC   transgenic non-human animals capable of producing the proteins. The
CC   present sequence is that of a scanning oligonucleotide useful in examples
CC   of the invention.
CC   Note: The present sequence did not form part of the printed
CC   specification, but is based on sequence information supplied to Derwent
CC   by the European Patent Office.
XX
SQ   Sequence 25 BP; 6 A; 12 C; 3 G; 4 T; 0 other;

  Query Match              1.3%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 48;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        263 TGGGCTGGCTGATCAAAGAGG 283
              |||||||| |||||| |||||
Db         25 TGGGCTGGGTGATCACAGAGG 5


RESULT 10
ABV92614/c
ID   ABV92614 standard; DNA; 25 BP.
XX
AC   ABV92614;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Human POSHL1 scanning oligonucleotide SEQ ID NO 3327.
XX
KW   Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW   Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW   gene therapy; transgenic; ss.
XX
OS   Homo sapiens.
XX
PN   EP1239051-A2.
XX
PD   11-SEP-2002.
XX
PF   28-JAN-2002; 2002EP-0001165.
XX
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00666.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   30-JAN-2001; 2001WO-US00670.
PR   23-MAY-2001; 2001US-0864761.
PR   10-OCT-2001; 2001US-0328205.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M;
XX
DR   WPI; 2002-684061/74.
XX
PT   Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,
PT   POSHL-1, useful for treating disorders associated with decreased
PT   expression or activity of human POSHL1 -
XX
PS   Example 2; SEQ ID NO 3327; 60pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated SH3 domain (POSH)-like signalling
CC   protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC   acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC   (S1) having 95% deviations, especially conservative substitutions or a
CC   fragment of the sequences comprising at least 8 contiguous amino acids.
CC   Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC   adaptor protein that interacts with Rho family small GTPases as well as
CC   downstream components of the signal transduction pathway. (I) is useful
CC   for identifying a specific binding partner. (I) and nucleic acids (II)
CC   encoding (I) are useful for diagnosing, monitoring disease and treating
CC   caused by altered expression of human POSHL1 including diagnosing and
CC   treating cancer, they useful in the development of vaccines and (II) is
CC   useful in gene therapy. (II) is useful for constructing microarrays which
CC   are useful for measuring and for surveying gene expression and creating
CC   transgenic non-human animals capable of producing the proteins. The
CC   present sequence is that of a scanning oligonucleotide useful in examples
CC   of the invention.
CC   Note: The present sequence did not form part of the printed
```

```
CC   specification, but is based on sequence information supplied to Derwent
CC   by the European Patent Office.
XX
SQ   Sequence 25 BP; 5 A; 12 C; 3 G; 5 T; 0 other;

  Query Match             1.3%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 48;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        263 TGGGCTGGCTGATCAAAGAGG 283
              ||||||||| |||||| |||||
Db         24 TGGGCTGGGTGATCACAGAGG 4


RESULT 11
AAC95776
ID   AAC95776 standard; DNA; 25 BP.
XX
AC   AAC95776;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DRB1 gene PCR primer #20.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP03636.
XX
PR   26-APR-1999;   99EP-0303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences
PT   of specific length  -
XX
PS   Claim 14; Page 39; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular.
XX
SQ   Sequence 25 BP; 4 A; 2 C; 6 G; 13 T; 0 other;

  Query Match             1.3%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 53;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTGGAAGTAAAGC 1167
              ||||||| |||||||||||    |||
Db          1 TTTTTTTTTTTTTTGGAAGACGAGC 24


RESULT 12
AAC96237
ID   AAC96237 standard; DNA; 25 BP.
XX
AC   AAC96237;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #204.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP03636.
XX
PR   26-APR-1999;   99EP-0303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences
PT   of specific length  -
XX
PS   Claim 14; Page 47; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular.
XX
SQ   Sequence 25 BP; 5 A; 2 C; 4 G; 14 T; 0 other;

  Query Match             1.3%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 53;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTGGAAGTAAAGC 1167
              ||||||| |||||| ||||| | |
Db          1 TTTTTTTTTTTTTTGCAAGTAGAAC 24


RESULT 13
ABT33591/c
ID   ABT33591 standard; DNA; 22 BP.
XX
AC   ABT33591;
XX
DT   22-MAY-2003  (first entry)
XX
DE   NOV reverse PCR primer SEQ ID No 507.
XX
KW   Hepatotropic; immunosuppressive; cardiant; hypertensive; tranquilizer;
KW   vulnerary; virucide; antibacterial; protozoacide; fungicide; nootropic;
KW   antiparasitic; neuroprotective; cerebroprotective; antiparkinsonian;
KW   anticonvulsant; antiaddictive; analgesic; dermatological; keratolytic;
KW   antiseborrheic; antirheumatic; antiarthritic; antiinflammatory; anti-HIV;
KW   cytostatic; antiasthmatic; antipsoriatic; hypotensive; osteopathic;
KW   antiulcer; anorectic; antidiabetic; antiallergic; haemostatic;
KW   neuroleptic; antidepressant; antiinfertility; NOVX; human disease;
KW   NOVX-associated disorder; trauma; viral; bacterial; fungal; protozoal;
KW   parasitic infection; Alzheimer's disease; stroke; forensic biology;
```

```
KW   immunogen; non-human transgenic animal; gene therapy; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200281517-A2.
XX
PD   17-OCT-2002.
XX
PF   22-JAN-2002; 2002WO-US02064.
XX
PR   19-JAN-2001; 2001US-262892P.
PR   23-JAN-2001; 2001US-263598P.
PR   24-JAN-2001; 2001US-263799P.
PR   25-JAN-2001; 2001US-264117P.
PR   25-JAN-2001; 2001US-264139P.
PR   26-JAN-2001; 2001US-264478P.
PR   30-JAN-2001; 2001US-263351P.
PR   02-MAR-2001; 2001US-272870P.
PR   14-MAR-2001; 2001US-275927P.
PR   14-MAR-2001; 2001US-275990P.
PR   15-MAR-2001; 2001US-276449P.
PR   20-MAR-2001; 2001US-277358P.
PR   23-MAR-2001; 2001US-278151P.
PR   29-MAR-2001; 2001US-279857P.
PR   20-APR-2001; 2001US-285140P.
PR   20-APR-2001; 2001US-285141P.
PR   30-APR-2001; 2001US-287484P.
PR   17-MAY-2001; 2001US-291701P.
PR   08-JUN-2001; 2001US-296960P.
PR   10-JUL-2001; 2001US-304353P.
PR   10-JUL-2001; 2001US-304355P.
PR   12-JUL-2001; 2001US-304886P.
PR   09-AUG-2001; 2001US-311289P.
PR   13-AUG-2001; 2001US-311975P.
PR   16-AUG-2001; 2001US-312937P.
PR   18-OCT-2001; 2001US-330227P.
PR   29-NOV-2001; 2001US-334198P.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Decristofaro MF,  Padigaru M,  Miller C,  Tchernev V,  Zhong H;
PI   Zhong M,  Anderson D,  Ballinger R,  Gerlach V,  Spytek KA;
PI   Rastelli L,  Kekuda R,  Guo X,  Zerhusen B,  Andrew D,  Mezes P;
PI   Patturajan M,  Burgess CE,  Eisen A,  Wolenc A,  Baumgartner J;
PI   Shimkets RA,  Gusev V,  Vernet CAM,  Taupier RJ,  Pena C,  Shenoy S;
PI   Li L,  Casman S,  Boldog F,  Fernandes E,  Smithson G,  Malyankar U;
PI   Taillon B,  Liu X;
XX
DR   WPI; 2003-058504/05.
XX
PT   New polypeptides, designated as NOVX, useful for diagnosing and
PT   treating infections, neurological diseases, cancer, allergy, and bone,
PT   immunological, skin, renal, brain, muscle and autoimmune disorders -
XX
PS   Example 3; Page 659; 672pp; English.
XX
CC   The invention relates to a novel isolated polypeptide, designated NOVX
CC   (NOV1 - 33), consisting of a mature form of one of 61 sequences, given
CC   in the specification, or its variant, where amino acid residue(s) in the
CC   variant differ from the mature form, provided that the variant differs
CC   in not more than 15 % of the amino acids from the sequence of the mature
CC   form. The NOVX polypeptides, nucleic acids encoding the polypeptides, and
CC   an antibody to the polypeptides, are useful for treating or preventing a
CC   NOVX-associated disorder in humans and for treating a syndrome associated
CC   with a human disease (NOVX-associated disorder). NOVX polypeptides and
CC   the encoding nucleic acids, are useful for determining the presence of or
CC   predisposition to a disease associated with altered levels of NOVX
CC   polypeptide and polynucleotide, by measuring the level of polypeptide
CC   expression or the amount of nucleic acid from a mammal and comparing it
CC   with another mammal not having or not predisposed to the disease. NOVX
CC   polypeptide is also useful for identifying an agent that binds to NOVX
CC   and a cell expressing NOVX is useful for identifying an agent that
CC   modulates the expression or activity of NOVX. The antibodies and a
CC   polypeptide having 95 % sequence identity to NOVX polypeptide are useful
CC   for treating a pathological state in a mammal. The antibodies are also
CC   useful for determining the presence or amount of NOVX in a sample. NOVX
CC   polypeptides, polynucleotides and antibodies specific for the
CC   polypeptides are useful for treating or preventing disorders or syndromes
CC   including trauma, viral, bacterial, fungal, protozoal, and parasitic
CC   infections. They can also treat disorders such as e.g., Alzheimer's
CC   disease or a stroke. The NOVX encoding nucleic acids are useful for
CC   expressing the NOVX proteins, to detect NOVX mRNA, or a genetic lesion in
CC   a NOVX gene and to modulate NOVX activity. NOVX sequences are also useful
CC   for identifying a cell or tissue type in a biological sample, to amplify
CC   DNA sequences from very small biological samples such as tissues e.g.
CC   hair or skin or body fluids in forensic biology and as primers and probes
CC   for use in identifying and/or cloning NOVX homologues in other cell
CC   types. The NOVX proteins are useful as an immunogen to generate
CC   antibodies which are useful for diagnostically monitoring protein levels
CC   and modulating NOVX activity. Cells comprising NOVX nucleic acids are
CC   useful for producing non-human transgenic animals which are useful for
CC   studying the function and/or activity of NOVX protein and for identifying
CC   and/or evaluating modulators of NOVX protein activity. The NOVX nucleic
CC   acids can be used in gene therapy. This polynucleotide sequence
CC   represents a NOVX PCR primer of the invention.
XX
SQ   Sequence 22 BP; 3 A; 2 C; 11 G; 6 T; 0 other;

  Query Match             1.3%;  Score 17.2;  DB 1;  Length 22;
  Best Local Similarity   86.4%;  Pred. No. 53;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        562 CACACACTGCTCCAGCAGGCCC 583
              |||| ||| ||||| |||||||
Db         22 CACAAACTCCTCCATCAGGCCC 1


RESULT 14
AAL45714
ID   AAL45714 standard; DNA; 24 BP.
XX
AC   AAL45714;
XX
DT   27-JUN-2002  (first entry)
XX
DE   AML cancer cells detection oligonucleotide #3.
XX
KW   Cancer; extranuclear DNA; stem-loop; DNA-binding protein; cytostatic;
KW   tumour cell detection; probe; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "digoxygenin-11-dUTP"
FT   misc_RNA        1
FT                   /*tag=  b
FT   modified_base   24
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "digoxygenin-11-dUTP"
FT   misc_RNA        24
FT                   /*tag=  d
XX
PN   DE10046318-A1.
XX
PD   28-MAR-2002.
XX
PF   19-SEP-2000; 2000DE-1046318.
XX
PR   19-SEP-2000; 2000DE-1046318.
XX
PA   (ABKE/) ABKEN H.
XX
```

```
PI   Abken H,  Schinkoethe T;
XX
DR   WPI; 2002-331116/37.
XX
PT   Detecting tumor cells from presence of specific stem-loop DNA molecules
PT   outside the nucleus, useful for diagnosis and monitoring of tumors -
XX
PS   Example 2; Page 7; 27pp; German.
XX
CC   The present invention relates to a method of detecting tumour cells, by
CC   detecting extranuclear DNA consisting of a single-strand with a
CC   double-stranded stem-loop structure containing at least 2 binding sites
CC   for DNA binding proteins. The method can be used to detect cancer cells
CC   in tissue sections, biopsies, body fluids etc, and can be used in the
CC   diagnosis and monitoring of cancer. The present sequence is an
CC   oligonucleotide used to detect AML leukaemia cells in a demonstration of
CC   the invention.
XX
SQ   Sequence 24 BP; 8 A; 0 C; 2 G; 12 T; 2 U; 0 other;

  Query Match             1.3%;  Score 17.2;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 60;
  Matches   18;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTGGAAGTAAA 1165
              :|||||| ||||||||  |||
Db          1 UTTTTTTTTTTTTTGGAAAAAAA 22


RESULT 15
AAT46092
ID   AAT46092 standard; DNA; 21 BP.
XX
AC   AAT46092;
XX
DT   19-FEB-1997  (first entry)
XX
DE   Primer for STS associated with EDA gene.
XX
KW   STS; sequence-tagged site; primer; EDA; anhidrotic ectodermal dysplasia;
KW   yeast artificial chromosome; Homo sapiens; ss.
XX
OS   Synthetic.
XX
PN   US5556786-A.
XX
PD   17-SEP-1996.
XX
PF   27-APR-1993;   93US-0052997.
XX
PR   27-APR-1993;   93US-0052997.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   De La Chapelle A,  Kere J,  Schlessinger D;
XX
DR   WPI; 1996-432990/43.
XX
PT   Cloning vector contg. the human anhydrotic ecto-dermal dysplasia
PT   gene  - for diagnosis of EDA related diseases
XX
PS   Claim 5; Column 28; 19pp; English.
XX
CC   EDA is an X-chromosomal recessive disorder linked with the absence or
CC   hypoplasia of hair, teeth and sweat glands. The EDA gene has been mapped
CC   to Xq12-q13 by genetic linkage analysis using restriction fragment
CC   length polymorphisms (RFLP) markers. Translocation breakpoints were also
CC   used to define the localisation of the gene as well as the recovery of
CC   yeast artificial chromosome (YAC) clones from the region using RFLP
CC   markers and new unique markers. AAT46079-92 are primers for
CC   sequence-tagged sites associated with the anhidrotic ectodermal dysplasia
CC   (EDA) gene. AAT46083-92 are associated with new markers labelled sWXD632,
CC   sWXD178, sWXD634, sWXD635 and sWXD636.
XX
SQ   Sequence 21 BP; 6 A; 5 C; 4 G; 6 T; 0 other;

  Query Match             1.2%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 60;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          78 TGAATAATAGCAGTTCTACC 97
               |||||||||||| |||| ||
Db           2 TGAATAATAGCACTTCTGCC 21


RESULT 16
AAZ26500/c
ID   AAZ26500 standard; DNA; 21 BP.
XX
AC   AAZ26500;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 689.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US05419.
XX
PR   20-MAR-1997;   97US-0041057.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for
PT   diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic
PT   plaque, dysplastic lesions, endometriosis or graft versus host disease
XX
PS   Disclosure; Figure 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is
CC   active on a gene vital for cell growth or viability, and where the gene
CC   is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can
CC   be used in the diagnosis, prevention and treatment of LOH disorders,
CC   e.g. cancers, atherosclerotic plaques, premalignant metaplastic or
CC   dysplastic lesions, benign tumours, endometriosis, polycystic kidney
CC   disease, and graft versus host disease. The method can also be used to
CC   remove malignant cells from bone marrow transplants. AAZ25812-Z26825
CC   represent human polymorphic sites described in the method of the
CC   invention.
XX
SQ   Sequence 21 BP; 15 A; 2 C; 0 G; 4 T; 0 other;
```

```
  Query Match             1.2%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 60;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTGGAAGTA 1163
              ||||||| |||||| |||||
Db         20 TTTTTTTTTTTTTTGAAAGTA 1
```

RESULT 17
AAV05879
ID AAV05879 standard; DNA; 21 BP.
XX
AC AAV05879;
XX
DT 01-JUN-1998 (first entry)
XX
DE Primer #10 for STS locus DXS339.
XX
KW Human; anhidrotic ectodermal dysplasia; X chromosome; genetic linkage;
KW translocation; CpG island; foetal development; hair; sweat gland; ss;
KW tooth; primer; PCR; amplification; sequence tagged site; STS.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5700926-A.
XX
PD 23-DEC-1997.
XX
PF 22-JUL-1996; 96US-0684672.
XX
PR 22-JUL-1996; 96US-0684672.
PR 27-APR-1993; 93US-0052997.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI De La Chapelle A, Kere J, Schlessinger D, Srivastava AK;
XX
DR WPI; 1998-062436/06.
XX
PT Human anhidrotic ectodermal dysplasia gene - useful for research
PT into hair growth
XX
PS Disclosure; Column 7; 37pp; English.
XX
CC Primers AAV05858-V05879 were used to PCR amplify sequence tagged sites
CC (STS's) in the search for the sequence encoding the human anhidrotic
CC ectodermal dysplasia (EDA) gene (AAV05851). This primer is used to
CC amplify the STS at locus DXS339. The amplified fragments can be used
CC as probes for isolating the EDA gene. The EDA gene has been mapped to
CC the region Xq12-q13 by genetic linkage analysis and has been shown to
CC contain a 200 kb intron inserted in the 3' end of the coding sequence.
CC Deficiencies in the gene are observed by translocations with a
CC breakpoint in the transcribed CpG island 3 at the Xq12-q13 locus. The
CC EDA gene can be used to study the dynamics of EDA gene expression during
CC foetal development, and processes affecting normal hair growth in
CC adults. The EDA gene can also be used to study hair, sweat gland and
CC tooth formation and growth, and ectodermal dysplasias.
XX
SQ Sequence 21 BP; 6 A; 5 C; 4 G; 6 T; 0 other;

```
  Query Match             1.2%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 60;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         78 TGAATAATAGCAGTTCTACC 97
              |||||||||||| |||| ||
Db          2 TGAATAATAGCACTTCTGCC 21
```

RESULT 18
ABK94277
ID ABK94277 standard; DNA; 21 BP.
XX
AC ABK94277;
XX
DT 27-AUG-2002 (first entry)
XX
DE Endothelin converting enzyme 1 (ECE-1) SNP detection primer #65.
XX
KW Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
KW EDNR; signaling system; cardiovascular disease; coronary heart disease;
KW hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;
KW diabetes; familial hypercholesterolaemia; forensic marker;
KW transgenic animal; solid support; cardiovascular regulator; SNP;
KW single nucleotide polymorphism; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO200224747-A2.
XX
PD 28-MAR-2002.
XX
PF 31-AUG-2001; 2001WO-EP10087.
XX
PR 19-SEP-2000; 2000EP-0120123.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Brinkmann U, Hoffmeyer S;
XX
DR WPI; 2002-435060/46.
XX
PT Novel polynucleotide of the endothelin/endothelin converting
PT enzyme/receptors of endothelin and endothelin converting enzyme
PT signaling system associated with cardiovascular disease, useful for
PT treating the disease -
XX
PS Claim 1; Page 63; 190pp; English.
XX
CC The invention describes a polynucleotide (I) of the endothelin
CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
CC signaling system which is associated with a cardiovascular disease. (I),
CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
CC or (II) is useful for producing cells capable of expressing a molecular
CC variant polypeptide which is associated with a cardiovascular disease.
CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
CC a molecular variant gene comprising (I) is useful for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
CC or its gene product, or for identifying and obtaining an inhibitor of
CC the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
CC signaling system or its gene product. The isolated proteins and
CC polynucleotides encoding them are useful for preparation of a
CC pharmaceutical composition for treating a cardiovascular disease such as
CC coronary heart disease, hypertension, atherosclerosis, or related to
CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
CC hypercholesterolaemia. The gene or a polynucleotide fragment of the
CC EDN/ECE/EDNR signaling system are useful as forensic markers, for
CC creating a transgenic animal and in creation of a solid support
CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or
CC host cells of the invention. This sequence represents a PCR primer used
CC to identify single nucleotide polymorphisms in DNA encoding
CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway.
XX
SQ Sequence 21 BP; 6 A; 3 C; 11 G; 1 T; 0 other;

```
  Query Match             1.2%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 60;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        463 AGCAGCCTGCAGGGGGAGGA 482
              ||||| |||||||| |||||
Db          1 AGCAGGCTGCAGGGAGAGGA 20
```

```
RESULT 19
ABK94278/c
ID   ABK94278 standard; DNA; 21 BP.
XX
AC   ABK94278;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Endothelin converting enzyme 1 (ECE-1) SNP detection primer #66.
XX
KW   Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
KW   EDNR; signaling system; cardiovascular disease; coronary heart disease;
KW   hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;
KW   diabetes; familial hypercholesterolaemia; forensic marker;
KW   transgenic animal; solid support; cardiovascular regulator; SNP;
KW   single nucleotide polymorphism; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200224747-A2.
XX
PD   28-MAR-2002.
XX
PF   31-AUG-2001; 2001WO-EP10087.
XX
PR   19-SEP-2000; 2000EP-0120123.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI   Brinkmann U,  Hoffmeyer S;
XX
DR   WPI; 2002-435060/46.
XX
PT   Novel polynucleotide of the endothelin/endothelin converting
PT   enzyme/receptors of endothelin and endothelin converting enzyme
PT   signaling system associated with cardiovascular disease, useful for
PT   treating the disease  -
XX
PS   Claim 1; Page 63; 190pp; English.
XX
CC   The invention describes a polynucleotide (I) of the endothelin
CC   (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
CC   signaling system which is associated with a cardiovascular disease. (I),
CC   the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
CC   or (II) is useful for producing cells capable of expressing a molecular
CC   variant polypeptide which is associated with a cardiovascular disease.
CC   (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
CC   a molecular variant gene comprising (I) is useful for identifying and
CC   obtaining a pro-drug or drug capable of modulating the activity of a
CC   molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
CC   or its gene product, or for identifying and obtaining an inhibitor of
CC   the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
CC   signaling system or its gene product. The isolated proteins and
CC   polynucleotides encoding them are useful for preparation of a
CC   pharmaceutical composition for treating a cardiovascular disease such as
CC   coronary heart disease, hypertension, atherosclerosis, or related to
CC   abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
CC   hypercholesterolaemia. The gene or a polynucleotide fragment of the
CC   EDN/ECE/EDNR signaling system are useful as forensic markers, for
CC   creating a transgenic animal and in creation of a solid support
CC   comprising polynucleotides, genes, vectors, polypeptides, antibodies or
CC   host cells of the invention. This sequence represents a PCR primer used
CC   to identify single nucleotide polymorphisms in DNA encoding
CC   cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway.
XX
SQ   Sequence 21 BP; 1 A; 11 C; 3 G; 6 T; 0 other;

  Query Match             1.2%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 60;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        463 AGCAGCCTGCAGGGGGAGGA 482
              ||||| |||||||| |||||
Db         21 AGCAGGCTGCAGGGAGAGGA 2


RESULT 20
AAV48107
ID   AAV48107 standard; DNA; 18 BP.
XX
AC   AAV48107;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Beta-globin fusion primer 18.155.
XX
KW   In situ translation; RNA-protein fusion; binding reagent; antibody;
KW   industrial catalyst; ss; PCR; primer; amplification.
XX
OS   Synthetic.
XX
PN   WO9831700-A1.
XX
PD   23-JUL-1998.
XX
PF   14-JAN-1998;   98WO-US00807.
XX
PR   06-NOV-1997;   97US-0064491.
PR   21-JAN-1997;   97US-0035963.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Liu R,  Roberts RW,  Szostak JW;
XX
DR   WPI; 1998-414032/35.
XX
PT   Selection of specific protein by screening protein-RNA fusions
PT   generated in vitro or in situ - useful for, e.g. identifying enzymes
PT   and antibodies with altered properties, potentially useful as
PT   catalysts or for therapy or diagnosis
XX
PS   Disclosure; Page 49; 94pp; English.
XX
CC   The primers AAV48107 and AAV48108 were used in the synthesis of a
CC   beta-globin fusion construct.  This was used in the selection of a
CC   specific protein or RNA, by in vitro or in situ translation of candidate
CC   RNA molecules to produce RNA-protein fusions, then selecting specific RNA
CC   protein fusions. The method is used to select proteins (or DNA encoding
CC   them) having altered properties, e.g. for identification of new binding
CC   reagents, to identify improved human antibodies or new enzymes.  These
CC   proteins are potentially useful in diagnosis and therapy, or as
CC   industrial catalysts. The methods allow many rounds of selection and
CC   amplification to be performed, resulting in enrichment of even very rare
CC   molecules and allowing isolation of proteins that bind specifically to
CC   almost any compound or catalyse almost any reaction.
XX
SQ   Sequence 18 BP; 3 A; 2 C; 7 G; 6 T; 0 other;

  Query Match             1.2%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 58;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        679 GTGGTATTTGGGAGCCAG 696
              |||||||||| |||||||
Db          1 GTGGTATTTGTGAGCCAG 18


RESULT 21
AAC67511
ID   AAC67511 standard; DNA; 18 BP.
XX
AC   AAC67511;
XX
DT   14-FEB-2001  (first entry)
XX
```

```
DE   Alzheimer's disease-linked mitochondrial SNP PCR primer #211.
XX
KW   Human; mitochondrial genome; single nucleotide polymorphism; SNP;
KW   Alzheimer's disease; mtDNA; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200063441-A2.
XX
PD   26-OCT-2000.
XX
PF   19-APR-2000; 2000WO-US10906.
XX
PR   20-APR-1999;   99US-0130447.
PR   22-OCT-1999;   99US-0160901.
XX
PA   (MITO-) MITOKOR.
XX
PI   Herrnstadt C,  Davis RE;
XX
DR   WPI; 2000-672748/65.
XX
PT   Diagnosing a subject at the risk for or having Alzheimer's disease
PT   comprises determining at least one single nucleotide polymorphism in
PT   mitochondrial DNA associated with the disease in the sample from the
PT   subject  -
XX
PS   Example 9; Page 51; 89pp; English.
XX
CC   The present invention describes a novel method for determining the risk
CC   of or diagnosing Alzheimer's disease using single nucleotide
CC   polymorphisms (SNPs) present in an individual's mitochondrial DNA
CC   (mtDNA). In additon, the SNPs identified can be used to identify agents
CC   suitable for use in treating Alzheimer's disease. Sequences
CC   AAC67301-C67610 are PCR primers used to demonstrate the method of the
CC   invention.
XX
SQ   Sequence 18 BP; 7 A; 7 C; 3 G; 1 T; 0 other;

  Query Match             1.2%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 58;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         23 AAACCAAACCCAGCTACG 40
              |||||| ||||||||||
Db          1 AAACCAGACCCAGCTACG 18


RESULT 22
AAA94334
ID   AAA94334 standard; DNA; 18 BP.
XX
AC   AAA94334;
XX
DT   11-JAN-2001  (first entry)
XX
DE   Human beta-globin mRNA reverse transcription primer 18.155.
XX
KW   Human; beta-globin; RNA-protein fusion; protein library;
KW   protein isolation; gene cloning; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200047775-A1.
XX
PD   17-AUG-2000.
XX
PF   01-FEB-2000; 2000WO-US02589.
XX
PR   09-FEB-1999;   99US-0247190.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Szostak JW,  Roberts RW,  Liu R;
XX
DR   WPI; 2000-533022/48.
XX
PT   Producing protein or DNA libraries which are useful for improving
PT   existing proteins, by in vitro translating protein coding sequences to
PT   produce RNA-protein fusions and incubating these protein fusions under
PT   high salt conditions -
XX
PS   Disclosure; Page 55; 121pp; English.
XX
CC   The present sequence is a primer which was used to generate beta-globin
CC   cDNA from mRNA by reverse transcription. The cDNA was used in a method
CC   for generating beta-globin RNA-protein fusions. RNA-protein fusions
CC   comprise a protein covalently linked to the 3' end of its own mRNA. The
CC   fusions are made by synthesis and in vitro or in situ translation of an
CC   mRNA molecule with a peptide acceptor attached to its 3' end. The
CC   RNA-protein fusions are incubated under high salt conditions to produce
CC   a protein library. This method is useful for improving or altering
CC   existing proteins, as well as for isolating new proteins and nucleic
CC   acid or small molecule targets. It may also be used to improve human or
CC   humanised single-chain antibodies for the treatment of a number of
CC   diseases. The method is useful for the isolation of proteins with
CC   specific binding properties, for screening cDNA libraries and cloning
CC   new genes on the basis of protein-protein interactions. Unlike prior
CC   art, the new method does not rely on maintaining the integrity of an
CC   mRNA:ribosome:nascent chain ternary complex, which is very fragile and
CC   is therefore of limited use. The method does not rely on topological
CC   links between the protein and the nucleic acid so that the information
CC   of the protein is retained and can be recovered in readable, nucleic
CC   acid form.
XX
SQ   Sequence 18 BP; 3 A; 2 C; 7 G; 6 T; 0 other;

  Query Match             1.2%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 58;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        679 GTGGTATTTGGGAGCCAG 696
              |||||||||| |||||||
Db          1 GTGGTATTTGTGAGCCAG 18


RESULT 23
AAZ26499/c
ID   AAZ26499 standard; DNA; 21 BP.
XX
AC   AAZ26499;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 688.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US05419.
XX
PR   20-MAR-1997;   97US-0041057.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
```

XX
DR WPI; 1998-521232/44.
XX
PT Identifying target genes for allele-specific drugs - used for
PT diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic
PT plaque, dysplastic lesions, endometriosis or graft versus host disease
XX
PS Disclosure; Figure 7; 605pp; English.
XX
CC This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is
CC active on a gene vital for cell growth or viability, and where the gene
CC is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can
CC be used in the diagnosis, prevention and treatment of LOH disorders,
CC e.g. cancers, atherosclerotic plaques, premalignant metaplastic or
CC dysplastic lesions, benign tumours, endometriosis, polycystic kidney
CC disease, and graft versus host disease. The method can also be used to
CC remove malignant cells from bone marrow transplants. AAZ25812-Z26825
CC represent human polymorphic sites described in the method of the
CC invention.
XX
SQ Sequence 21 BP; 13 A; 3 C; 0 G; 5 T; 0 other;

Query Match 1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 79;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1145 TTTTTTCTTTTTGGAAGTAAA 1165
|||||| |||||| ||||| |
Db 21 TTTTTTTTTTTTGAAAGTAGA 1

RESULT 24
AAC67429/c
ID AAC67429 standard; DNA; 21 BP.
XX
AC AAC67429;
XX
DT 14-FEB-2001 (first entry)
XX
DE Alzheimer's disease-linked mitochondrial SNP PCR primer #129.
XX
KW Human; mitochondrial genome; single nucleotide polymorphism; SNP;
KW Alzheimer's disease; mtDNA; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200063441-A2.
XX
PD 26-OCT-2000.
XX
PF 19-APR-2000; 2000WO-US10906.
XX
PR 20-APR-1999; 99US-0130447.
PR 22-OCT-1999; 99US-0160901.
XX
PA (MITO-) MITOKOR.
XX
PI Herrnstadt C, Davis RE;
XX
DR WPI; 2000-672748/65.
XX
PT Diagnosing a subject at the risk for or having Alzheimer's disease
PT comprises determining at least one single nucleotide polymorphism in
PT mitochondrial DNA associated with the disease in the sample from the
PT subject -
XX
PS Example 4; Page 40; 89pp; English.
XX
CC The present invention describes a novel method for determining the risk
CC of or diagnosing Alzheimer's disease using single nucleotide
CC polymorphisms (SNPs) present in an individual's mitochondrial DNA
CC (mtDNA). In additon, the SNPs identified can be used to identify agents
CC suitable for use in treating Alzheimer's disease. Sequences
CC AAC67301-C67610 are PCR primers used to demonstrate the method of the
CC invention.
XX
SQ Sequence 21 BP; 5 A; 2 C; 8 G; 6 T; 0 other;

Query Match 1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 79;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 51 GCATACTCCTCAATTACCCAC 71
|||||||| ||||| | ||||
Db 21 GCATACTCTTCAATCAGCCAC 1

RESULT 25
AAZ57277/c
ID AAZ57277 standard; DNA; 21 BP.
XX
AC AAZ57277;
XX
DT 30-MAR-2000 (first entry)
XX
DE Human mitochondrial DNA NADH dehydrogenase PCR primer SEQ ID NO:76.
XX
KW Human; mitochondrial DNA; extramitochondrial DNA; mtDNA; exmtDNA;
KW diagnosis; quantification; detection; dystonia; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; schizophrenia; stroke;
KW non-insulin dependent diabetes mellitus; mitochondrial encephalopathy;
KW lactic acidosis; myoclonic epilepsy ragged red fibre syndrome;
KW Leber's hereditary optic neuropathy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO9966075-A2.
XX
PD 23-DEC-1999.
XX
PF 14-JUN-1999; 99WO-US13426.
XX
PR 15-JUN-1998; 98US-0097889.
PR 15-JUN-1998; 98US-0098079.
PR 30-APR-1999; 99US-0302681.
XX
PA (MITO-) MITOKOR.
XX
PI Herrnstadt C, Ghosh SS, Clevenger W, Fahy ED, Davis RE;
XX
DR WPI; 2000-097754/08.
XX
PT Quantification of extramitochondrial DNA for diagnosis of, e.g.
PT Alzheimer's, Huntington's and Parkinson's disease -
XX
PS Disclosure; Page 32; 157pp; English.
XX
CC The present invention describes a method for the quantification of
CC extramitochondrial DNA (exmtDNA) by determining the ratio of a first
CC and second biological sample containing exmtDNA and mitochondrial DNA
CC (mtDNA) to determine the risk or presence of a disease associated with
CC altered mitochondrial function. The method can be used to determine
CC the risk of or presence of a disease associated with altered
CC mitochondrial function, especially Alzheimer's disease, Huntington's
CC disease, Parkinson's disease, dystonia, schizophrenia, non-insulin
CC dependent diabetes mellitus, mitochondrial encephalopathy, lactic
CC acidosis, stroke, myoclonic epilepsy ragged red fibre syndrome and

```
CC   Leber's hereditary optic neuropathy. The method can also be used to
CC   identify agents suitable for treating such diseases, in particular
CC   Alzheimer's disease. AAZ57202 to AAZ57313 represent nucleotide sequences
CC   used in the exemplification of the present invention. More specifically
CC   AAZ57206 to AAZ57313 are PCR primers used in the detection of exmtDNA
CC   and mtDNA.
XX
SQ   Sequence 21 BP; 5 A; 2 C; 8 G; 6 T; 0 other;

  Query Match             1.2%;  Score 16.2;  DB 1;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 79;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 GCATACTCCTCAATTACCCAC 71
              ||||||||| ||||| | ||||
Db         21 GCATACTCTTCAATCAGCCAC 1


RESULT 26
AAQ64857/c
ID   AAQ64857 standard; DNA; 23 BP.
XX
AC   AAQ64857;
XX
DT   25-MAR-2003  (updated)
DT   18-OCT-1994  (first entry)
XX
DE   Ig gamma chain probe gamma-CH1.
XX
KW   SpA domain D; Ig binding region; gamma chain; B-cell superantigen; sAg;
KW   superantigen; heavy chain variable region; VH3 restricted antibody;
KW   VH; protein-A; VH26C; combinatorial library; B-lymphocyte;
KW   vaccine; DNA probe; hybridization; ss.
XX
OS   Synthetic.
XX
PN   WO9409818-A1.
XX
PD   11-MAY-1994.
XX
PF   29-OCT-1993;   93WO-US10555.
XX
PR   30-OCT-1992;   92US-0969936.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Silverman GJ;
XX
DR   WPI; 1994-167127/20.
XX
PT   Stimulating prodn. of variable region gene family restricted
PT   antibodies - through B-cell super-antigen vaccination
XX
PS   Disclosure; Page 24; 130pp; English.
XX
CC   A B-cell superantigen (sAg) is a fragment of SpA D domain that
CC   specifically binds the Fab portion of variable region restricted
CC   antibodies.  The sAg is used to enhance production of VH, especially
CC   VH3, restricted Abs.  To detect Ig gamma chain expression, the
CC   antisense sequence given in AAQ64857 was used as probe.  Detection of
CC   VH families used the sense oligonucleotides given in AAQ64858-60.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 23 BP; 4 A; 8 C; 8 G; 3 T; 0 other;

  Query Match             1.2%;  Score 16.2;  DB 1;  Length 23;
  Best Local Similarity   85.7%;  Pred. No. 90;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        261 CCTGGGCTGGCTGATCAAAGA 281
              ||||||||| ||| |||| ||
Db         22 CCTGGGCTGCCTGGTCAAGGA 2


RESULT 27
AAX22417
ID   AAX22417 standard; DNA; 20 BP.
XX
AC   AAX22417;
XX
DT   20-MAR-2003  (updated)
DT   19-MAY-1999  (first entry)
XX
DE   EP-897990 Seq ID 6.
XX
KW   Cross-contamination; amplification; N-lauroylsarcosine; inhibition;
KW   reactivation; uracil-N-glycosylase; UNG; false negative; primer; ss.
XX
OS   Synthetic.
XX
PN   EP897990-A2.
XX
PD   24-FEB-1999.
XX
PF   18-AUG-1998;   98EP-0115491.
XX
PR   20-AUG-1997;   97DE-1036062.
XX
PA   (BOEF ) BOEHRINGER MANNHEIM GMBH.
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Haberhausen G,  Jaeger S,  Sobek H;
XX
DR   WPI; 1999-134649/12.
XX
PT   Prevention of cross-contamination in DNA amplification - using
PT   nucleic-acid-degrading enzyme and reagent that inhibits reactivation
PT   of inactivated enzyme
XX
PS   Example 2; Page 8; 17pp; German.
XX
CC   This sequence is used to describe a method for reducing
CC   cross-contamination during the amplification of nucleic acids in a
CC   sample. The method involves (i) treating the sample with an enzyme
CC   that degrades nucleic acids from other amplification reactions; (ii)
CC   inactivating the enzyme; and (iii) amplifying the nucleic acids in the
CC   sample in the presence of a reagent that inhibits reactivation of the
CC   enzyme. N-lauroylsarcosine is used to inhibit reactivation of
CC   uracil-N-glycosylase (UNG). The new method prevents cross-contamination
CC   from amplification products containing artificially introduced dUTP
CC   units by using UNG and inhibiting reactivation of the UNG as above
CC   eliminates false negatives.
CC   (Updated on 20-MAR-2003 to correct PA field.)
XX
SQ   Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 other;

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 89;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGCAG 292
              ||||| |||||||| ||||
Db          1 ATCAATGAGGAAGCTGCAG 19


RESULT 28
AAC68751/c
ID   AAC68751 standard; DNA; 20 BP.
XX
AC   AAC68751;
XX
DT   20-FEB-2001  (first entry)
XX
DE   Human FUT3 antisense oligonucleotide SEQ ID NO: 2.
XX
KW   Human; fucosyltransferase; FUT3; FUT6; cancer; antisense oligonucleotide;
```

KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200064262-A1.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-US10547.
XX
PR 26-APR-1999; 99US-0131068.
XX
PA (UYNC-) UNIV NORTH CAROLINA.
XX
PI Weston BW, Hiller KM;
XX
DR WPI; 2000-687246/67.
XX
PT Novel antisense human fucosyltransferase sequences useful for treating
PT cancer including breast, lung, gastric, renal and uterine cancer -
XX
PS Claim 6; Page 32; 53pp; English.
XX
CC The present invention provides antisense oligonucleotides to the human
CC fucosyltransferase coding sequences, particularly FUT3 and FUT6. These
CC antisense sequences can be used in the treatment of cancer, especially
CC colon, pancreatic, ovarian, gastric, breast, lung, hepatocellular,
CC prostate, bladder, renal cell and uterine cancers. In additon, they can
CC also be used in the treatment of animals such as dogs, cats and horses.
XX
SQ Sequence 20 BP; 11 A; 3 C; 3 G; 3 T; 0 other;

Query Match 1.2%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1322 CTTTTGTAGATCTTGTGTT 1340
||||||||||||||| |||
Db 19 CTTTTGTAGATCTTCAGTT 1

RESULT 29
AAZ45870
ID AAZ45870 standard; DNA; 20 BP.
XX
AC AAZ45870;
XX
DT 25-APR-2000 (first entry)
XX
DE PCR primer R1570RAP used to amplify a portion of the RAP3 gene.
XX
KW RAP3; regeneration association protein 3; liver regeneration;
KW liver proliferation; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200003013-A2.
XX
PD 20-JAN-2000.
XX
PF 12-JUL-1999; 99WO-EP04938.
XX
PR 10-JUL-1998; 98EP-0202336.
XX
PA (AMST-) AMSTERDAM MOLECULAR THERAPEUTICS BV.
XX
PI Chamuleau RAFM, Groenink M, Van Der Vliet HN, Leegwater ACJ;
XX
DR WPI; 2000-147615/13.
XX
PT Isolated RAP3 gene, protein and antibody useful for diagnosing liver
PT regeneration and/or cell proliferation -
XX
PS Disclosure; Page 3; 42pp; English.
XX
CC AAZ45854-71 represent PCR primers, derived from the human RAP3 cDNA
CC sequence. The RAP3 (regeneration association protein 3) gene is
CC involved in regeneration processes of the liver. The RAP3 gene was
CC found to be upregulated 6 hours after partial hepatectomy, after
CC which it is downregulated. The PCR primers are useful for detecting
CC nucleotide sequences in a source material. The RAP3 cDNA sequence
CC is useful as a marker of liver proliferation. The RAP3 protein is
CC useful for the diagnosis of liver regeneration and liver cell
CC proliferation. RAP3 antibodies, PCR primers and probes are useful
CC for detecting the occurrence of liver cell proliferation in a patient.
CC The RAP3 protein is also is useful for enhancing the growth of
CC regeneration of liver tissue comprising treating the liver tissue
CC such as extracorporeal or intracorporeal.
XX
SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 other;

Query Match 1.2%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 551 TGGCAGGCATGCACACACT 569
||||||| ||| |||||||
Db 1 TGGCAGGGATGTACACACT 19

RESULT 30
AAZ60204
ID AAZ60204 standard; cDNA; 20 BP.
XX
AC AAZ60204;
XX
DT 25-APR-2000 (first entry)
XX
DE PCR primer F1570RAP for RAP3 identification or amplification.
XX
KW RAP3; rat; liver regeneration; hepatic cell proliferation; liver biopsy;
KW liver transplant; bioartificial liver; PCR primer; ss.
XX
OS Rattus sp.
XX
PN EP976824-A1.
XX
PD 02-FEB-2000.
XX
PF 10-JUL-1998; 98EP-0202336.
XX
PR 10-JUL-1998; 98EP-0202336.
XX
PA (AMST-) AMSTERDAM MOLECULAR THERAPEUTICS BV.
XX
PI Chamuleau RAFM, Groenink M, Van der Vliet HN, Leegwater ACJ;
XX
DR WPI; 2000-147615/13.
XX
PT Isolated RAP3 gene, protein and antibody useful for diagnosing liver
PT regeneration and/or cell proliferation -
XX
PS Claim 15; Page 3; 31pp; English.
XX
CC This sequence represents a PCR primer which is based on the rat RAP3
CC gene. The RAP3 gene and rap3 protein are involved in the regeneration
CC processes of the liver, and the RAP3 gene is expressed specifically in
CC the liver. The RAP3 gene is useful for designing PCR primers (such as the
CC present sequence) and probes for detecting nucleotide sequences in a
CC source material and as a marker of liver proliferation. The rap3 protein
CC is useful for the diagnosis of liver regeneration and/or liver cell
CC proliferation. Anti-rap3 antibodies, PCR primers and nucleotide sequences
CC which act as probes are useful for detecting the occurrence of liver cell
CC proliferation in a patient. Single stranded oligonucleotides that are
CC complementary to RAP3 can be used as probes to detect the amount of mRNA
CC transcribed from RAP3 present in a sample such as a liver biopsy, plasma

```
CC   or serum of a tissue or body fluid in comparison to a reference sample.
CC   The probes can also be used for screening a liver cDNA or genomic
CC   library. The rap3 protein is useful for enhancing the growth or
CC   regeneration of liver tissue. The methods of the invention can be used to
CC   establish the efficacy of therapeutic agents stimulating liver
CC   regeneration and for patients who have undergone liver transplantation
CC   and for monitoring patients treated with a bioartificial liver.
XX
SQ   Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 other;

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 89;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        551 TGGCAGGCATGCACACACT 569
              ||||||| ||| |||||||
Db          1 TGGCAGGGATGTACACACT 19


RESULT 31
AAZ56049
ID   AAZ56049 standard; DNA; 20 BP.
XX
AC   AAZ56049;
XX
DT   23-MAR-2000  (first entry)
XX
DE   PCR primer for beta-actin.
XX
KW   Nuclear factor of activated T cells; NFATp; bone fracture; osteoporosis;
KW   calcineurin interaction region; cartilage cell differentiation;
KW   endochondral ossification; chondrosarcoma; rheumatoid arthritis;
KW   osteoarthritis; osteosarcoma; fibrous sarcoma; chondroma; enchondroma;
KW   PCR primer; beta-actin; ss.
XX
OS   Mus sp.
XX
PN   WO9961908-A1.
XX
PD   02-DEC-1999.
XX
PF   28-MAY-1999;   99WO-US11941.
XX
PR   28-MAY-1998;   98US-0087139.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Glimcher LH,  Ranger AM;
XX
DR   WPI; 2000-086734/07.
XX
PT   Modulating growth or differentiation of cartilage cells useful for
PT   treating chondrosarcoma, osteochondroma and arthritis in mammals  -
XX
PS   Example 6; Page 57; 90pp; English.
XX
CC   PCR primers AAZ56049-Z56050 are used to amplify beta-actin from wild
CC   type and NFATp-/- cartilage cultures. The primers are used in the
CC   identification of the role that NFATp plays in cartilage cell growth and
CC   differentiation. The modulation of growth or differentiation of
CC   cartilage can be carried out through contacting cells deficient in the
CC   NFAT family genes, with a  test compound. Modulating growth or
CC   differentiation of cartilage cells can achieved by contacting the cells
CC   with a modulator of NFATp activity, where the modulator comprises a
CC   peptidic compound derived from the calcineurin interacting region of
CC   NFATp. The methods of the invention are useful for modulating the growth
CC   or differentiation of cartilage cells and endochondral ossification
CC   useful for repairing bone defects and fractures in mammals including
CC   humans, monkeys, dogs, cats, mice etc. The compound that modulates
CC   cartilage cell growth and differentiation is useful for diagnosing
CC   disorders such as chondrosarcoma, osteochondroma, chondromyxoid fibroma,
CC   chondroma, enchondroma, chondroblastoma, osteoblastoma, fibrous
CC   dysplasia, ossifying fibroma, osteosarcoma or osteocartilaginous
CC   exostosis, which are associated with a change (elevated, reduced or
CC   mutated) in the expression of NFATp in cartilage cell. NFATp inhibitory
CC   compounds are useful for treating disorders such as rheumatoid arthritis,
CC   osteoarthritis and osteoporosis associated with cartilage degradation.
XX
SQ   Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 other;

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 89;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        934 CTGGAGAAGAGGTGTGAGC 952
              |||||||||| | |||||
Db          1 CTGGAGAAGAGCTATGAGC 19


RESULT 32
AAH25407
ID   AAH25407 standard; DNA; 20 BP.
XX
AC   AAH25407;
XX
DT   22-AUG-2001  (first entry)
XX
DE   Detection probe for a HIV DNA fragment.
XX
KW   Magnetic glass particle; nucleic acid purification; probe; ss.
XX
OS   Human immunodeficiency virus.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "ruthenium3+-(tris-bipyridyl)-derivatisation"
XX
PN   WO200137291-A1.
XX
PD   25-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-EP11459.
XX
PR   17-NOV-1999;   99EP-0122853.
PR   12-MAY-2000; 2000EP-0110165.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Weindel K,  Riedling M,  Geiger A;
XX
DR   WPI; 2001-381247/40.
XX
PT   Novel composition of magnetic glass particles for purification of DNA
PT   or RNA in automated processes  -
XX
PS   Example 7; Page 96; 105pp; English.
XX
CC   The specification describes a composition of magnetic glass particles,
CC   which contain at least one magnetic object with a mean diameter between
CC   5-500 nm. The composition is useful for the purification of nucleic
CC   acids. The composition can be used to process large quantities of
CC   nucleic acid samples, because it does not involve the particles being
CC   centrifuged or the fluids being drawn through glass fiber filters.
CC   The present sequence represents a probe for a HIV DNA fragment. The
CC   DNA fragment can be purified using the method of the invention.
XX
SQ   Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 other;

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 89;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGCAG 292
              ||||| |||||||| ||||
Db          1 ATCAATGAGGAAGCTGCAG 19
```

```
RESULT 33
ABS73911/c
ID   ABS73911 standard; DNA; 20 BP.
XX
AC   ABS73911;
XX
DT   06-DEC-2002  (first entry)
XX
DE   Human cytohesin-1 coding region antisense oligonucleotide, ISIS#111004.
XX
KW   Human; antisense; cytohesin-1; guanine nucleotide exchange protein;
KW   ARF; ADP ribosylation factor; inflammation; antiinflammatory; tumour;
KW   cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200268584-A2.
XX
PD   06-SEP-2002.
XX
PF   30-OCT-2001; 2001WO-US47583.
XX
PR   22-FEB-2001; 2001US-0791243.
XX
PA   (ISIS-) ISIS PHARM INC.
PA   (BOEH ) BOEHRINGER INGELHEIM PHARM INC.
XX
PI   Bennett CF,  Rothlein R,  Kishimoto TK,  Cowsert LM;
XX
DR   WPI; 2002-723198/78.
XX
PT   New antisense oligonucleotide encoding human cytohesin-1, useful for
PT   preventing or treating a disease or condition associated with
PT   cytohesin-1 expression e.g. tumor or inflammation  -
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to a new antisense compound, comprising 8-30
CC   nucleobases targeted to a nucleic acid molecule encoding human
CC   cytohesin-1, specifically hybridises with, and inhibits the expression
CC   of, human cytohesin-1, a guanine nucleotide exchange protein for ARF
CC   (ADP ribosylation factor). The antisense compound may be used in a
CC   pharmaceutical composition for inhibiting the expression of
CC   cytohesin-1 in human cells or tissues, and in treating a disease or
CC   condition associated with cytohesin-1 by administering to the human the
CC   antisense compound e.g. tumour or inflammation. The antisense
CC   compound is also useful for diagnostics, therapeutics, prophylaxis and
CC   as research reagents and kits. The present sequence is an antisense
CC   oligonucleotide targeting human cytohesin-1.
XX
SQ   Sequence 20 BP; 3 A; 6 C; 8 G; 3 T; 0 other;

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 89;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        521 ACCTGCCGGAGGAGCAGCT 539
              ||||||||||||||||  ||
Db         20 ACCTGCCGGAGGAGCTCCT 2


RESULT 34
ABN83653
ID   ABN83653 standard; DNA; 20 BP.
XX
AC   ABN83653;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Human immunodeficiency virus capture probe.
XX
KW   Nucleic acid detection; infection; subtilisin; esperase; diagnosis;
KW   HIV; probe; ss.
XX
OS   Human immunodeficiency virus.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Ruthenium-tris(bipyridyl) label"
XX
PN   EP1201752-A1.
XX
PD   02-MAY-2002.
XX
PF   31-OCT-2000; 2000EP-0123728.
XX
PR   31-OCT-2000; 2000EP-0123728.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Schmuck R,  Staepels J,  Meier T,  Wehnes U,  Russmann E;
XX
DR   WPI; 2002-396142/43.
XX
PT   Use of Bacillus lentus subtilisin 147 to analyze one or more target
PT   non-proteinaceous components from a mixture of non-proteinaceous and
PT   proteinaceous components derived from a biological sample useful e.g.
PT   diagnostically  -
XX
PS   Example; Page 24; 36pp; English.
XX
CC   The present sequence is a human immunodeficiency virus (HIV)
CC   capture probe, labeled with ruthenium-tris(bipyridyl) label.  The
CC   probe was used with HIV PCR primers (see ABN83651-52) in an example
CC   from the invention for the amplification and detection of HIV RNA
CC   in a plasma sample.  The invention provides a method for the
CC   analysis of non-proteinaceous components, especially DNA and/or
CC   RNA, in a mixture of proteinaceous and non-proteinaceous components
CC   in a biological sample.  The sample is incubated with protease
CC   subtilisin 147 (see ABB76400) of Bacillus lentus variant 147
CC   (NCIB 10147), and the target DNA or RNA is then amplified by PCR
CC   and determined or detected.  In the present example, the
CC   ruthenium-tris(bipyridyl)-labeled capture probe provided a
CC   sensitive nonisotopic approach to detection based on
CC   electrochemiluminescence following specific hybridisation to
CC   biotinylated denatured HIV amplicons.  The method is useful in
CC   environmental, food and medical analysis, e.g. to detect viral
CC   infection, and in molecular biological research, and can be
CC   performed using a high throughput format.
XX
SQ   Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 other;

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 89;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGCAG 292
              ||||| |||||||| ||||
Db          1 ATCAATGAGGAAGCTGCAG 19


RESULT 35
ABQ66447/c
ID   ABQ66447 standard; DNA; 20 BP.
XX
AC   ABQ66447;
XX
DT   22-AUG-2002  (first entry)
XX
DE   Human cytohesin-1 mRNA levels inhibitor #16.
XX
KW   Cytohesin-1; CT1; inhibit; cytostatic; antiinflammatory; cytostatic;
```

KW anti-infective; antisense gene therapy; infection; inflammation; tumour;
KW human; ss; inhibitor.
XX
OS Synthetic.
XX
PN US6383809-B1.
XX
PD 07-MAY-2002.
XX
PF 30-OCT-2000; 2000US-0702246.
XX
PR 30-OCT-2000; 2000US-0702246.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowsert LM;
XX
DR WPI; 2002-478385/51.
XX
PT New antisense compounds directed against human cytohesin-1, useful for
PT treating and preventing infection, inflammation and tumors -
XX
PS Claim 14; Column 41; 40pp; English.
XX
CC The invention relates to a novel antisense compound of 16-30 nucleotides
CC targeted to any of 71 specified regions of the sequence that encodes
CC human cytohesin-1 (CT1), where the compound hybridises and inhibits
CC expression of human CT1. The compound of the invention has
CC antiinflammatory, cytostatic, and anti-infective activity. The
CC antisense compounds may have a use in antisense gene therapy. The
CC antisense compounds are useful for treating or preventing disorders
CC associated with expression of human CT1, e.g. infections, inflammation
CC and tumours, and as research and diagnostic reagents. Sequences
CC ABQ66432-ABQ66511 represent chimeric phosphorothioate oligonucleotides,
CC with 2'-MOE wings and a deoxy gap. The claimed sequences inhibit
CC production of cytohesin-1 mRNA.
XX
SQ Sequence 20 BP; 3 A; 6 C; 8 G; 3 T; 0 other;

Query Match 1.2%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 521 ACCTGCCGGAGGAGCAGCT 539
||||||||||||||| ||
Db 20 ACCTGCCGGAGGAGCTCCT 2

RESULT 36
ABK51604
ID ABK51604 standard; DNA; 20 BP.
XX
AC ABK51604;
XX
DT 13-AUG-2002 (first entry)
XX
DE Human immunodeficiency virus (HIV) protease, probe.
XX
KW Subtilisin 147; medical analysis; environmental analysis;
KW food analysis; diagnostic; virus infection; probe; ss;
KW human immunodeficiency virus; HIV; protease.
XX
OS Human immunodeficiency virus.
XX
PN EP1201753-A1.
XX
PD 02-MAY-2002.
XX
PF 26-OCT-2001; 2001EP-0125322.
XX
PR 31-OCT-2000; 2000EP-0123728.
PR 15-MAR-2001; 2001EP-0106308.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Russmann E, Schmuck R, Meier T, Staepels J, Wehnes U;
XX
DR WPI; 2002-428566/46.
XX
PT Use of Bacillus lentus subtilisin 147 to analyse a target
PT non-proteinaceous component from a mixture of non-proteinaceous and
PT proteinaceous components derived from a biological sample useful e.g.
PT diagnostically to detect viruses -
XX
PS Example 2; Page 26; 38pp; English.
XX
CC The invention describes a target non-proteinaceous component is
CC analysed from a mixture of non-proteinaceous and proteinaceous components
CC derived from a biological sample by incubating the mixture with a
CC protease having at least 80 % identity to the known amino acid sequence
CC for subtilisin 147 from Bacillus lentus. The methods are useful for
CC analysis of biological samples e.g. in medical, environmental or food
CC analysis or in molecular biological research. They are especially useful
CC in diagnostics e.g. to detect virus infections. They can be used to
CC enrich a mixture for a target non-proteinaceous component or
CC purify/isolate the component, the component can especially be a nucleic
CC acid, e.g. from a virus/microorganism. The methods can be used to
CC isolate non-proteinaceous components useful as substrates in enzymatic
CC reactions, or (in the case of nucleic acids) for sequencing, as probes
CC etc. They can be used in high throughput formats, enabling analysis of
CC large numbers of samples in a short time. Kits for undertaking the
CC methods, comprising the preferred polypeptide, optionally a material
CC with an affinity to nucleic acids (especially preferred materials as
CC above) and/or optionally lysis, washing and elution buffers are provided.
CC This sequence represents a probe used to detect DNA sequences encoding
CC Human immunodeficiency virus proteases.
XX
SQ Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 other;

Query Match 1.2%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 274 ATCAAAGAGGAAGCAGCAG 292
||||| |||||||| ||||
Db 1 ATCAATGAGGAAGCTGCAG 19

RESULT 37
ABA04617/c
ID ABA04617 standard; DNA; 20 BP.
XX
AC ABA04617;
XX
DT 21-FEB-2002 (first entry)
XX
DE MOL2 forward PCR primer.
XX
KW MOL; G-coupled protein-receptor; cardiomyopathy; atherosclerosis;
KW cell signal processing; metabolic disorder; diabetes; cancer;
KW neurodegenerative disorder; immune disorder; cardiac disorder;
KW lung disease; autoimmune disease; developmental disorder; antidiabetic;
KW Cytostatic; Neuroprotective; Antiatherosclerotic; Immunosuppressive;
KW Gene therapy; Vaccine; antiinflammatory; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200181578-A2.
XX
PD 01-NOV-2001.
XX
PF 26-APR-2001; 2001WO-US13578.
XX
PR 26-APR-2000; 2000US-200158P.
PR 28-APR-2000; 2000US-200613P.

PR 28-APR-2000; 2000US-200780P.
PR 01-MAY-2000; 2000US-201006P.
PR 01-MAY-2000; 2000US-201007P.
PR 01-MAY-2000; 2000US-201236P.
PR 01-MAY-2000; 2000US-201238P.
PR 02-MAY-2000; 2000US-201186P.
PR 03-MAY-2000; 2000US-201474P.
PR 03-MAY-2000; 2000US-201508P.
PR 25-JUL-2000; 2000US-220591P.
PR 15-SEP-2000; 2000US-232678P.
PR 22-JAN-2001; 2001US-263217P.
PR 30-JAN-2001; 2001US-265160P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Vernet CAM, Fernandes ER, Gerlach V, Shimkets RA, Malyankar UM;
PI Boldog FL, Zerhusen BD, Spytek KA, Majumder K, Tchernev VT;
PI Padigaru M, Patturajan M, Burgess CE, Gangolli EA, Smithson G;
PI Rastelli L, Macdougall JR, Taupier RJ, Grosse WM, Szekeres ES;
PI Alsobrook JP;
XX
DR WPI; 2002-049278/06.
XX
PT Novel G-protein coupled receptor-related polypeptides and
PT polynucleotides for diagnosing, preventing and treating cardiomyopathy,
PT atherosclerosis, disorders related to cell signal processing and for
PT identifying modulators -
XX
PS Example 1; Page 156; 227pp; English.
XX
CC The present invention relates to novel G-coupled protein-receptor related
CC proteins and coding sequences (MOLX, where X is a number from 1 to 10,
CC ABA04589-ABA04603 and AAM47659-AAM47673). MOLX proteins and coding
CC sequences are useful for treating or preventing a MOLX-associated
CC disorder, such as cardiomyopathy, atherosclerosis, disorders related to
CC cell signal processing and metabolic pathway modulation, diabetes and
CC cancer. Additionally, MOLX proteins and coding sequences are useful for
CC preventing and treating a variety of disorders including metabolic
CC disorders, nutritional oedema, chronic and hereditary pancreatitis,
CC obesity, infectious disease, anorexia, neurodegenerative disorders,
CC Alzheimer's disease, Parkinson's disease, stroke, immune disorders,
CC haematopoietic disorders and various dyslipidaemias, metabolic syndrome X
CC and wasting disorders associated with chronic diseases and cancers,
CC cardiac disorders, hypertension, hypercalcaemia, cirrhosis, angiogenesis
CC and wound healing, trauma, glomerulonephritis, hyper and hypothyroidism,
CC multiple sclerosis, lung diseases including asthma, Crohn's disease,
CC scleroderma, autoimmune diseases, developmental disorders and neural tube
CC defects. The present sequence is a PCR primer, which was used to
CC illustrate the invention.
XX
SQ Sequence 20 BP; 5 A; 2 C; 7 G; 6 T; 0 other;

Query Match 1.2%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 641 TCTGCATCCCCCAAGACCT 659
||||||||| ||||||| |
Db 19 TCTGCATCCACCAAGACAT 1

RESULT 38
AAV47652
ID AAV47652 standard; DNA; 21 BP.
XX
AC AAV47652;
XX
DT 07-DEC-1998 (first entry)
XX
DE Mouse focal adhesion kinase cDNA 3' PCR primer.
XX
KW Protein tyrosine kinase 2; PYK2; mouse; cell adhesion kinase-beta;
KW related adhesion focal tyrosine kinase; focal adhesion kinase;
KW platelet; PCR; primer; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN WO9835016-A1.
XX
PD 13-AUG-1998.
XX
PF 09-FEB-1998; 98WO-US02494.
XX
PR 11-FEB-1997; 97US-0037561.
XX
PA (MERI) MERCK & CO INC.
XX
PI Duong LT, Rodan GA;
XX
DR WPI; 1998-447214/38.
XX
PT New nucleic acid encoding murine protein tyrosine kinase 2 and cells
PT expressing the recombinant kinase - used to identify specific
PT modulators, potentially useful for controlling the level of
PT platelets
XX
PS Example 2; Page 6; 25pp; English.
XX
CC This 3' primer and a 5' primer (see AAV47651) are based on an area
CC of non-homology between murine protein tyrosine kinase 2 (PYK2)
CC and focal adhesion kinase (FAK) that is adjacent to the C-terminus
CC of the kinase domain. They were used in a PCR amplification of
CC cDNAs of mouse osteoblastic MB1.8. The PCR product (700 bp) was
CC used as a FAK-specific probe to isolate mouse FAK cDNA. The
CC invention relates to new nucleic acid (see AAV47653) encoding mouse
CC PYK2 (see AAW61196), a member of the FAK family. PYK2 can be used in
CC a claimed method for identifying specific modulators of PYK2
CC activity.
XX
SQ Sequence 21 BP; 5 A; 7 C; 4 G; 5 T; 0 other;

Query Match 1.2%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 95;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 604 CTGAAGCCTGACACCTTCA 622
||||||| ||||||| |||
Db 2 CTGAAGCTTGACACCCTCA 20

RESULT 39
AAV49607
ID AAV49607 standard; DNA; 21 BP.
XX
AC AAV49607;
XX
DT 24-NOV-1998 (first entry)
XX
DE Focal adhesion kinase 3' PCR primer.
XX
KW Focal adhesion kinase; protein tyrosine kinase 2; PYK2 gene; mouse;
KW podosome; related adhesion focal tyrosine kinase;
KW cell adhesion kinase; ligand; monocyte; osteoporosis;
KW inflammation; therapy; PCR; primer; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN WO9835056-A1.
XX
PD 13-AUG-1998.
XX
PF 09-FEB-1998; 98WO-US02797.
XX
PR 11-FEB-1997; 97US-0037560.

XX
PA (MERI) MERCK & CO INC.
XX
PI Duong Le T, Rodan GA;
XX
DR WPI; 1998-447250/38.
XX
PT Identifying agents that bind and modulate protein tyrosine kinase 2
PT - useful for inhibiting migration, adhesion or activity of monocytic
PT cells, particularly for treatment and prevention of osteoporosis and
PT inflammation
XX
PS Example 3; Page 20; 56pp; English.
XX
CC This oligonucleotide is based on a non-homologous region, found
CC adjacent to the C-terminal of the kinase domain, of murine
CC protein tyrosine kinase 2 (PYK2) and focal adhesion kinase (FAK)
CC sequences. It was used as a 3' primer, together with a 5' primer
CC (see AAV49606), in the PCR amplification of mouse osteoblastic MB1.8
CC cell cDNA. The PCR product was used as a FAK-specific probe to
CC isolate full-length FAK cDNA. FAK shows homology to murine PYK2
CC (see AAW64568), another cell adhesion-dependent kinase. Agents that
CC bind to and modulate PYK2 are isolated using methods of the
CC invention, and are useful in treating osteoporosis and/or
CC inflammation.
XX
SQ Sequence 21 BP; 5 A; 7 C; 4 G; 5 T; 0 other;

Query Match 1.2%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 95;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 604 CTGAAGCCTGACACCTTCA 622
||||||| ||||||| |||
Db 2 CTGAAGCTTGACACCCTCA 20

RESULT 40
AAZ76174/c
ID AAZ76174 standard; DNA; 21 BP.
XX
AC AAZ76174;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:10530.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX
PS Claim 9; Page 2475; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 21 BP; 12 A; 4 C; 3 G; 2 T; 0 other;

Query Match 1.2%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 95;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1107 TGTAGTTTTCTGTTTAATT 1125
|||||| ||||||||| ||
Db 20 TGTAGTGTTCTGTTTATTT 2

RESULT 41
AAA63852/c
ID AAA63852 standard; DNA; 21 BP.
XX
AC AAA63852;
XX
DT 04-DEC-2000 (first entry)
XX
DE PCR primer used to amplify cDNA encoding full length human DAGKbeta.
XX
KW Human; diacylglycerol kinase beta; DAGKbeta; diacylglycerol; DAG;
KW phosphatidic acid; DAG-dependent protein kinase C activation;
KW mood disorder; epilepsy; neurodegenerative disorder; anxiety;
KW schizophrenia; migraine; drug dependence; stroke; Alzheimer's dementia;
KW Parkinson's disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200047723-A2.
XX
PD 17-AUG-2000.
XX
PF 23-DEC-1999; 99WO-GB04421.
XX
PR 15-FEB-1999; 99GB-0003430.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Caricasole A, Caldara F, Sala CF;
XX
DR WPI; 2000-506093/45.
XX
PT New human diacylglycerol kinase beta (hDAGKbeta) protein and its
PT modulating compounds, useful for treatment of neurodegenerative and
PT mood disorders -
XX
PS Disclosure; Page 15; 57pp; English.
XX
CC PCR primers AAA63851-52 were used to amplify cDNA encoding full
CC length human diacylglycerol kinase beta (DAGKbeta). DAGK converts
CC diacylglycerol (DAG) to phosphatidic acid and attenuates DAG-dependent
CC protein kinase C activation. Compounds that modulate the activity
CC of DAGKbeta may be administered to a human patient for the treatment

```
CC   or prophylaxis of a disorder that is responsive to modulation of
CC   DAGK activity. The disorder may be a mood disorder, epilepsy, a
CC   neurodegenerative disorder, anxiety, schizophrenia, migraine, drug
CC   dependence, stroke, Alzheimer's dementia or Parkinson's disease.
XX
SQ   Sequence 21 BP; 3 A; 7 C; 5 G; 6 T; 0 other;

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 95;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        934 CTGGAGAAGAGGTGTGAGC 952
              ||||||||||| | |||||
Db         19 CTGGAGAAGAGCTATGAGC 1


RESULT 42
AAA47627/c
ID   AAA47627 standard; cDNA; 21 BP.
XX
AC   AAA47627;
XX
DT   08-NOV-2000  (first entry)
XX
DE   Intronic primer (5a) used to map KCNQ4 potassium channel gene.
XX
KW   KCNQ4; potassium channel; cardiac arrhythmia; neonatal epilepsy;
KW   deafness; probes; treatment; therapy; transgenic animal; antibody;
KW   agonist; antagonist; tinnitus; hearing loss; neonatal deafness;
KW   presbyacusis; affective disorder, Alzheimer's disease; anxiety;
KW   ataxia; cognitive deficits; compulsive behavior; dementia;
KW   depression; Huntington's disease; mania; memory impairment;
KW   motor disorders; neurodegenerative disease; Parkinson's disease;
KW   Pick's disease; psychosis; schizophrenia; spinal cord damage;
KW   stroke; tremor; ss.
XX
OS   Synthetic.
XX
PN   WO200044786-A1.
XX
PD   03-AUG-2000.
XX
PF   19-JAN-2000; 2000WO-DK00024.
XX
PR   26-JAN-1999;   99DK-0000076.
PR   19-MAY-1999;   99DK-0000693.
XX
PA   (NEUR-) NEUROSEARCH AS.
XX
PI   Jentsch TJ;
XX
DR   WPI; 2000-548813/50.
XX
PT   Nucleic acids encoding the novel KCNQ4 potassium channel subunit,
PT   useful e.g. for treating tinnitus, deafness, Alzheimer's and
PT   Parkinson's diseases
XX
PS   Example 2; Page 24; 65pp; English.
XX
CC   Mutations in 3 known genes of the KCNQ branch of the potassium
CC   channel gene family underlie inherited cardiac arrhythmia's, neonatal
CC   epilepsy and in some cases associated with deafness. KCNQ4 has been
CC   mapped to the DFNA2 locus for autosomal dominant hearing loss, and
CC   a dominant negative KCNQ4 mutation that causes deafness in a DFNA2
CC   pedigree has been identified. KCNQ4 is the first potassium channel
CC   gene underlying non-syndromic deafness. KCNQ4 forms heteromeric
CC   channels with other KCNQ channel subunits, especially KCNQ3.
CC   Nucleotides encoding the KCNQ4 protein and the protein itself may be
CC   used in the prevention, treatment and diagnosis of diseases
CC   associated with inappropriate KCNQ4 expression. The nucleotides may
CC   also be used as DNA probes in diagnostic assays (e.g. polymerase
CC   chain reactions (PCR)) to detect and quantitate the presence of
CC   similar nucleic acid sequences in samples and to identify mutations
CC   within them, and hence which patients may be in need of restorative
CC   therapy. They may also be used to study the expression and function
CC   of KCNQ4 polypeptides and their role in metabolism, for example
CC   through the production of transgenic animals. The KCNQ4 polypeptides
CC   may be used as antigens in the production of antibodies and to
CC   identify modulators (agonists and antagonists) of KCNQ4 expression
CC   and activity. The anti-KCNQ4 antibodies and KCNQ4 antagonists may
CC   also be used to down regulate KCNQ4 expression and activity. They may
CC   be used in this way to treat tinnitus, loss of hearing (especially
CC   progressive hearing loss, neonatal deafness and presbyacusis
CC   (deafness of the elderly)) and disease or adverse conditions of the
CC   central nervous system (CNS) such as affective disorder, Alzheimer's
CC   disease, anxiety, ataxia, CNS damage caused by trauma, stroke or
CC   neurodegenerative illness, cognitive deficits, compulsive behavior,
CC   dementia, depression, Huntington's disease, mania, memory impairment,
CC   memory disorders and dysfunctions, motion disorders, motor disorders,
CC   neurodegenerative diseases, Parkinson's disease, Parkinson-like motor
CC   disorders, phobias, Pick's disease, psychosis, schizophrenia, spinal
CC   cord damage, stroke and/or tremor. Conversely, antisense nucleic acid
CC   molecules may be administered to down regulate KCNQ4 expression by
CC   binding with the cells own KCNQ4 genes and preventing their
CC   expression. Fourteen intronic primer pairs were used map the KCNQ4
CC   gene by amplifying KCNQ4 exons with adjacent short intronic sequences
CC   (See AAA47619-A47646). This primer was used to amplify exon 5 and
CC   generated a 286 nucleotide fragment.
XX
SQ   Sequence 21 BP; 3 A; 7 C; 5 G; 6 T; 0 other;

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 95;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        120 CGTCCACACGGGACAGGGA 138
              | |||||||||||| |||||
Db         20 CTTCCACACGGGAAAGGGA 2


RESULT 43
AAL47730
ID   AAL47730 standard; DNA; 21 BP.
XX
AC   AAL47730;
XX
DT   18-SEP-2002  (first entry)
XX
DE   Ras gene PCR primer SEQ ID NO: 26.
XX
KW   K-ras; N-ras; H-ras; ras; oncogene; mutation detection; PCR; primer;
KW   probe; restriction mediated selection PCR; cancer; ss.
XX
OS   Unidentified.
XX
PN   WO200229005-A2.
XX
PD   11-APR-2002.
XX
PF   02-OCT-2001; 2001WO-US42422.
XX
PR   02-OCT-2000; 2000US-237416P.
XX
PA   (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI   Belly RT,  Todd AV,  Fuery CJ;
XX
DR   WPI; 2002-479599/51.
XX
PT   Amplifying and determining mutant sequences in DNA sample using
PT   thermostable restriction enzyme so that during thermocycling mutant
PT   sequences are enriched while wild-type sequences and/or primer induced
PT   sites are cleaved  -
XX
PS   Claim 1; Page 74; 116pp; English.
XX
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CC The present invention relates to a method of amplifying and determining
CC target mutant Ras sequences in a DNA sample, involving the use of a
CC thermostable restriction enzyme and primers shown in AAL47705-AAL47771.
CC The method used is designated restriction mediated selection polymerase
CC chain reaction (REMS-PCR). The method can be used to detect H-ras, K-ras
CC and N-ras mutations, which may lead to cancer. The present sequence is a
CC PCR primer useful in the method of the invention.
XX
SQ Sequence 21 BP; 3 A; 9 C; 6 G; 3 T; 0 other;

Query Match 1.2%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 95;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 687 TGGGAGCCAGCGGCCCCTC 705
|| || ||||||||||||||
Db 2 TGTGACCCAGCGGCCCCTC 20

RESULT 44
ABK94275
ID ABK94275 standard; DNA; 21 BP.
XX
AC ABK94275;
XX
DT 27-AUG-2002 (first entry)
XX
DE Endothelin converting enzyme 1 (ECE-1) SNP detection primer #63.
XX
KW Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
KW EDNR; signaling system; cardiovascular disease; coronary heart disease;
KW hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;
KW diabetes; familial hypercholesterolaemia; forensic marker;
KW transgenic animal; solid support; cardiovascular regulator; SNP;
KW single nucleotide polymorphism; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO200224747-A2.
XX
PD 28-MAR-2002.
XX
PF 31-AUG-2001; 2001WO-EP10087.
XX
PR 19-SEP-2000; 2000EP-0120123.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Brinkmann U, Hoffmeyer S;
XX
DR WPI; 2002-435060/46.
XX
PT Novel polynucleotide of the endothelin/endothelin converting
PT enzyme/receptors of endothelin and endothelin converting enzyme
PT signaling system associated with cardiovascular disease, useful for
PT treating the disease -
XX
PS Example 6; Page 63; 190pp; English.
XX
CC The invention describes a polynucleotide (I) of the endothelin
CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
CC signaling system which is associated with a cardiovascular disease. (I),
CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
CC or (II) is useful for producing cells capable of expressing a molecular
CC variant polypeptide which is associated with a cardiovascular disease.
CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
CC a molecular variant gene comprising (I) is useful for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
CC or its gene product, or for identifying and obtaining an inhibitor of
CC the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
CC signaling system or its gene product. The isolated proteins and
CC polynucleotides encoding them are useful for preparation of a
CC pharmaceutical composition for treating a cardiovascular disease such as
CC coronary heart disease, hypertension, atherosclerosis, or related to
CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
CC hypercholesterolaemia. The gene or a polynucleotide fragment of the
CC EDN/ECE/EDNR signaling system are useful as forensic markers, for
CC creating a transgenic animal and in creation of a solid support
CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or
CC host cells of the invention. This sequence represents a PCR primer used
CC to identify single nucleotide polymorphisms in DNA encoding
CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway.
XX
SQ Sequence 21 BP; 5 A; 3 C; 11 G; 1 T; 1 other;

Query Match 1.2%; Score 15.8; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 95;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 463 AGCAGCCTGCAGGGGGAGGA 482
||||| |||| ||| |||||
Db 1 AGCAGGCTGCNGGGAGAGGA 20

RESULT 45
ABK94276/c
ID ABK94276 standard; DNA; 21 BP.
XX
AC ABK94276;
XX
DT 27-AUG-2002 (first entry)
XX
DE Endothelin converting enzyme 1 (ECE-1) SNP detection primer #64.
XX
KW Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
KW EDNR; signaling system; cardiovascular disease; coronary heart disease;
KW hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;
KW diabetes; familial hypercholesterolaemia; forensic marker;
KW transgenic animal; solid support; cardiovascular regulator; SNP;
KW single nucleotide polymorphism; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO200224747-A2.
XX
PD 28-MAR-2002.
XX
PF 31-AUG-2001; 2001WO-EP10087.
XX
PR 19-SEP-2000; 2000EP-0120123.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Brinkmann U, Hoffmeyer S;
XX
DR WPI; 2002-435060/46.
XX
PT Novel polynucleotide of the endothelin/endothelin converting
PT enzyme/receptors of endothelin and endothelin converting enzyme
PT signaling system associated with cardiovascular disease, useful for
PT treating the disease -
XX
PS Example 6; Page 63; 190pp; English.
XX
CC The invention describes a polynucleotide (I) of the endothelin
CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
CC signaling system which is associated with a cardiovascular disease. (I),
CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
CC or (II) is useful for producing cells capable of expressing a molecular
CC variant polypeptide which is associated with a cardiovascular disease.
CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
CC a molecular variant gene comprising (I) is useful for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
CC or its gene product, or for identifying and obtaining an inhibitor of

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CC   the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
CC   signaling system or its gene product. The isolated proteins and
CC   polynucleotides encoding them are useful for preparation of a
CC   pharmaceutical composition for treating a cardiovascular disease such as
CC   coronary heart disease, hypertension, atherosclerosis, or related to
CC   abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
CC   hypercholesterolaemia. The gene or a polynucleotide fragment of the
CC   EDN/ECE/EDNR signaling system are useful as forensic markers, for
CC   creating a transgenic animal and in creation of a solid support
CC   comprising polynucleotides, genes, vectors, polypeptides, antibodies or
CC   host cells of the invention. This sequence represents a PCR primer used
CC   to identify single nucleotide polymorphisms in DNA encoding
CC   cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway.
XX
SQ   Sequence 21 BP; 1 A; 11 C; 3 G; 5 T; 1 other;

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 95;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        463 AGCAGCCTGCAGGGGGAGGA 482
              ||||| |||| ||| |||||
Db         21 AGCAGGCTGCNGGGAGAGGA 2


RESULT 46
ABQ80130
ID   ABQ80130 standard; DNA; 22 BP.
XX
AC   ABQ80130;
XX
DT   13-JUN-2003  (first entry)
XX
DE   Probe DBM0157P, identifies IL4R variant T1682.
XX
KW   Human; interleukin 4 receptor; IL4R; type 1; diabetes; allele;
KW   insulin dependent diabetes mellitus; IDDM; myasthenia gravis;
KW   single nucleotide polymorphism; SNP; autoimmune disease;
KW   T helper type 1 mediated disease; rheumatoid arthritis; probe;
KW   multiple sclerosis; inflammatory bowel disease; systemic sclerosis;
KW   systemic lupus erythematosus; psoriasis; scleroderma; Grave's disease;
KW   Guillain-Barre syndrome; Hashimoto's thyroiditis; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003010335-A2.
XX
PD   06-FEB-2003.
XX
PF   17-JUL-2002; 2002WO-EP07956.
XX
PR   20-JUL-2001; 2001US-306912P.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Mirel DB,  Erlich HA,  Bugawan TL,  Noble JA,  Valdez AM;
XX
DR   WPI; 2003-248086/24.
XX
PT   Determining an individual's risk for type 1 diabetes, comprises
PT   detecting the presence of an insulin dependent diabetes
PT   mellitus-associated interleukin 4 receptor allele in a nucleic acid
PT   sample of the individual  -
XX
PS   Example 1; Page 32; 79pp; English.
XX
CC   The sequences given in ABQ80119-35 represent probes which were used
CC   to identify wild type and variant loci in the human interleukin 4
CC   receptor (IL4R).  These probe sequences were used in the method
CC   of the invention for determining an individual's risk for type 1
CC   diabetes.  The method comprises detecting the presence of an insulin
CC   dependent diabetes mellitus (IDDM)-associated interleukin 4 receptor
CC   allele in a nucleic acid sample of the individual, where the presence
CC   of the allele indicates the individual's risk for type 1 diabetes.
CC   The method identifies one or more single nucleotide polymorphism
CC   (SNP) within the IL4R gene listed in the specification.  The method
CC   and the SNP's are useful for determining an individual's risk for type 1
CC   diabetes. The IL4R SNP's are also useful for determining an individual's
CC   risk for any autoimmune disease or condition or any T helper type 1
CC   mediated disease, e.g. rheumatoid arthritis, multiple sclerosis,
CC   inflammatory bowel disease, systemic lupus erythematosus, psoriasis,
CC   scleroderma, Grave's disease, systemic sclerosis, myasthenia gravis,
CC   Guillain-Barre syndrome, or Hashimoto's thyroiditis.
XX
SQ   Sequence 22 BP; 5 A; 4 C; 8 G; 5 T; 0 other;

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 22;
  Best Local Similarity   89.5%;  Pred. No. 1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        435 GTTCAGAAAGTTGCTGAAG 453
              | ||||| ||||||||||
Db          3 GCTCAGAGAGTTGCTGAAG 21


RESULT 47
ABQ80159
ID   ABQ80159 standard; DNA; 22 BP.
XX
AC   ABQ80159;
XX
DT   13-JUN-2003  (first entry)
XX
DE   Probe DBM0157P, identifies wild type IL4R SNP #6.
XX
KW   Human; interleukin 4 receptor; IL4R; type 1; diabetes; allele;
KW   insulin dependent diabetes mellitus; IDDM; myasthenia gravis;
KW   single nucleotide polymorphism; SNP; autoimmune disease;
KW   T helper type 1 mediated disease; rheumatoid arthritis; probe;
KW   multiple sclerosis; inflammatory bowel disease; systemic sclerosis;
KW   systemic lupus erythematosus; psoriasis; scleroderma; Grave's disease;
KW   Guillain-Barre syndrome; Hashimoto's thyroiditis; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003010335-A2.
XX
PD   06-FEB-2003.
XX
PF   17-JUL-2002; 2002WO-EP07956.
XX
PR   20-JUL-2001; 2001US-306912P.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Mirel DB,  Erlich HA,  Bugawan TL,  Noble JA,  Valdez AM;
XX
DR   WPI; 2003-248086/24.
XX
PT   Determining an individual's risk for type 1 diabetes, comprises
PT   detecting the presence of an insulin dependent diabetes
PT   mellitus-associated interleukin 4 receptor allele in a nucleic acid
PT   sample of the individual  -
XX
PS   Example 4; Page 36; 79pp; English.
XX
CC   The sequences given in ABQ80153-69 represent probes which were used
CC   to identify wild type and variant loci in the human interleukin 4
CC   receptor (IL4R).  These probe sequences were used in the method
CC   of the invention for determining an individual's risk for type 1
CC   diabetes.  The method comprises detecting the presence of an insulin
CC   dependent diabetes mellitus (IDDM)-associated interleukin 4 receptor
CC   allele in a nucleic acid sample of the individual, where the presence
CC   of the allele indicates the individual's risk for type 1 diabetes.
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CC   The method identifies one or more single nucleotide polymorphism
CC   (SNP) within the IL4R gene listed in the specification. The method
CC   and the SNP's are useful for determining an individual's risk for type 1
CC   diabetes. The IL4R SNP's are also useful for determining an individual's
CC   risk for any autoimmune disease or condition or any T helper type 1
CC   mediated disease, e.g. rheumatoid arthritis, multiple sclerosis,
CC   inflammatory bowel disease, systemic lupus erythematosus, psoriasis,
CC   scleroderma, Grave's disease, systemic sclerosis, myasthenia gravis,
CC   Guillain-Barre syndrome, or Hashimoto's thyroiditis.
XX
SQ   Sequence 22 BP; 5 A; 4 C; 8 G; 5 T; 0 other;

  Query Match             1.2%;  Score 15.8;  DB 1;  Length 22;
  Best Local Similarity   89.5%;  Pred. No. 1e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        435 GTTCAGAAAGTTGCTGAAG 453
              | ||||| ||||||||||
Db          3 GCTCAGAGAGTTGCTGAAG 21


RESULT 48
ABK85826/c
ID   ABK85826 standard; DNA; 18 BP.
XX
AC   ABK85826;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Myotonic dystrophy protein kinase (DMPK) isoform, primer 57.
XX
KW   Myotonic dystrophy; DM; protein kinase; DMPK; myocardial infarction;
KW   muscle damage; dysfunction; reverse transcriptase PCR; RT-PCR;
KW   primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002061571-A1.
XX
PD   23-MAY-2002.
XX
PF   20-MAR-2001; 2001US-0813289.
XX
PR   20-MAR-2000; 2000US-190590P.
XX
PA   (MAHA/) MAHADEVAN M S.
PA   (TISC/) TISCORNIA G.
XX
PI   Mahadevan MS,  Tiscornia G;
XX
DR   WPI; 2002-507644/54.
XX
PT   A new isoform of myotonic dystrophy protein kinase includes a sequence
PT   encoded by exon 16 of the gene and is useful to detect presence or risk
PT   of myotonic dystrophy, myocardial infarction or a condition associated
PT   with muscle damage -
XX
PS   Example; Page 7; 26pp; English.
XX
CC   The invention describes an isolated and purified polypeptide, comprising
CC   an amino acid sequence encoded by exon 16 of the myotonic dystrophy
CC   protein kinase (DMPK) gene. The invention is used to detect presence or
CC   risk of myotonic dystrophy, myocardial infarction or a condition
CC   associated with muscle damage or dysfunction. This sequence represents a
CC   reverse transcriptase PCR primer used to isolate cDNA encoding exon 16 of
CC   the novel Myotonic dystrophy protein kinase DMPK isoform studied in the
CC   invention.
XX
SQ   Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 other;

  Query Match             1.1%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 92;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        578 AGGCCCTCCGTCTGCCC 594
              ||||||||| |||||||
Db         17 AGGCCCTCCATCTGCCC 1


RESULT 49
AAI71035
ID   AAI71035 standard; DNA; 18 BP.
XX
AC   AAI71035;
XX
DT   18-MAR-2002  (first entry)
XX
DE   Human tumour suppressor gene THW forward PCR primer 312f6.
XX
KW   THW; tumour suppressor gene; human; breast cancer; melanoma;
KW   metastasis; diagnosis; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200190353-A1.
XX
PD   29-NOV-2001.
XX
PF   17-MAY-2001; 2001WO-EP05627.
XX
PR   19-MAY-2000; 2000EP-0110692.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Hildebrandt T,  Van Muijen G,  Weidle U;
XX
DR   WPI; 2002-106197/14.
XX
PT   Detecting nucleic acids in a sample for determining whether a cancer
PT   cell-containing test sample from a human has potential for tumour
PT   development, by using a THW nucleic acid down regulated in human tumours
PT   cells as probe -
XX
PS   Example 3; Page 17; 42pp; English.
XX
CC   The present sequence is that of primer 312f6, which was used in the
CC   PCR amplification of cDNA derived from human melanoma metastasis
CC   cell line 530. The primer is based on a 301 bp clone obtained by
CC   differential display analysis of 530 cells. RT-PCR was performed
CC   to identify the 5' extended region of the cDNA. Human THW cDNA
CC   was obtained (see AAI71033). THW is a tumour suppressor gene that
CC   shows downregulated expression in tumour cells. It is capable of
CC   suppressing tumour progression and/or metastasis, especially in
CC   malignant melanoma and mammary carcinoma cells. A process for
CC   determining whether a cancer cell-containing test sample has
CC   potential for tumour development, progression or metastasis involves
CC   determining the approximate level of hybridisation of a probe
CC   comprising the THW gene to the sample. A test sample having no or
CC   low potential for tumour progression or metastasis will have a
CC   higher amount of the THW nucleic acid than does a cancer cell
CC   sample which has a high tumour progression potential or a
CC   metastatic potential.
XX
SQ   Sequence 18 BP; 1 A; 11 C; 3 G; 3 T; 0 other;

  Query Match             1.1%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 92;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        141 CCCGCTCGGCTCCGCTC 157
              ||||||| |||||||||
Db          2 CCCGCTCCGCTCCGCTC 18


RESULT 50
AAT03278
```

```
ID   AAT03278 standard; DNA; 20 BP.
XX
AC   AAT03278;
XX
DT   11-APR-1996  (first entry)
XX
DE   Mycobacterium tuberculosis detecting hybridisation probe-PCR primer.
XX
KW   Tuberculosis; detection; primer; probe; ss.
XX
OS   Mycobacterium tuberculosis.
XX
PN   JP07213288-A.
XX
PD   15-AUG-1995.
XX
PF   04-FEB-1994;   94JP-0012724.
XX
PR   04-FEB-1994;   94JP-0012724.
XX
PA   (TOYM ) TOYOBO KK.
XX
DR   WPI; 1995-315927/41.
XX
PT   Oligo:nucleotide for detection of Mycobacterium tuberculosis -
PT   useful as a labelled hybridisation probe or as a primer for PCR
PT   amplification
XX
PS   Claim 2; Page 7; 8pp; Japanese.
XX
CC   AAT03277-T03280 are oligonucleotides which may be used for the
CC   detection of Mycobacterim tuberculosis in humans. They may be used
CC   either as labelled hybridisation probes or as polymerase chain
CC   reaction primers. The oligonucleotides allow direct, rapid and
CC   reliable detection of Mycobacterium tuberculosis.
XX
SQ   Sequence 20 BP; 3 A; 4 C; 6 G; 7 T; 0 other;

  Query Match             1.1%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        497 TGCAGCGTCTTGGGGTC 513
              ||||||||||||| ||||
Db          2 TGCAGCGTCTTGAGGTC 18


RESULT 51
AAZ77095/c
ID   AAZ77095 standard; DNA; 20 BP.
XX
AC   AAZ77095;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human biallelic marker downstream amplification primer SEQ ID NO:11451.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   amplification; single nucleotide polymorphism; SNP; PCR primer;
KW   diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB00822.
XX
PR   21-APR-1998;   98US-0082614.
PR   23-NOV-1998;   98US-0109732.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome  -
XX
PS   Claim 9; Page 2672; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the
CC   invention have a variety of uses: they can be used for high density
CC   mapping of the human genome, and in complex association studies and
CC   haplotyping studies which are useful in determining the genetic basis
CC   for disease states. Compositions and methods of the invention can also
CC   be useful for the identification of the targets for the development of
CC   pharmaceutical agents and diagnostic methods, as well as the
CC   characterisation of the differential efficacious responses to and side
CC   effects from pharmaceutical agents acting on a disease as well as other
CC   treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC   and 3367, are not actually given a sequence in the Sequence Listing
CC   from the present invention.
XX
SQ   Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 other;

  Query Match             1.1%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        225 TCCTCAGCCTCAGGCAT 241
              |||||| ||||||||||
Db         17 TCCTCATCCTCAGGCAT 1


RESULT 52
AAQ75612
ID   AAQ75612 standard; DNA; 21 BP.
XX
AC   AAQ75612;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-0112515.
XX
PR   16-APR-1993;   93JP-0112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA
PT   followed by digestion with restriction enzymes
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an
```

```
CC   aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC   and a plural type of labelled reverse transcription primers
CC   (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC   template for each reverse transcription primer; (b) digesting each of
CC   the prepared aggregates of the double-stranded cDNAs with restriction
CC   enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC   seperate lanes. The method can be used to analyse gene expression
CC   rapidly and easily.
XX
SQ   Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 other;

  Query Match             1.1%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTGGAA 1160
              ||||||| |||||||||
Db          5 TTTTTTTTTTTTTGGAA 21


RESULT 53
AAT84695/c
ID   AAT84695 standard; DNA; 21 BP.
XX
AC   AAT84695;
XX
DT   02-JAN-1998  (first entry)
XX
DE   KSHV DNA polymerase antisense oligonucleotide HVLQB.
XX
KW   KSHV; gamma herpes virus; glycoprotein B; vaccine; infection;
KW   human Kaposi's sarcoma-associated herpes virus; probe; primer;
KW   DNA polymerase; ss.
XX
OS   Synthetic.
XX
PN   WO9712042-A2.
XX
PD   03-APR-1997.
XX
PF   26-SEP-1996;   96WO-US15702.
XX
PR   26-SEP-1995;   95US-0004297.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Bosch ML,  Rose TM,  Strand K;
XX
DR   WPI; 1997-212901/19.
XX
PT   DNA encoding glycoprotein B of retroperitoneal fibromatosis and
PT   Kaposi's sarcoma associated herpes viruses - useful in vaccines for
PT   treatment of herpes infection or for detection of viral DNA
XX
PS   Claim 37; Page 76; 138pp; English.
XX
CC   Claimed type 3 oligonucleotides (AAT84694-96) are specific
CC   non-degenerate oligonucleotides for the human Kaposi's sarcoma-
CC   associated herpes virus (KSHV) DNA polymerase (gB).  They can
CC   be used for detecting, amplifying or characterising KSHV
CC   polynucleotides encoding DNA polymerase (see AAT84697).
XX
SQ   Sequence 21 BP; 3 A; 4 C; 11 G; 3 T; 0 other;

  Query Match             1.1%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        569 TGCTCCAGCAGGCCCTC 585
              | |||||||||||||||
Db         17 TCCTCCAGCAGGCCCTC 1


RESULT 54
AAT51587/c
ID   AAT51587 standard; DNA; 21 BP.
XX
AC   AAT51587;
XX
DT   06-NOV-1997  (first entry)
XX
DE   KSHV DNA polymerase specific oligonucleotide HVLQB.
XX
KW   Retroperitoneal fibromatosis herpes virus; detection; infection;
KW   Kaposi's sarcoma herpes virus; viral DNA; viral RNA; vaccine;
KW   antigen; antibody; ss.
XX
OS   Synthetic.
XX
PN   WO9704105-A1.
XX
PD   06-FEB-1997.
XX
PF   12-JUL-1996;   96WO-US11688.
XX
PR   11-JUL-1996;   96US-0001148.
PR   14-JUL-1995;   95US-0001148.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Bosch ML,  Rose TM,  Strand K,  Todaro GJ;
XX
DR   WPI; 1997-132644/12.
XX
PT   Herpes virus DNA polymerase and corresponding nucleotide sequence -
PT   used in the detection and treatment of herpes virus infection
XX
PS   Claim 26; Page 92; 132pp; English.
XX
CC   The present sequence represents oligonucleotide HVLQB which is
CC   specific for polynucleotides encoding DNA polymerases from Kaposi's
CC   sarcoma herpes virus (KSHV). The oligonucleotide may be used for
CC   detecting viral DNA or RNA in a sample of primate origin, especially
CC   in the diagnosis of herpes viral infection. Herpes virus DNA
CC   polymerases of this invention, may be used in vaccines for the
CC   protection against infection by a herpes virus of the RFHV/KSHV
CC   family. They may also be used in the design and screening of
CC   anti-viral drugs. Antibodies raised against the polymerase or
CC   fragments of it, may be used in the detection of herpes virus
CC   infection and for drug targetting for the therapy of herpes virus
CC   infection.
XX
SQ   Sequence 21 BP; 3 A; 4 C; 11 G; 3 T; 0 other;

  Query Match             1.1%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        569 TGCTCCAGCAGGCCCTC 585
              | |||||||||||||||
Db         17 TCCTCCAGCAGGCCCTC 1


RESULT 55
AAH91924/c
ID   AAH91924 standard; DNA; 21 BP.
XX
AC   AAH91924;
XX
DT   09-OCT-2001  (first entry)
XX
DE   Human inflammatory bowel disease associated polymorphic site #999.
XX
KW   Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW   single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KW   chromosome 5q31-33; forensic test; gene therapy; ds.
```

```
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    10
FT                   /*tag= a
FT                   /note= "SNP, optionally T or A at this position"
XX
PN   WO200142511-A2.
XX
PD   14-JUN-2001.
XX
PF   11-DEC-2000; 2000WO-US33632.
XX
PR   10-DEC-1999;   99US-0170257.
PR   10-APR-2000; 2000US-0196046.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
PI   Daly M,  Hudson TJ,  Lander ES,  Rioux J,  Siminovitch K;
XX
DR   WPI; 2001-367874/38.
XX
PT   Testing for the presence of polymorphisms associated with inflammatory
PT   bowel disease, using a hybridization assay -
XX
PS   Claim 1; Page 81; 463pp; English.
XX
CC   The present invention describes a method for detecting the presence of
CC   polymorphisms associated with inflammatory bowel diseases such as
CC   ulcerative colitis and Crohn's disease. The methods can be used to detect
CC   the presence of genetic polymorphisms associated with inflammatory bowel
CC   disease and correlating their occurrence with disease states. They may be
CC   used in this way for phenotypic correlations, forensics, paternity
CC   testing, medicine and genetic analysis. The present sequence is a
CC   polymorphic site described in the exemplification of the invention.
XX
SQ   Sequence 21 BP; 5 A; 5 C; 6 G; 4 T; 1 other;

  Query Match             1.1%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1064 TTCCCATCAGGCAGGCTC 1081
              || ||||||| |||||||
Db         20 TTGCCATCAGNCAGGCTC 3


RESULT 56
AAF96193
ID   AAF96193 standard; DNA; 21 BP.
XX
AC   AAF96193;
XX
DT   06-JUN-2001  (first entry)
XX
DE   Human gene single nucleotide polymorphism #954.
XX
KW   Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW   polymorphism; vascular disease; coronary artery disease; forensics;
KW   myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW   pulmonary embolism; paternity test; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,T)
FT                   /*tag= a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200118250-A2.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US24503.
XX
PR   10-SEP-1999;   99US-0153357.
PR   26-JUL-2000; 2000US-0220947.
PR   16-AUG-2000; 2000US-0225724.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lander ES,  Gargill M,  Ireland JS,  Bolk S,  Daley GQ,  McCarthy JJ;
XX
DR   WPI; 2001-226749/23.
XX
PT   Nucleic acids comprising single nucleotide polymorphisms, useful in
PT   applications such as forensics, paternity testing, medicine, genetic
PT   analysis and phenotype correlations to diseases such as diabetes and
PT   atherosclerosis -
XX
PS   Examples; Page 116; 242pp; English.
XX
CC   The present invention provides a method of diagnosing a vascular disease
CC   in an individual, involving determining the sequence at various
CC   polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC   genes. The sequences at a number of polymorphic sites are also provided
CC   in the specification. In particular, the method can be used in the
CC   diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC   disease, stroke, peripheral vascular diseases, venous thromboembolism
CC   and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC   useful in forensics, paternity testing, genetic analysis and phenotype
CC   correlations to diseases. The present sequence is an example of one of
CC   the human gene SNPS shown in the specification.
XX
SQ   Sequence 21 BP; 5 A; 8 C; 7 G; 1 T; 0 other;

  Query Match             1.1%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        513 CAGCGCCAACCTGCCGG 529
              |||||||||||||| ||
Db          1 CAGCGCCAACCTGCAGG 17


RESULT 57
AAQ65816/c
ID   AAQ65816 standard; DNA; 20 BP.
XX
AC   AAQ65816;
XX
DT   25-MAR-2003  (updated)
DT   20-DEC-1994  (first entry)
XX
DE   Type II procollagen PCR primer CW-12.
XX
KW   Type II procollagen; COL2A1; amplification; primer;
KW   polymerase chain reaction; PCR; osteoarthritis; cartilage; ss.
XX
OS   Synthetic.
XX
PN   WO9411532-A1.
XX
PD   26-MAY-1994.
XX
PF   12-NOV-1993;   93WO-US10964.
XX
PR   13-NOV-1992;   92US-0977284.
XX
PA   (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI   Ahmad NN,  Ala-Kokko L,  Baldwin C,  Hopkinson I,  Prockop DJ;
PI   Ritvaniemi P,  Williams CJ;
```

```
XX
DR   WPI; 1994-183530/22.
XX
PT   Detecting genetic pre-disposition to osteoarthritis - and other
PT   diseases involving mutation in cartilage protein genes, by
PT   amplification and analysis of DNA and comparison with standards
XX
PS   Claim 18; Page 25; 112pp; English.
XX
CC   Claim 18 claims primers for use in detecting mutations in a
CC   mammalian gene for a structural protein of cartilage comprising
CC   a sequence identified in Table I (Page 18-31).  Table I includes
CC   179 primer sequences (see AAQ65728-Q65906).
CC   The following details are given for primer CW-12:
CC   Region/exon: 29/31
CC   Direction: sense
CC   Primer position: 12313
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 20 BP; 1 A; 8 C; 4 G; 7 T; 0 other;

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.2e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        282 GGAAGCAGCAGCAATGTCTG 301
              ||||||||||||| || | |
Db         20 GGAAGCAGCAGCAGTGACAG 1


RESULT 58
AAT39478/c
ID   AAT39478 standard; DNA; 20 BP.
XX
AC   AAT39478;
XX
DT   21-MAY-1997  (first entry)
XX
DE   Steroidogenesis acute regulatory protein antisense PCR primer 2.
XX
KW   Human; steroidogenesis; acute regulatory protein; hStAR; analysis;
KW   mutation; detection; prenatal; genetic defect; congenital; protein;
KW   lipoid adrenal hyperplasia; treatment; prevention; gene;
KW   replacement therapy; hypercholesterolaemia; primer; PCR;
KW   polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   WO9629338-A1.
XX
PD   26-SEP-1996.
XX
PF   22-MAR-1996;   96WO-US03896.
XX
PR   23-MAR-1995;   95US-0410540.
XX
PA   (REGC ) UNIV CALIFORNIA.
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Lin D,  Miller WL,  Strauss JF;
XX
DR   WPI; 1996-443130/44.
XX
PT   Isolated human steroidogenesis acute regulatory protein gene - used
PT   for detection of mutation(s) of this gene that cause congenital
PT   lipoid adrenal hyperplasia
XX
PS   Example 7; Page 4; 89pp; English.
XX
CC   The present sequence is a PCR primer (nt 717-738) for the human
CC   steroidogenesis acute regulatory protein (hStAR) cDNA. The hStAR
CC   gene can be analysed for mutations to detect (e.g. prenatally)
CC   genetic defects associated with congenital lipoid adrenal
CC   hyperplasia (CAH), or its transmission to children. CAH can be
CC   treated by protein or gene replacement therapy, which can also be
CC   used to prevent or treat hypercholesterolaemia.
CC   A human adrenal cortex cDNA library was screened with a mouse StAR
CC   probe to isolate a 1.6 kb insert, including an ORF for a 285
CC   residue protein. When it was cloned into pSPORT and expressed in
CC   COS-1 cells cotransfected with pP450scc abd pADX, it increased the
CC   level of pregnenolone synthesis from cholesterol or
CC   20-alpha-hydroxycholesterol.
XX
SQ   Sequence 20 BP; 4 A; 7 C; 6 G; 3 T; 0 other;

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.2e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        548 TGCTGGCAGGCATGCACACA 567
              ||||||| ||||||  ||||
Db         20 TGCTGGCTGGCATGGCCACA 1


RESULT 59
AAZ04965
ID   AAZ04965 standard; DNA; 20 BP.
XX
AC   AAZ04965;
XX
DT   07-OCT-1999  (first entry)
XX
DE   PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
KW   Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW   paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW   nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer;
KW   bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
OS   Synthetic.
OS   Chlamydia trachomatis.
XX
PN   WO9928475-A2.
XX
PD   10-JUN-1999.
XX
PF   27-NOV-1998;   98WO-IB01939.
XX
PR   04-NOV-1998;   98US-0107077.
PR   28-NOV-1997;   97FR-0015041.
PR   17-DEC-1997;   97FR-0016034.
XX
PA   (GEST ) GENSET.
XX
PI   Griffais R;
XX
DR   WPI; 1999-371125/31.
XX
PT   Genome sequence of Chlamydia trachomatis
XX
PS   Disclosure; Page 1732; 1755pp; English.
XX
CC   PCR primers AAZ01426-Z06209 were used to amplify open reading frames
CC   (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC   encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC   against Chlamydia trachomatis. Antisense and ribozyme sequences
CC   can also be used to control growth of the microorganism. Chlamydia
CC   trachomatis is responsible for a large number of diseases, e.g. eye
CC   diseases such as conventional trachoma, nonendemic trachoma,
CC   paratrachoma, and inclusion conjunctivitis; genital diseases such as
CC   nongonococcal uretritis, epidymitis, cervicitis, salpingitis,
CC   perihepatitis, bartholinitis; pneumopathy in breast feeding infants;
CC   and venereal lymphogranulomatosis. The polypeptides of the
CC   invention may be of use in treating these diseases.
XX
SQ   Sequence 20 BP; 8 A; 1 C; 8 G; 3 T; 0 other;
```

```
  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.2e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        922 GAGATGGCAGATCTGGAGAA 941
              |||| ||  ||||||||||
Db          1 GAGAAGGATGATCTGGAGAA 20


RESULT 60
AAX94626/c
ID   AAX94626 standard; DNA; 20 BP.
XX
AC   AAX94626;
XX
DT   13-SEP-1999  (first entry)
XX
DE   PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW   Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW   sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW   vaccine; neutralising epitope; PCR primer; ss.
XX
OS   Synthetic.
OS   Chlamydia pneumoniae.
XX
PN   WO9927105-A2.
XX
PD   03-JUN-1999.
XX
PF   20-NOV-1998;   98WO-IB01890.
XX
PR   04-NOV-1998;   98US-0107078.
PR   21-NOV-1997;   97FR-0014673.
XX
PA   (GEST ) GENSET.
XX
PI   Griffais R;
XX
DR   WPI; 1999-357842/30.
XX
PT   Genome sequence of Chlamydia pneumoniae
XX
PS   Page 1684; Disclosure; 1912pp; English.
XX
CC   AAX91991-X97517 represent PCR primers used to amplify open reading
CC   frames and other nucleic acid sequences from the genome of
CC   Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory
CC   disease such as pneumonia and bronchitis and is thought to be a
CC   contributing factor in heart disease, sarcoidosis, sinusitis, purulent
CC   otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
CC   by the open reading frames of the C. pneumoniae genome (see AAY34584-
CC   AAY35879) can be used in immunogenic compositions as vaccines. Vectors
CC   containing C. pneumoniae nucleotides sequences can also be used as
CC   immunogenic compositions, especially where the vector directs the
CC   expression of a neutralising epitope of C. pneumoniae.
XX
SQ   Sequence 20 BP; 4 A; 4 C; 5 G; 7 T; 0 other;

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.2e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         17 TGGATTAAACCAAACCCAGC 36
              ||||||| |||| ||| |||
Db         20 TGGATTATACCAGACCAAGC 1


RESULT 61
AAX92281/c
ID   AAX92281 standard; DNA; 20 BP.
XX
AC   AAX92281;
XX
DT   13-SEP-1999  (first entry)
XX
DE   PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW   Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW   sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW   vaccine; neutralising epitope; PCR primer; ss.
XX
OS   Synthetic.
OS   Chlamydia pneumoniae.
XX
PN   WO9927105-A2.
XX
PD   03-JUN-1999.
XX
PF   20-NOV-1998;   98WO-IB01890.
XX
PR   04-NOV-1998;   98US-0107078.
PR   21-NOV-1997;   97FR-0014673.
XX
PA   (GEST ) GENSET.
XX
PI   Griffais R;
XX
DR   WPI; 1999-357842/30.
XX
PT   Genome sequence of Chlamydia pneumoniae
XX
PS   Page 1499; Disclosure; 1912pp; English.
XX
CC   AAX91991-X97517 represent PCR primers used to amplify open reading
CC   frames and other nucleic acid sequences from the genome of
CC   Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory
CC   disease such as pneumonia and bronchitis and is thought to be a
CC   contributing factor in heart disease, sarcoidosis, sinusitis, purulent
CC   otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
CC   by the open reading frames of the C. pneumoniae genome (see AAY34584-
CC   AAY35879) can be used in immunogenic compositions as vaccines. Vectors
CC   containing C. pneumoniae nucleotides sequences can also be used as
CC   immunogenic compositions, especially where the vector directs the
CC   expression of a neutralising epitope of C. pneumoniae.
XX
SQ   Sequence 20 BP; 2 A; 5 C; 5 G; 8 T; 0 other;

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.2e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGCAGC 293
              ||||||   ||||||||||||
Db         20 ATCAAATGCGAAGCAGCAGC 1


RESULT 62
AAX33259
ID   AAX33259 standard; DNA; 20 BP.
XX
AC   AAX33259;
XX
DT   30-JUN-1999  (first entry)
XX
DE   PEBP2 alpha A gene expression regulating DNA PCR primer SEQ ID NO:16.
XX
KW   PEBP2 alpha A gene; expression; regulation; bone disease;
KW   osteoporosis; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9911787-A1.
XX
PD   11-MAR-1999.
```

```
XX
PF   02-SEP-1998;   98WO-JP03920.
XX
PR   08-APR-1998;   98JP-0114135.
PR   02-SEP-1997;   97JP-0254250.
PR   15-OCT-1997;   97JP-0299407.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
XX
PI   Fujiwara M,  Harada H,  Katsumata T,  Nakatsuka M;
PI   Ogawa S,  Tagashira S;
XX
DR   WPI; 1999-243621/20.
XX
PT   DNA regulating expression of PEBP2 alphaA gene to produce regulator
PT   protein, useful as promoter for prevention or/and treatment of bone
PT   diseases e.g. osteoporosis
XX
PS   Example 2; Page 29; 118pp; Japanese.
XX
CC   The present invention describes DNA which participates in the regulation
CC   of expression of PEBP2 alpha A gene. The DNA produces a regulator
CC   protein with the activity of promoting bone formation and can serve as a
CC   promoter for prevention and treatment of bone diseases including
CC   osteoporosis. The present sequence represents a PCR primer used in an
CC   example from the present invention.
XX
SQ   Sequence 20 BP; 3 A; 11 C; 4 G; 2 T; 0 other;

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.2e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        592 CCCCCCACCAGCCTGAAGCC 611
              ||| ||| ||||||| ||||
Db          1 CCCTCCAGCAGCCTGCAGCC 20


RESULT 63
ABS74296
ID   ABS74296 standard; DNA; 20 BP.
XX
AC   ABS74296;
XX
DT   09-DEC-2002  (first entry)
XX
DE   Human calcium channel alpha2delta SSCP PCR primer  #20.
XX
KW   Human; ss; primer; calcium channel alpha2delta; splice isoform; CACNA2D2;
KW   gene therapy; Lambert-Eaton myasthenic syndrome; LEMS; PCR;
KW   autoimmune disease; epilepsy; migraine; episodic ataxia; cancer; stroke;
KW   brain trauma; Alzheimer's disease; multiinfarct dementia; convulsion;
KW   Korsa-koff's disease; amyotrophic lateral sclerosis; seizure;
KW   Huntington's disease; amnesia; cardiac arrhythmia; angina pectoris;
KW   hypoxia; ischaemia; myocardial infarction; congestive heart failure;
KW   muscular dystrophy; hypertension; chromosome 3p21.3; lung cancer;
KW   breast cancer; preneoplastic lesion; hyperplasia; dysplasia; carcinoma;
KW   SSCP; single strand change polymorphism.
XX
OS   Homo sapiens.
XX
PN   US6441156-B1.
XX
PD   27-AUG-2002.
XX
PF   22-DEC-1999;   99US-0470443.
XX
PR   30-DEC-1998;   98US-114359P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Lerman MI,  Latif F,  Wei M,  Duh F,  Minna JD,  Sekido Y,  Gao B;
XX
DR   WPI; 2002-730574/79.
XX
PT   Novel purified nucleic acid sequence encoding human calcium channel
PT   alpha2delta subunit protein, useful for detecting, preventing and
PT   treating cancer, stroke, brain trauma, Huntington's disease, myocardial
PT   infarction  -
XX
PS   Example 7; Column 46; 77pp; English.
XX
CC   The invention relates to a purified nucleic acid sequence (referred as
CC   CACNA2D2 gene which encodes human calcium channel alpha2delta-2 subunit
CC   protein) comprising a fully defined alpha2delta splice isoform 1, 2 or 3
CC   nucleic acid sequence, or its complement and the encoded proteins.
CC   Also include are: (1) a method of producing a calcium channel protein
CC   which involves introducing a recombinant expression vector comprising the
CC   CACNA2D2 nucleic acids and encoding the calcium channel protein, into
CC   a cultured host cell under conditions such that the host cell expresses
CC   the amino acid sequences; and (2) a method for co-expressing calcium
CC   channel proteins, comprising carrying out the method of (1), but with one
CC   or more than one expression vector comprising one or more nucleic acid
CC   sequences encoding the splice variants. CACNA2D2 nucleic acid is useful
CC   for producing a calcium channel protein. The recombinantly expressed
CC   polypeptide is useful for treating patients with Lambert-Eaton myasthenic
CC   syndrome (LEMS) (an autoimmune disease) and for identifying compounds
CC   useful for treating other diseases associated with abnormal calcium
CC   channel protein activity (e.g. epilepsy, migraine, episodic ataxia,
CC   cancer, stroke, brain trauma, Alzheimer's disease, multiinfarct dementia,
CC   Korsa-koff's disease, amyotrophic lateral sclerosis, convulsions,
CC   seizures, Huntington's disease, amnesia, cardiac arrhythmia, angina
CC   pectoris, hypoxic damage to the cardiovascular system, ischaemic damage
CC   to the cardiovascular system, myocardial infarction, congestive heart
CC   failure, muscular dystrophy and hypertension) CACNA2D2 nucleic acid is
CC   useful as primers and probes for detecting presence of nucleic acid
CC   sequence encoding at least a portion of calcium channel protein, in
CC   detection, identification and isolation of alpha2delta sequences
CC   diagnosing and typing of preneoplasias and cancers, since genetic
CC   disruption of 3p21.3 region (in which the alpha_2delta gene is located)
CC   is common in cancer (e.g. lung cancer and breast cancer) and
CC   preneoplastic lesion (e.g. hyperplasia, dysplasia, carcinoma in situ).
CC   The present is an SSCP (single strand change polymorphism) PCR primer
CC   used to detect polymorphisms in sequences encoding a human calcium
CC   channel alpha2delta splice isoform protein.
XX
SQ   Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 other;

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.2e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        335 CTGGTGATAGTCACAGTGGC 354
              |||||||| |||||||  ||
Db          1 CTGGTGATGGTCACAGGAGC 20


RESULT 64
ABS74306
ID   ABS74306 standard; DNA; 20 BP.
XX
AC   ABS74306;
XX
DT   09-DEC-2002  (first entry)
XX
DE   Human calcium channel alpha2delta SSCP PCR primer  #30.
XX
KW   Human; ss; primer; calcium channel alpha2delta; splice isoform; CACNA2D2;
KW   gene therapy; Lambert-Eaton myasthenic syndrome; LEMS; PCR;
KW   autoimmune disease; epilepsy; migraine; episodic ataxia; cancer; stroke;
KW   brain trauma; Alzheimer's disease; multiinfarct dementia; convulsion;
KW   Korsa-koff's disease; amyotrophic lateral sclerosis; seizure;
KW   Huntington's disease; amnesia; cardiac arrhythmia; angina pectoris;
KW   hypoxia; ischaemia; myocardial infarction; congestive heart failure;
KW   muscular dystrophy; hypertension; chromosome 3p21.3; lung cancer;
KW   breast cancer; preneoplastic lesion; hyperplasia; dysplasia; carcinoma;
```

KW SSCP; single strand change polymorphism.
XX
OS Homo sapiens.
XX
PN US6441156-B1.
XX
PD 27-AUG-2002.
XX
PF 22-DEC-1999; 99US-0470443.
XX
PR 30-DEC-1998; 98US-114359P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Lerman MI, Latif F, Wei M, Duh F, Minna JD, Sekido Y, Gao B;
XX
DR WPI; 2002-730574/79.
XX
PT Novel purified nucleic acid sequence encoding human calcium channel
PT alpha2delta subunit protein, useful for detecting, preventing and
PT treating cancer, stroke, brain trauma, Huntington's disease, myocardial
PT infarction -
XX
PS Example 7; Column 47; 77pp; English.
XX
CC The invention relates to a purified nucleic acid sequence (referred as
CC CACNA2D2 gene which encodes human calcium channel alpha2delta-2 subunit
CC protein) comprising a fully defined alpha2delta splice isoform 1, 2 or 3
CC nucleic acid sequence, or its complement and the encoded proteins.
CC Also include are: (1) a method of producing a calcium channel protein
CC which involves introducing a recombinant expression vector comprising the
CC CACNA2D2 nucleic acids and encoding the calcium channel protein, into
CC a cultured host cell under conditions such that the host cell expresses
CC the amino acid sequences; and (2) a method for co-expressing calcium
CC channel proteins, comprising carrying out the method of (1), but with one
CC or more than one expression vector comprising one or more nucleic acid
CC sequences encoding the splice variants. CACNA2D2 nucleic acid is useful
CC for producing a calcium channel protein. The recombinantly expressed
CC polypeptide is useful for treating patients with Lambert-Eaton myasthenic
CC syndrome (LEMS) (an autoimmune disease) and for identifying compounds
CC useful for treating other diseases associated with abnormal calcium
CC channel protein activity (e.g. epilepsy, migraine, episodic ataxia,
CC cancer, stroke, brain trauma, Alzheimer's disease, multiinfarct dementia,
CC Korsa-koff's disease, amyotrophic lateral sclerosis, convulsions,
CC seizures, Huntington's disease, amnesia, cardiac arrhythmia, angina
CC pectoris, hypoxic damage to the cardiovascular system, ischaemic damage
CC to the cardiovascular system, myocardial infarction, congestive heart
CC failure, muscular dystrophy and hypertension) CACNA2D2 nucleic acid is
CC useful as primers and probes for detecting presence of nucleic acid
CC sequence encoding at least a portion of calcium channel protein, in
CC detection, identification and isolation of alpha2delta sequences
CC diagnosing and typing of preneoplasias and cancers, since genetic
CC disruption of 3p21.3 region (in which the alpha_2delta gene is located)
CC is common in cancer (e.g. lung cancer and breast cancer) and
CC preneoplastic lesion (e.g. hyperplasia, dysplasia, carcinoma in situ).
CC The present is an SSCP (single strand change polymorphism) PCR primer
CC used to detect polymorphisms in sequences encoding a human calcium
CC channel alpha2delta splice isoform protein.
XX
SQ Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 other;

```
  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.2e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        335 CTGGTGATAGTCACAGTGGC 354
              ||||||||  |||||||  ||
Db          1 CTGGTGATGGTCACAGGAGC 20
```

RESULT 65
ABS76637
ID ABS76637 standard; DNA; 20 BP.
XX
AC ABS76637;
XX
DT 11-DEC-2002 (first entry)
XX
DE Novel metalloprotease MP1 associated primer #2.
XX
KW Metalloprotease; MP-1; immune disorder; glutamate transport; cancer;
KW motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes;
KW reproductive disorder; Kleinfelter's syndrome; germinal cell aplasia;
KW genital wart; metabolic disorder; premature puberty; Kallman syndrome;
KW Cushing's syndrome; neurodegenerative disease; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis;
KW liver disease; renal disease; immune disorder; rheumatoid arthritis;
KW acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumonia;
KW emphysema; cystic fibrosis; vascular disorder; inflammatory disorder;
KW neurological disorder; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200272751-A2.
XX
PD 19-SEP-2002.
XX
PF 05-FEB-2002; 2002WO-US03353.
XX
PR 05-FEB-2001; 2001US-266518P.
PR 10-APR-2001; 2001US-282814P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Chen J, Feder J, Nelson TC, Duclos F, Krystek S;
XX
DR WPI; 2002-723329/78.
XX
PT New isolated nucleic acid encoding MP-1 protein, useful for preventing,
PT treating, or ameliorating diseases associated with aberrant
PT metalloproteinase activity, e.g. immune, metabolic, inflammatory and
PT neurological disorders -
XX
PS Claim 16; Page 270; 473pp; English.
XX
CC The invention describes an isolated nucleic acid molecule (I) encoding
CC a metalloprotease (MP-1). (I) is useful for preventing, treating, or
CC ameliorating a medical condition, particularly an immune disorder, an
CC aberrant glutamate transport or motor neuron disorder, such as
CC amyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like
CC condition. The compositions and methods are also useful for diagnosing,
CC prognosticating, treating, ameliorating and/or treating disorders
CC associated with MP-1 activity, e.g. diabetes, cancer, reproductive
CC disorders (e.g. Kleinfelter's syndrome, genital warts, or germinal cell
CC aplasia), metabolic disorders (e.g. premature puberty, Kallman
CC syndrome, or Cushing's syndrome), neurodegenerative diseases
CC (Alzheimer's disease, Parkinson's disease, Huntington's disease or
CC Tourette syndrome), liver and renal diseases and immune disorders (e.g.
CC AIDS, rheumatoid arthritis or sepsis), pulmonary diseases (e.g.
CC pneumonia, emphysema or cystic fibrosis) and vascular, inflammatory and
CC neurological disorders (e.g. Alzheimer's disease or Parkinson's
CC disease). This sequence represents a primer associated with the novel
CC human metalloprotease MP1 polynucleotide.
XX
SQ Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 other;

```
  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.2e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        299 CTGCTGTGGGGGCTGCAACT 318
              |||||||| || || ||||
Db          1 CTGCTGTGGTGGATGAAACT 20
```

RESULT 66

```
ABS67685/c
ID   ABS67685 standard; DNA; 20 BP.
XX
AC   ABS67685;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Casein kinase-2 antisense oligonucleotide ISIS127185.
XX
KW   ss; antisense therapy; casein kinase-2 alpha; cytostatic; antidiabetic;
KW   antiinflammatory; diabetes; hyperproliferative disorder; cancer; human;
KW   breast cancer; prostate cancer; liver cancer; infection; inflammation;
KW   tumour; mouse.
XX
OS   Homo sapiens.
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..20
FT                   /*tag=  a
FT                   /label= OTHER
FT                   /note= "All cytidines are 5-methylcytidine.
FT                   Phosphorothioate backbone"
FT   modified_base   1..5
FT                   /*tag=  b
FT                   /label= OTHER
FT                   /note= "2'-methoxyethyl nucleotides"
FT   modified_base   16..20
FT                   /*tag=  c
FT                   /label= OTHER
FT                   /note= "2'-methoxyethyl nucleotides"
XX
PN   WO200262818-A2.
XX
PD   15-AUG-2002.
XX
PF   31-JAN-2002; 2002WO-US02942.
XX
PR   08-FEB-2001; 2001US-0780172.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   McKay R,  Freier SM,  Wyatt JR;
XX
DR   WPI; 2002-627521/67.
XX
PT   New antisense oligonucleotides targeted to nucleic acid encoding casein
PT   kinase 2-alpha, useful in diagnostic and research applications, or for
PT   treating a disease or condition associated with expression of casein
PT   kinase 2-alpha  -
XX
PS   Claim 3; Page 95; 166pp; English.
XX
CC   The invention relates to a compound 8-50 nucleobases in length targeted
CC   to a nucleic acid molecule encoding casein kinase 2-alpha. The compound
CC   specifically hybridises with and inhibits the expression of casein
CC   kinase 2-alpha, or specifically hybridises with at least an
CC   8-nucleobase portion of an active site on a nucleic acid molecule
CC   encoding casein kinase 2-alpha i.e. an antisense oligonucleotide.
CC   Also included are: (1) a composition comprising the compound and a
CC   carrier or diluent; (2) inhibiting the expression of casein kinase
CC   2-alpha in cells or tissues by contacting the cells or tissues with the
CC   novel compound; and (3) treating an animal having a disease or condition
CC   associated with casein kinase 2-alpha by administering to the animal the
CC   compound cited above so that expression of casein kinase 2-alpha is
CC   inhibited. The antisense compounds are useful for modulating the
CC   expression of casein kinase 2-alpha and for treating diseases or
CC   conditions associated with expression of casein kinase 2-alpha, e.g.
CC   diabetes or hyperproliferative disorder, particularly cancer, such as
CC   breast cancer, prostate cancer, or liver cancer. The antisense
CC   compounds are also useful for diagnostics, therapeutics, prophylaxis,
CC   e.g. to prevent or delay infection, inflammation or tumour formation, as
CC   research reagents and kits, and in distinguishing between functions of
CC   various members of a biological pathway. The present sequence is a
CC   casein kinase-2 alpha antisense oligonucleotide of the invention.
XX
SQ   Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 other;

  Query Match             1.1%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.2e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1070 TCAGGCAGGCTCTTCAGTGA 1089
                || |||||||||  ||||||
Db         20 TCTGGCAGGCTCACCAGTGA 1


RESULT 67
ABK69390
ID   ABK69390 standard; DNA; 20 BP.
XX
AC   ABK69390;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Chimeric phosphorothioate oligonucleotide #142 for caspase 9 inhibition.
XX
KW   Antisense compound; caspase 9; C9; hyperproliferative disorder; stroke;
KW   haematopoietic disorder; cholesterol disorder; bone metabolism disorder;
KW   brain injury; neurodegenerative disease; infection; inflammation; tumour;
KW   phosphorothioate backbone linkage; 2'-methoxyethyl; 2'-MOE; ss.
XX
OS   Chimeric - Mus musculus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base   1..20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate nucleotides, all cytidine
FT                         residues are 5-methylcytidines"
FT   modified_base   16..20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN   WO200222641-A1.
XX
PD   21-MAR-2002.
XX
PF   10-SEP-2001; 2001WO-US28233.
XX
PR   11-SEP-2000; 2000US-0659845.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Zhang H,  Watt AT;
XX
DR   WPI; 2002-351874/38.
XX
PT   New antisense oligonucleotide which modulates expression of caspase 9,
PT   useful to treat tumour, inflammation or to prevent infection in humans
PT   -
XX
PS   Claim 26; Page 95; 145pp; English.
XX
CC   The present invention relates to a new antisense compound targeted to a
CC   nucleic acid molecule encoding caspase 9 (C9). The compound specifically
CC   hybridises with and inhibits the expression of caspase 9. The invention
CC   also describes an antisense compound that specifically hybridises with
CC   an 8 nucleotide portion of an active site of the nucleic acid. The
CC   invention is useful for inhibiting the expression of C9 in cells or
```

CC tissues and is also useful for treating an animal having a disease or
CC condition associated with C9, including a hyperproliferative,
CC haematopoietic or cholesterol disorder, bone metabolism disorder, stroke,
CC brain injury or neurodegenerative disease. The compound is commonly
CC useful as a research and diagnostics reagent. It is also useful to
CC distinguish between functions of various members of a biological pathway.
CC The invention is also be useful prophylactically e.g. to prevent or
CC delay infection, inflammation or tumour formation. The antisense compound
CC of the invention is often preferred over native form because of enhanced
CC cellular uptake, enhanced affinity for nucleic acid target and increased
CC stability in presence of nucleases. The present nucleic acid sequence
CC represents one of a collection (ABK69249-ABK69396) of chimeric
CC phosphorothioate oligonucleotides having 2'-methoxyethyl (2'-MOE) wings.
CC This sequence was used in the methods of the invention for inhibition
CC of caspase 9.
XX
SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 other;

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 567 ACTGCTCCAGCAGGCCCTCC 586
||||||||||| | ||| |||
Db 1 ACTGCTCCAGAATGCCATCC 20

RESULT 68
AAZ26599/c
ID AAZ26599 standard; DNA; 21 BP.
XX
AC AAZ26599;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human polymorphic region 788.
XX
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS Homo sapiens.
XX
PN WO9841648-A2.
XX
PD 24-SEP-1998.
XX
PF 19-MAR-1998; 98WO-US05419.
XX
PR 20-MAR-1997; 97US-0041057.
XX
PA (VARI-) VARIAGENICS INC.
XX
PI Housman D, Ledley FD, Stanton VP;
XX
DR WPI; 1998-521232/44.
XX
PT Identifying target genes for allele-specific drugs - used for
PT diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic
PT plaque, dysplastic lesions, endometriosis or graft versus host disease
XX
PS Disclosure; Figure 7; 605pp; English.
XX
CC This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is
CC active on a gene vital for cell growth or viability, and where the gene
CC is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can
CC be used in the diagnosis, prevention and treatment of LOH disorders,
CC e.g. cancers, atherosclerotic plaques, premalignant metaplastic or
CC dysplastic lesions, benign tumours, endometriosis, polycystic kidney
CC disease, and graft versus host disease. The method can also be used to
CC remove malignant cells from bone marrow transplants. AAZ25812-Z26825
CC represent human polymorphic sites described in the method of the
CC invention.
XX
SQ Sequence 21 BP; 3 A; 6 C; 5 G; 7 T; 0 other;

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 118 ACCGTCCACACGGGACAGGG 137
| |||||||| ||||||||
Db 21 AACGTCCACATAGGACAGGG 2

RESULT 69
AAC58095/c
ID AAC58095 standard; DNA; 21 BP.
XX
AC AAC58095;
XX
DT 25-JAN-2001 (first entry)
XX
DE Human PRO2038 hybridisation probe SEQ ID NO:117.
XX
KW Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
KW identification; tumourigenesis; anticancer; detection; hybridisation;
KW probe; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200053750-A1.
XX
PD 14-SEP-2000.
XX
PF 02-DEC-1999; 99WO-US28551.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 01-SEP-1999; 99WO-US20111.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28634.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;
XX
DR WPI; 2000-594320/56.
XX
PT Antibodies specific for PRO polypeptides, used to diagnose and inhibit
PT the growth of tumors in mammals, and to identify inhibitors of PRO
PT polypeptide activity or expression -
XX
PS Example 20; Page 126; 226pp; English.
XX
CC The present invention describes an antibody that binds to a human
CC protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780;
CC PRO3434; PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354;
CC PRO4397; PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has
CC anticancer activity and can be used to diagnose tumours in mammals, by
CC detecting complex formation when the antibody is contacted with test
CC cells. Increased expression of genes encoding (I) can also be detected
CC to diagnose tumours. Agents which inhibit the activity of (I),
CC especially the antibodies, or an antisense oligonucleotide which

CC hybridises to genes encoding (I), can be used to inhibit tumour growth,
CC preferably by inducing cell death. Methods from the present invention
CC can be used to identify compounds which inhibit the biological activity
CC of (I). AAC58019 to AAC58102 represent PCR primers and hybridisation
CC probes used in examples from the present invention for human PRO
CC sequences. AAC58103 to AAC58122 and AAB24021 to AAB24040 represent human
CC PRO polynucleotide and protein sequences given in the exemplification of
CC the present invention.
XX
SQ Sequence 21 BP; 1 A; 11 C; 3 G; 6 T; 0 other;

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 462 CAGCAGCCTGCAGGGGGAGG 481
|||||| ||||||||||
Db 21 CAGCAGGAAGCAGGGGGAGG 2

RESULT 70
AAA31011/c
ID AAA31011 standard; DNA; 21 BP.
XX
AC AAA31011;
XX
DT 30-JUN-2000 (first entry)
XX
DE Primer used to assess activity of HIV-1 specific antibodies.
XX
KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease; ss;
KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
XX
OS Synthetic.
XX
PN AU9948756-A.
XX
PD 17-FEB-2000.
XX
PF 16-SEP-1999; 99AU-0048756.
XX
PR 16-SEP-1999; 99AU-0048756.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Burton DR, Barbas CF, Lerner RA;
XX
DR WPI; 2000-293393/26.
XX
PT Novel human monoclonal antibodies which immunoreact with and neutralise
PT human immunodeficiency virus useful for treating HIV infections -
XX
PS Example 8; Page 155; 366pp; English.
XX
CC The present sequence is used in the production of anti-human
CC immunodeficiency virus type 1 (HIV-1) antibodies. The invention relates
CC to a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
CC in vitro virus infectivity assay by 50%, at a concentration of less than
CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
CC immunotherapy of HIV induced disease. They are useful as neutralising
CC field isolates and provide useful information regarding the
CC immunocompetence of an immune response in HIV infected patients. The
CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
CC which can be used to screen human monoclonal antibodies to identify
CC whether the antibody has the same binding specificity as the antibodies
CC of the invention. The neutralising antibodies define new epitopes on the
CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
CC immunotherapeutic human monoclonal antibodies. A major advantages of the
CC monoclonal antibodies derives from the fact that they are encoded by a
CC human polynucleotides sequence. Thus in vivo use of the monoclonal
CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
CC reduces the problems of significant host immune response to the passively
CC administered antibodies which is a problem commonly encountered when
CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
CC An additional major advantage of the monoclonal antibodies described
CC derives from the fact that they immunoreact with a unique determinant
CC present on mature HIV glycoprotein gp120. This class of antibodies is
CC particularly effective at neutralising field isolates of HIV.
XX
SQ Sequence 21 BP; 4 A; 7 C; 7 G; 3 T; 0 other;

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 262 CTGGGCTGGCTGATCAAAGA 281
|||||||| ||| |||| ||
Db 21 CTGGGCTGCCTGGTCAACGA 2

RESULT 71
AAA32137/c
ID AAA32137 standard; DNA; 21 BP.
XX
AC AAA32137;
XX
DT 04-JUL-2000 (first entry)
XX
DE Primer used to assess activity of HIV-1 specific antibodies.
XX
KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
KW passive immunotherapy; reduce severity; HIV-induced disease;
KW immunocompetence; active immunisation; ss.
XX
OS Synthetic.
XX
PN AU9948754-A.
XX
PD 17-FEB-2000.
XX
PF 16-SEP-1999; 99AU-0048754.
XX
PR 16-SEP-1999; 99AU-0048754.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Burton DR, Barbas CF, Lerner RA;
XX
DR WPI; 2000-246867/22.
XX
PT Human neutralizing monoclonal antibodies to human immunodeficiency
PT virus (HIV) used for providing passive immunotherapy to HIV are
PT specific for glycoprotein-120 -
XX
PS Example 8; Page 155; 374pp; English.
XX
CC This sequence represents a polynucleotide used in the preparation of the
CC antibodies of the invention. The invention relates to the production of
CC an anti-HIV (human immunodeficiency virus) glycoprotein (gp)-120
CC monoclonal antibody capable of reducing an HIV infectivity titre in an
CC in vitro virus infectivity assay by 50% at a concentration of less than
CC 70 ng/ml. The method for the production of the antibody comprises:
CC (a) providing a first polynucleotide encoding a heavy chain
CC immunoglobulin amino acid sequence (which does not comprise the sequence
CC represented by AAY98206) and a second polynucleotide encoding a light
CC chain immunoglobulin amino acid sequence;
CC (b) inserting the first and second polynucleotide sequences into a host
CC cell;
CC (c) maintaining the host cell in conditions which allow the amino acid
CC sequences encoded by the polynucleotides to be expressed in the host
CC cell; and
CC (d) isolating the antibody comprising the heavy and light chain

CC immunoglobulin amino acid sequences from the host cell.
CC The anti-HIV gp-120 monoclonal antibody is used for providing passive
CC immunotherapy to HIV in a human. They can be administered to high-risk
CC patients to reduce the likelihood and/or severity of HIV-induced disease
CC and to patients who are already HIV-infected. The antibodies are used
CC for neutralising field isolates which provides information about the
CC immunocompetence of an immune response in HIV patients, for detecting
CC HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for
CC producing anti-idiotypic antibodies which can be used for active
CC immunisation and to screen human monoclonal antibodies to identify those
CC with the same binding specificity and to monitor the course of HIV
CC disease therapy by measuring the changes in concentration of HIV present
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
CC monoclonal antibodies are encoded by a human polynucleotide sequence and
CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
CC reduce the problems of significant host immune response to the
CC antibodies associated with monoclonal antibodies of xenogeneic or
CC chimeric derivation.
XX
SQ Sequence 21 BP; 4 A; 7 C; 7 G; 3 T; 0 other;

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 262 CTGGGCTGGCTGATCAAAGA 281
||||||||| ||| |||| ||
Db 21 CTGGGCTGCCTGGTCAACGA 2

RESULT 72
AAF75464
ID AAF75464 standard; DNA; 21 BP.
XX
AC AAF75464;
XX
DT 14-MAY-2001 (first entry)
XX
DE Codon-optimised HPV16 E2 fragment 13856-307-2PD.
XX
KW Human papillomavirus; HPV; HPV16; HPV6a; HPV18; L1; E2; E7; E1;
KW antiviral; immunostimulant; vaccine; immunogen; infection; ss.
XX
OS Human papillomavirus.
OS Synthetic.
XX
PN WO200114416-A2.
XX
PD 01-MAR-2001.
XX
PF 21-AUG-2000; 2000WO-US22932.
XX
PR 25-AUG-1999; 99US-0150728.
PR 07-JUN-2000; 2000US-0210143.
XX
PA (MERI) MERCK & CO INC.
XX
PI Neeper MP, McClements WL, Jansen KU, Schultz LD, Chen L, Wang X;
XX
DR WPI; 2001-218428/22.
XX
PT Novel synthetic polynucleotide encoding human papillomavirus (HPV)
PT protein or mutated HPV protein useful as anti-HPV vaccines, comprises
PT optimized-codons for expression of the viral proteins in human host
PT cells -
XX
PS Example 4; Fig 19; 119pp; English.
XX
CC The present sequence is an oligomer which was used in the assembly of
CC one of a number of synthetic polynucleotides that encode a human
CC papillomavirus (HPV) protein, or a mutated form of a HPV protein. The
CC mutated HPV proteins have reduced protein function as compared to wild
CC type proteins but maintain immunogenicity. The proteins comprise codons
CC for optimised expression in humans. The polynucleotides are useful as a
CC vaccine which provides effective immunoprophylaxis against
CC papillomavirus infection through stimulation of neutralising antibody
CC and cell-mediated immunity.
XX
SQ Sequence 21 BP; 2 A; 7 C; 6 G; 6 T; 0 other;

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 813 GCCGAGCGTCCTGATGCAGC 832
|||| || || |||||||||
Db 1 GCCGTGCTTCTTGATGCAGC 20

RESULT 73
ABK94273
ID ABK94273 standard; DNA; 21 BP.
XX
AC ABK94273;
XX
DT 27-AUG-2002 (first entry)
XX
DE Endothelin converting enzyme 1 (ECE-1) SNP detection primer #61.
XX
KW Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
KW EDNR; signaling system; cardiovascular disease; coronary heart disease;
KW hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;
KW diabetes; familial hypercholesterolaemia; forensic marker;
KW transgenic animal; solid support; cardiovascular regulator; SNP;
KW single nucleotide polymorphism; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO200224747-A2.
XX
PD 28-MAR-2002.
XX
PF 31-AUG-2001; 2001WO-EP10087.
XX
PR 19-SEP-2000; 2000EP-0120123.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Brinkmann U, Hoffmeyer S;
XX
DR WPI; 2002-435060/46.
XX
PT Novel polynucleotide of the endothelin/endothelin converting
PT enzyme/receptors of endothelin and endothelin converting enzyme
PT signaling system associated with cardiovascular disease, useful for
PT treating the disease -
XX
PS Example 6; Page 63; 190pp; English.
XX
CC The invention describes a polynucleotide (I) of the endothelin
CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
CC signaling system which is associated with a cardiovascular disease. (I),
CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
CC or (II) is useful for producing cells capable of expressing a molecular
CC variant polypeptide which is associated with a cardiovascular disease.
CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
CC a molecular variant gene comprising (I) is useful for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
CC or its gene product, or for identifying and obtaining an inhibitor of
CC the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
CC signaling system or its gene product. The isolated proteins and
CC polynucleotides encoding them are useful for preparation of a
CC pharmaceutical composition for treating a cardiovascular disease such as
CC coronary heart disease, hypertension, atherosclerosis, or related to
CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial

CC hypercholesterolaemia. The gene or a polynucleotide fragment of the
CC EDN/ECE/EDNR signaling system are useful as forensic markers, for
CC creating a transgenic animal and in creation of a solid support
CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or
CC host cells of the invention. This sequence represents a PCR primer used
CC to identify single nucleotide polymorphisms in DNA encoding
CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway.
XX
SQ Sequence 21 BP; 5 A; 3 C; 12 G; 1 T; 0 other;

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 463 AGCAGCCTGCAGGGGGAGGA 482
||||| |||| ||| |||||
Db 1 AGCAGGCTGCGGGGAGAGGA 20

RESULT 74
ABK94274/c
ID ABK94274 standard; DNA; 21 BP.
XX
AC ABK94274;
XX
DT 27-AUG-2002 (first entry)
XX
DE Endothelin converting enzyme 1 (ECE-1) SNP detection primer #62.
XX
KW Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
KW EDNR; signaling system; cardiovascular disease; coronary heart disease;
KW hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;
KW diabetes; familial hypercholesterolaemia; forensic marker;
KW transgenic animal; solid support; cardiovascular regulator; SNP;
KW single nucleotide polymorphism; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO200224747-A2.
XX
PD 28-MAR-2002.
XX
PF 31-AUG-2001; 2001WO-EP10087.
XX
PR 19-SEP-2000; 2000EP-0120123.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Brinkmann U, Hoffmeyer S;
XX
DR WPI; 2002-435060/46.
XX
PT Novel polynucleotide of the endothelin/endothelin converting
PT enzyme/receptors of endothelin and endothelin converting enzyme
PT signaling system associated with cardiovascular disease, useful for
PT treating the disease -
XX
PS Example 6; Page 63; 190pp; English.
XX
CC The invention describes a polynucleotide (I) of the endothelin
CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
CC signaling system which is associated with a cardiovascular disease. (I),
CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
CC or (II) is useful for producing cells capable of expressing a molecular
CC variant polypeptide which is associated with a cardiovascular disease.
CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
CC a molecular variant gene comprising (I) is useful for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
CC or its gene product, or for identifying and obtaining an inhibitor of
CC the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
CC signaling system or its gene product. The isolated proteins and
CC polynucleotides encoding them are useful for preparation of a
CC pharmaceutical composition for treating a cardiovascular disease such as
CC coronary heart disease, hypertension, atherosclerosis, or related to
CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
CC hypercholesterolaemia. The gene or a polynucleotide fragment of the
CC EDN/ECE/EDNR signaling system are useful as forensic markers, for
CC creating a transgenic animal and in creation of a solid support
CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or
CC host cells of the invention. This sequence represents a PCR primer used
CC to identify single nucleotide polymorphisms in DNA encoding
CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway.
XX
SQ Sequence 21 BP; 1 A; 12 C; 3 G; 5 T; 0 other;

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 463 AGCAGCCTGCAGGGGGAGGA 482
||||| |||| ||| |||||
Db 21 AGCAGGCTGCGGGGAGAGGA 2

RESULT 75
AAX31672
ID AAX31672 standard; DNA; 15 BP.
XX
AC AAX31672;
XX
DT 21-MAY-1999 (first entry)
XX
DE Tag sequence of a transcript increased in pancreatic cancer.
XX
KW Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
KW diagnosis; prognosis; treatment; ss.
XX
OS Homo sapiens.
XX
PN WO9853319-A2.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US10277.
XX
PR 21-MAY-1997; 97US-0047352.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Kinzler KW, Vogelstein B;
XX
DR WPI; 1999-070161/06.
XX
PT Use of isolated gene transcripts - useful for developing products
PT for the diagnosis, prognosis and treatment of cancers, particularly
PT colon and pancreatic cancer
XX
PS Claim 13; Page 68; 120pp; English.
XX
CC AAX30947-31815 represent tag sequences of transcripts that are
CC differentially expressed in colorectal cancer, in pancreatic
CC cancer, or in both. The tag sequences can be used to identify
CC genes by matching the tag to a gen data base member, or by using
CC the tag sequences as probes to isolate unidentified genes from
CC cDNA libraries. The tag sequences can also be used in a method
CC for diagnosing colon or pancreatic cancer in a sample suspected
CC of being neoplastic. The method comprises comparing the level of
CC at least one transcript in a first sample of a tissue to a second
CC sample, where the first sample is a colonic tissue suspected of
CC being neoplastic and the second sample is a normal human colonic
CC tissue. The transcript is identified by a tag selected from
CC AAX30947-31815. The methods of the invention can be used in the
CC diagnosis, prognosis and treatment of cancer.
XX
SQ Sequence 15 BP; 2 A; 3 C; 3 G; 7 T; 0 other;

```
  Query Match             1.1%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 86;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        745 CATGTTGCTGACTTT 759
              |||||||||||||||
Db          1 CATGTTGCTGACTTT 15


RESULT 76
ABK32626
ID   ABK32626 standard; DNA; 15 BP.
XX
AC   ABK32626;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human pancreatic cancer SAGE tag #178.
XX
KW   Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
KW   serial analysis of gene expression; diagnostic; prognostic; probe;
KW   cancer marker; ss.
XX
OS   Homo sapiens.
XX
PN   US6333152-B1.
XX
PD   25-DEC-2001.
XX
PF   20-MAY-1998;   98US-0081646.
XX
PR   20-MAY-1998;   98US-0081646.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW,  Zhang L,  Zhou W;
XX
DR   WPI; 2002-153821/20.
XX
PT   New human nucleic acid containing specific SAGE tags, useful as
PT   diagnostic markers for cancer, also derived probes -
XX
PS   Disclosure; Column 82; 161pp; English.
XX
CC   The invention relates to an isolated, purified human nucleic acid (I)
CC   that has the same sequence as a mRNA found in humans and is a SAGE
CC   (serial analysis of gene expression) tag comprising a single stranded
CC   probe containing at least 10 consecutive nucleotides. SAGE tags, are
CC   diagnostic and prognostic markers of cancer, especially of the colon and
CC   pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
CC   SAGE tags of the invention.
XX
SQ   Sequence 15 BP; 2 A; 3 C; 3 G; 7 T; 0 other;

  Query Match             1.1%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 86;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        745 CATGTTGCTGACTTT 759
              |||||||||||||||
Db          1 CATGTTGCTGACTTT 15


RESULT 77
ABK12664/c
ID   ABK12664 standard; DNA; 17 BP.
XX
AC   ABK12664;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Rat interleukin 11 (IL-11), reverse PCR primer.
XX
KW   Interleukin 11; IL-11; cerebroprotective; neuroprotective;
KW   gene therapy; stroke; neuropathy; rat; PCR; primer; ss.
XX
OS   Rattus sp.
XX
PN   WO200220609-A2.
XX
PD   14-MAR-2002.
XX
PF   27-AUG-2001; 2001WO-EP09923.
XX
PR   04-SEP-2000; 2000GB-0021668.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Bates SA,  Gloger IS,  Read S;
XX
DR   WPI; 2002-304371/34.
XX
PT   Treating stroke or neuropathy, using interleukin-11 or its mimic,
PT   related nucleic acid, or modulator of its receptor -
XX
PS   Example 2; Page 22; 39pp; English.
XX
CC   The invention describes a treatment for stroke or neuropathy using
CC   compounds including an interleukin-11 (IL-11) polypeptide, or its
CC   mimic, a compound that activates, or inhibits activation of the IL-11
CC   receptor, or polynucleotide that encodes IL-11. The polynucleotides
CC   can be used in gene therapy to replace defective IL-11 or enhance
CC   IL-11 production in acute illnesses such as stroke. Agonists and
CC   antagonists of IL-11 can also be used in the manufacture of a
CC   medicament. This sequence represents a PCR primer used to study the
CC   induction of IL-11 in rat cerebral cortex following permanent middle
CC   cerebral artery occlusion (pMCAO).
XX
SQ   Sequence 17 BP; 3 A; 7 C; 5 G; 2 T; 0 other;

  Query Match             1.1%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        536 AGCTGGGTGCCCTGC 550
              |||||||||||||||
Db         15 AGCTGGGTGCCCTGC 1


RESULT 78
AAF62379/c
ID   AAF62379 standard; DNA; 18 BP.
XX
AC   AAF62379;
XX
DT   06-JUN-2001  (first entry)
XX
DE   LSR-leptin interaction modulation related oligo SEQ ID NO: 104.
XX
KW   Leptin; human; LSR; lipolysis stimulated receptor; obesity;
KW   hypertension; anorexia; cachexia; stroke; atherosclerosis; ds.
XX
OS   Synthetic.
XX
PN   WO200121647-A2.
XX
PD   29-MAR-2001.
XX
PF   22-SEP-2000; 2000WO-IB01470.
XX
PR   22-SEP-1999;   99US-0155506.
XX
PA   (GEST ) GENSET.
XX
PI   Yen F,  Erickson MR,  Fruebis J,  Bihain B;
```

XX
DR WPI; 2001-218642/22.
XX
PT New leptin polypeptide fragment and related polynucleotides, useful for
PT the prevention and treatment of obesity and obesity-related diseases
PT such as hypertension and diabetes -
XX
PS Disclosure; Page 247; 247pp; English.
XX
CC The present invention provides the protein and coding sequences of leptin
CC fragments which modulate the activity of lipolysis stimulated factor
CC (LSR). These sequences are useful in the treatment of obesity related
CC diseases, including obesity, anorexia, cachexia, cardiac and coronary
CC insufficiency, stroke, hypertension, atheromatous disease,
CC atherosclerosis, non-insulin dependent diabetes, hyperlipidaemia,
CC hyperuricaemia and syndrome X.
XX
SQ Sequence 18 BP; 0 A; 2 C; 14 G; 2 T; 0 other;

Query Match 1.1%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 186 CCCCGCCGCCCACCC 200
||||||||||||||||
Db 18 CCCCGCCGCCCACCC 4

RESULT 79
AAZ26122
ID AAZ26122 standard; DNA; 21 BP.
XX
AC AAZ26122;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human polymorphic region 311.
XX
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS Homo sapiens.
XX
PN WO9841648-A2.
XX
PD 24-SEP-1998.
XX
PF 19-MAR-1998; 98WO-US05419.
XX
PR 20-MAR-1997; 97US-0041057.
XX
PA (VARI-) VARIAGENICS INC.
XX
PI Housman D, Ledley FD, Stanton VP;
XX
DR WPI; 1998-521232/44.
XX
PT Identifying target genes for allele-specific drugs - used for
PT diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic
PT plaque, dysplastic lesions, endometriosis or graft versus host disease
XX
PS Disclosure; Figure 7; 605pp; English.
XX
CC This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is
CC active on a gene vital for cell growth or viability, and where the gene
CC is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can
CC be used in the diagnosis, prevention and treatment of LOH disorders,
CC e.g. cancers, atherosclerotic plaques, premalignant metaplastic or
CC dysplastic lesions, benign tumours, endometriosis, polycystic kidney
CC disease, and graft versus host disease. The method can also be used to
CC remove malignant cells from bone marrow transplants. AAZ25812-Z26825
CC represent human polymorphic sites described in the method of the
CC invention.
XX
SQ Sequence 21 BP; 1 A; 11 C; 5 G; 4 T; 0 other;

Query Match 1.1%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1053 CAGCCCTGGCCTTCC 1067
|||||||||||||||
Db 5 CAGCCCTGGCCTTCC 19

RESULT 80
AAZ26123
ID AAZ26123 standard; DNA; 21 BP.
XX
AC AAZ26123;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human polymorphic region 312.
XX
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS Homo sapiens.
XX
PN WO9841648-A2.
XX
PD 24-SEP-1998.
XX
PF 19-MAR-1998; 98WO-US05419.
XX
PR 20-MAR-1997; 97US-0041057.
XX
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PS Disclosure; Figure 7; 605pp; English.
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CC potentially useful for treatment of cancer, where the inhibitor is
CC active on a gene vital for cell growth or viability, and where the gene
CC is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor

CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can
CC be used in the diagnosis, prevention and treatment of LOH disorders,
CC e.g. cancers, atherosclerotic plaques, premalignant metaplastic or
CC dysplastic lesions, benign tumours, endometriosis, polycystic kidney
CC disease, and graft versus host disease. The method can also be used to
CC remove malignant cells from bone marrow transplants. AAZ25812-Z26825
CC represent human polymorphic sites described in the method of the
CC invention.
XX
SQ Sequence 21 BP; 1 A; 11 C; 5 G; 4 T; 0 other;

Query Match 1.1%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1053 CAGCCCTGGCCTTCC 1067
||||||||||||||||
Db 4 CAGCCCTGGCCTTCC 18

RESULT 81
AAZ26124
ID AAZ26124 standard; DNA; 21 BP.
XX
AC AAZ26124;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human polymorphic region 313.
XX
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS Homo sapiens.
XX
PN WO9841648-A2.
XX
PD 24-SEP-1998.
XX
PF 19-MAR-1998; 98WO-US05419.
XX
PR 20-MAR-1997; 97US-0041057.
XX
PA (VARI-) VARIAGENICS INC.
XX
PI Housman D, Ledley FD, Stanton VP;
XX
DR WPI; 1998-521232/44.
XX
PT Identifying target genes for allele-specific drugs - used for
PT diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic
PT plaque, dysplastic lesions, endometriosis or graft versus host disease
XX
PS Disclosure; Figure 7; 605pp; English.
XX
CC This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is
CC active on a gene vital for cell growth or viability, and where the gene
CC is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can
CC be used in the diagnosis, prevention and treatment of LOH disorders,
CC e.g. cancers, atherosclerotic plaques, premalignant metaplastic or
CC dysplastic lesions, benign tumours, endometriosis, polycystic kidney
CC disease, and graft versus host disease. The method can also be used to
CC remove malignant cells from bone marrow transplants. AAZ25812-Z26825
CC represent human polymorphic sites described in the method of the
CC invention.
XX
SQ Sequence 21 BP; 2 A; 12 C; 4 G; 3 T; 0 other;

Query Match 1.1%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1053 CAGCCCTGGCCTTCC 1067
||||||||||||||||
Db 1 CAGCCCTGGCCTTCC 15

RESULT 82
ABK65504/c
ID ABK65504 standard; DNA; 21 BP.
XX
AC ABK65504;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human single nucleotide polymorphism #124.
XX
KW Human; single nucleotide polymorphism; SNP; sickle cell anaemia;
KW agammaglobulinaemia; diabetes insipidus; Lesch-Nyhan syndrome;
KW muscular dystrophy; Wiskott-Aldrich syndrome; Fabry's disease;
KW familial hypercholesterolaemia; polycystic kidney disease; cancer;
KW hereditary spherocytosis; Von Willebrand's disease; tuberous sclerosis;
KW hereditary haemorrhagic telangiectasia; familial colonic polyposis;
KW Ehlers-Danlos syndrome; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; inflammation; nervous system disorder;
KW infection; rheumatoid arthritis; multiple sclerosis; diabetes;
KW systemic lupus erythematosus; Graves disease; longevity; obesity;
KW baldness; fertility; forensic; paternity testing; ss.
XX
OS Homo sapiens.
XX
PN US2002037508-A1.
XX
PD 28-MAR-2002.
XX
PF 18-JAN-2001; 2001US-0765081.
XX
PR 19-JAN-2000; 2000US-176861P.
XX
PA (CARG/) CARGILL M.
PA (IREL/) IRELAND J S.
PA (LAND/) LANDER E S.
XX
PI Cargill M, Ireland JS, Lander ES;
XX
DR WPI; 2002-315108/35.
XX
PT Nucleic acid comprising single nucleotide polymorphisms, useful in
PT forensics, paternity testing and diagnosis of disease -
XX
PS Claim 1; Page 50; 96pp; English.
XX
CC The invention relates to a nucleic acid comprising single nucleotide
CC polymorphisms (SNPs) associated with diseases. The nucleic acids
CC comprising the SNPs and probes and primers for detecting them may be used
CC in assays for the diagnosis of diseases associated with SNPs (such as
CC sickle cell anaemia, agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan
CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
CC familial hypercholesterolaemia, polycystic kidney disease, hereditary
CC spherocytosis, Von Willebrand's disease, tuberous sclerosis, hereditary
CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos

CC syndrome, osteogenesis imperfecta, and acute intermittent porphyria,
CC symptoms of, or susceptibility to, multifactorial diseases of which a
CC component is or may be genetic, such as autoimmune diseases,
CC inflammation, cancer, diseases of the nervous system, and infection by
CC pathogenic microorganisms, autoimmune diseases including rheumatoid
CC arthritis, multiple sclerosis, diabetes (insulin-dependent and
CC non-independent), systemic lupus erythematosus and Graves disease,
CC cancers including cancers of the bladder, brain, breast, colon,
CC oesophagus, kidney, leukaemia, liver, lung, oral cavity, ovary, pancreas,
CC prostate, skin, stomach and uterus, longevity, appearance (e.g.,
CC baldness, obesity), strength, speed, endurance, fertility, and
CC susceptibility or receptivity to particular drugs or therapeutic
CC treatments), in forensics and in paternity testing. ABK65381-ABK65841
CC represent human single nucleotide polymorphisms of the invention.
XX
SQ Sequence 21 BP; 7 A; 3 C; 8 G; 2 T; 1 other;

Query Match 1.1%; Score 15; DB 1; Length 21;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 637 GAGCTCTGCATCCCCCA 653
||||||||:||| |||
Db 20 GAGCTCTGCMTCCTCCA 4

RESULT 83
ABK65804/c
ID ABK65804 standard; DNA; 21 BP.
XX
AC ABK65804;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human single nucleotide polymorphism #424.
XX
KW Human; single nucleotide polymorphism; SNP; sickle cell anaemia;
KW agammaglobulinaemia; diabetes insipidus; Lesch-Nyhan syndrome;
KW muscular dystrophy; Wiskott-Aldrich syndrome; Fabry's disease;
KW familial hypercholesterolaemia; polycystic kidney disease; cancer;
KW hereditary spherocytosis; Von Willebrand's disease; tuberous sclerosis;
KW hereditary haemorrhagic telangiectasia; familial colonic polyposis;
KW Ehlers-Danlos syndrome; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; inflammation; nervous system disorder;
KW infection; rheumatoid arthritis; multiple sclerosis; diabetes;
KW systemic lupus erythematosus; Graves disease; longevity; obesity;
KW baldness; fertility; forensic; paternity testing; ss.
XX
OS Homo sapiens.
XX
PN US2002037508-A1.
XX
PD 28-MAR-2002.
XX
PF 18-JAN-2001; 2001US-0765081.
XX
PR 19-JAN-2000; 2000US-176861P.
XX
PA (CARG/) CARGILL M.
PA (IREL/) IRELAND J S.
PA (LAND/) LANDER E S.
XX
PI Cargill M, Ireland JS, Lander ES;
XX
DR WPI; 2002-315108/35.
XX
PT Nucleic acid comprising single nucleotide polymorphisms, useful in
PT forensics, paternity testing and diagnosis of disease -
XX
PS Claim 1; Page 89; 96pp; English.
XX
CC The invention relates to a nucleic acid comprising single nucleotide
CC polymorphisms (SNPs) associated with diseases. The nucleic acids
CC comprising the SNPs and probes and primers for detecting them may be used
CC in assays for the diagnosis of diseases associated with SNPs (such as
CC sickle cell anaemia, agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan
CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
CC familial hypercholesterolaemia, polycystic kidney disease, hereditary
CC spherocytosis, Von Willebrand's disease, tuberous sclerosis, hereditary
CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC syndrome, osteogenesis imperfecta, and acute intermittent porphyria,
CC symptoms of, or susceptibility to, multifactorial diseases of which a
CC component is or may be genetic, such as autoimmune diseases,
CC inflammation, cancer, diseases of the nervous system, and infection by
CC pathogenic microorganisms, autoimmune diseases including rheumatoid
CC arthritis, multiple sclerosis, diabetes (insulin-dependent and
CC non-independent), systemic lupus erythematosus and Graves disease,
CC cancers including cancers of the bladder, brain, breast, colon,
CC oesophagus, kidney, leukaemia, liver, lung, oral cavity, ovary, pancreas,
CC prostate, skin, stomach and uterus, longevity, appearance (e.g.,
CC baldness, obesity), strength, speed, endurance, fertility, and
CC susceptibility or receptivity to particular drugs or therapeutic
CC treatments), in forensics and in paternity testing. ABK65381-ABK65841
CC represent human single nucleotide polymorphisms of the invention.
XX
SQ Sequence 21 BP; 4 A; 5 C; 9 G; 2 T; 1 other;

Query Match 1.1%; Score 15; DB 1; Length 21;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 794 CCCTGGCTCGCTCCCTG 810
|||||| ||:|||||||
Db 20 CCCTGGATCRCTCCCTG 4

RESULT 84
AAX67028/c
ID AAX67028 standard; RNA; 18 BP.
XX
AC AAX67028;
XX
DT 20-JUL-1999 (first entry)
XX
DE Mouse B7 hairpin ribozyme target SEQ ID NO:3660.
XX
KW Arthritic condition; graft tolerance; immune response; target; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
KW diagnosis; ss.
XX
OS Mus sp.
XX
PN WO9618736-A2.
XX
PD 20-JUN-1996.
XX
PF 22-NOV-1995; 95WO-US15516.
XX
PR 05-OCT-1995; 95US-0541365.
PR 13-DEC-1994; 94US-0354920.
PR 23-DEC-1994; 94US-0363253.
PR 23-DEC-1994; 94US-0363254.
PR 17-FEB-1995; 95US-0390850.
PR 20-APR-1995; 95US-0426124.
PR 02-MAY-1995; 95US-0432874.
PR 04-MAY-1995; 95US-0434509.
PR 07-JUL-1995; 95US-0000951.
PR 07-JUL-1995; 95US-0000974.
PR 07-AUG-1995; 95US-0512861.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Draper K, Gustofson J, McSwiggen J, Pavco P, Stinchcomb DT;
PI Beigelman L, Karpeisky A, Modak A, Usman N, Burgin A;

PI Matulic-Adamic J, Jarvis T, Thompson JD, Wincott F;
XX
DR WPI; 1996-300653/30.
XX
PT Enzymatic nucleic acid molecules having a hammer-head motif - used
PT for the treatment of arthritis, induction of graft tolerance or
PT treatment of auto-immune diseases
XX
PS Claim 10; Page 215; 307pp; English.
XX
CC The present invention describes a novel enzymatic nucleic acid (ENA)
CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose
CC residues; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii)
CC at least ten 2'-O-methyl modifications; and (iv) a 3'-end modification.
CC The ENA's can inhibit collagenase and stromelysin production in the
CC synovial membrane of joints for the treatment or prevention of arthritis,
CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
CC be used to treat antigen presenting cells of a donor to induce tolerance
CC in a recipient to an alloantigen of a donor. They can also be used for
CC enhancing graft tolerance or for treating autoimmune disease, and for
CC treating allergies and other inflammatory conditions. The ENA's can also
CC be used in diagnosis. Ribozyme therapy impacts on the expression of
CC stromelysin without introducing the non-specific effects upon gene
CC expression which accompany treatment with retinoids and dexamethasone.
CC The concentration of ribozyme required to affect a therapeutic treatment
CC is lower than that required of antisense molecules, and is highly
CC specific. The present sequence is used in the exemplification of the
CC present invention.
XX
SQ Sequence 18 BP; 1 A; 4 C; 4 G; 9 U; 0 other;

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 277 AAAGAGGAAGCAGCAGCA 294
||||| ||| ||||||||
Db 18 AAAGACGAATCAGCAGCA 1

RESULT 85
AAD52710
ID AAD52710 standard; DNA; 18 BP.
XX
AC AAD52710;
XX
DT 14-MAY-2003 (first entry)
XX
DE Psammomys obesus AGT-114 cDNA specific forward PCR primer.
XX
KW Obesity; anorexia; weight maintenance; impaired muscle development;
KW diabetes; alkylguanine alkyltransferase; energy imbalance; enzyme;
KW gene therapy; Israeli sand rat; AGT; PCR; primer; ss.
XX
OS Psammomys obesus.
XX
PN WO200295020-A1.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-AU00628.
XX
PR 21-MAY-2001; 2001AU-0005137.
XX
PA (AUTO-) AUTOGEN RES PTY LTD.
PA (UYDE-) UNIV DEAKIN.
PA (ITDI-) INT DIABETES INST.
XX
PI Collier G, Walder K, Miller JE;
XX
DR WPI; 2003-140372/13.
XX
PT New isolated nucleic acid molecule expressed in liver or stomach
PT tissue, useful for diagnosing or treating obesity, anorexia, diabetes
PT or energy imbalance, and as targets for agents which act as modulators
PT of physiological processes -
XX
PS Example 24; Page 72; 115pp; English.
XX
CC The invention relates to a novel nucleic acid molecule expressed
CC in liver or stomach tissue, useful for diagnosing or treating obesity,
CC anorexia etc. The nucleic acid molecule is useful as a diagnostic and
CC therapeutic agent or as a target for agents which act as modulators
CC and/or monitors of physiological processes associated with obesity,
CC anorexia, weight maintenance, impaired muscle development, diabetes
CC and/or metabolic energy levels and/or other physiological conditions.
CC Alkylguanine alkyltransferase (AGT)-117, AGT-110, AGT-199, AGT-107,
CC AGT-114, AGT-116, AGT-115 and/or AGT-108 genes of the invention and
CC the agent that modulate their expression or activity are useful in
CC manufacturing a medicament for treating a condition characterised by
CC obesity, anorexia, diabetes and/or energy imbalance. The invention is
CC useful in gene therapy. The present sequence is Israeli sand rat
CC (P. obesus) AGT cDNA specific PCR primer used in the exemplification
CC of the invention.
XX
SQ Sequence 18 BP; 5 A; 5 C; 6 G; 2 T; 0 other;

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 383 CTCCAGAGGTGGCAGCAA 400
| |||| ||||||||||
Db 1 CACCAGTGGTGGCAGCAA 18

RESULT 86
AAT96652
ID AAT96652 standard; cDNA; 19 BP.
XX
AC AAT96652;
XX
DT 25-MAR-2003 (updated)
DT 27-APR-1998 (first entry)
XX
DE Mouse tub gene primer 2.61F.
XX
KW TULP; tub gene; mouse; sensory neuron; neurosensory defect;
KW cochlear degeneration; hearing loss; deafness; retinal dystrophy;
KW retinitis pigmentosa; combined rod cone dystrophy; obesity;
KW animal model; transgenic animal; therapy; diagnosis; PCR; primer;
KW ss.
XX
OS Synthetic.
OS Mus musculus.
XX
PN WO9738004-A1.
XX
PD 16-OCT-1997.
XX
PF 10-APR-1997; 97WO-US05903.
XX
PR 17-SEP-1996; 96US-0714991.
PR 10-APR-1996; 96US-0630592.
PR 22-AUG-1996; 96US-0701380.
PR 04-SEP-1996; 96US-0706292.
XX
PA (JACK-) JACKSON LAB.
PA (SEQU-) SEQUANA THERAPEUTICS INC.
XX
PI Nishina P, Nobentrauth K, Naggert J, North M;
XX
DR WPI; 1997-512642/47.
XX
PT Mammalian TULP protein - used for detecting pre-disposition to
PT neuro-sensory defects

```
XX
PS   Disclosure; Page 28; 89pp; English.
XX
CC   Primer 2.61F (AAT96652) and primer C13R (AAT96653) were used to obtain
CC   a mouse tub gene probe DNA fragment for northern blots by
CC   amplifying mouse cDNA.  Tub mutation is associated with adult onset
CC   obesity.  Mouse Form I (see AAT96636) and Form II (see AAT96637) tub
CC   cDNAs have been isolated.  Tub is a member of the mammalian TULP
CC   gene family associated with various defects in sensory neurons such
CC   as cochlear defects, retinitis pigmentosa and combined rod-cone
CC   dystrophy.
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 19 BP; 6 A; 5 C; 6 G; 2 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 1.3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        822 CCTGATGCAGCTGAAGCT 839
              ||||| ||||| ||||||
Db          2 CCTGAGGCAGCAGAAGCT 19


RESULT 87
AAA94645
ID   AAA94645 standard; DNA; 19 BP.
XX
AC   AAA94645;
XX
DT   15-JAN-2001  (first entry)
XX
DE   Mouse tub gene PCR primer 2.61F.
XX
KW   Mouse; TULP; neurosensory defect; retina; retinal dystrophy; PCR primer;
KW   TUB; ss.
XX
OS   Mus sp.
XX
PN   US6114502-A.
XX
PD   05-SEP-2000.
XX
PF   27-FEB-1998;   98US-0032365.
XX
PR   22-AUG-1996;   96US-0701380.
PR   04-SEP-1996;   96US-0706292.
PR   10-APR-1996;   96US-0630592.
PR   17-SEP-1996;   96US-0714991.
PR   30-APR-1997;   97US-0850218.
PR   01-AUG-1997;   97US-0904699.
PR   17-SEP-1997;   97US-0932306.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   North M,  Nishina P,  Noben-Trauth K,  Naggert J;
XX
DR   WPI; 2000-586483/55.
XX
PT   Mammalian proteins expressed in retina and brain, useful for producing
PT   antibodies and for diagnosing neurosensory defects including cochlear
PT   degeneration, peripheral retinal degeneration and cone-rod retinal
PT   dystrophy -
XX
PS   Disclosure; Column 21; 61pp; English.
XX
CC   The present invention relates to human and murine cDNAs from a
CC   neurosensory defect associated gene family. The novel cDNAs are mouse
CC   tub form I (see AAA94629), mouse tub form II (see AAA94630), human TUB
CC   form 6 (see AAA94632), human TUB form 1 (see AAA94633), human TULP1 (see
CC   AAA94635), human TULP2 (see AAA94636), human TULP3 (see AAA94637) and
CC   mouse TULP4 (see AAA94638). The novel coding sequences are useful as
CC   immunogens to raise antibodies that specifically identify TUB/TULP
CC   expressing cells and in drug screening assays directed at neurosensory
CC   defects. The novel proteins encoded by the present sequence can be used
CC   for the treatment of neurosensory degenerative conditions e.g. retinal
CC   dystrophies. The present sequence is a PCR primer used to isolate the
CC   novel genes of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 5 C; 6 G; 2 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 1.3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        822 CCTGATGCAGCTGAAGCT 839
              ||||| ||||| ||||||
Db          2 CCTGAGGCAGCAGAAGCT 19


RESULT 88
AAA84761
ID   AAA84761 standard; DNA; 19 BP.
XX
AC   AAA84761;
XX
DT   04-DEC-2000  (first entry)
XX
DE   Cyclin F ribozyme binding site #29.
XX
KW   Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
KW   restenosis; ss.
XX
OS   Mammalia.
XX
PN   WO200032765-A2.
XX
PD   08-JUN-2000.
XX
PF   06-DEC-1999;   99WO-US28772.
XX
PR   04-DEC-1998;   98US-0110954.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Tritz R,  Welch PJ,  Barber JR,  Robbins JM;
XX
DR   WPI; 2000-412314/35.
XX
PT   New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT   RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT   PCNA and Cyclin B1  -
XX
PS   Disclosure; Page 82; 109pp; English.
XX
CC   The present invention relates to a hairpin or hammerhead ribozyme,
CC   designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC   other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC   Representative examples of ribozyme recognition sites are given in
CC   AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC   inhibiting restenosis by introduction of the ribozyme into cells.
CC   The ribozyme is resistant to endonuclease activity and hence is
CC   efficient in restenosis treatment.
XX
SQ   Sequence 19 BP; 3 A; 6 C; 6 G; 4 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 1.3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        877 GCCAAGTTCCAGGAGCTG 894
              ||||  ||||||||||||
Db          2 GCCAGCTTCCAGGAGCTG 19


RESULT 89
```

```
AAH59923
ID   AAH59923 standard; DNA; 19 BP.
XX
AC   AAH59923;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Cyclin F ribozyme binding site SEQ ID NO:2347.
XX
KW   Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW   recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW   proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW   cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW   matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW   antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW   antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW   atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW   basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW   sickle cell retinopathy; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200130362-A2.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US29500.
XX
PR   26-OCT-1999;   99US-0161532.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Robbins JM,  Tritz R;
XX
DR   WPI; 2001-300427/31.
XX
PT   Treating proliferative skin or eye diseases and scarring, using
PT   ribozymes that cleave RNA encoding cytokines involved in inflammation,
PT   matrix metalloproteinases, growth factors and cell-cycle dependent
PT   kinases -
XX
PS   Example 1; Page 242; 408pp; English.
XX
CC   The present invention describes a method for treating a proliferative
CC   skin or eye disease and scarring. The method involves administering a
CC   ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC   inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC   dependent kinase, growth factor or a reductase, or administering a
CC   nucleic acid molecule (II) comprising a promoter operably linked to a
CC   nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC   dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC   ophthalmological, vulnerary, keratolytic and virucide activities, and
CC   cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC   in gene therapy. (I) and (II) are useful for treating proliferative
CC   skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC   squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC   also be used for treating proliferative eye diseases such as diabetic
CC   retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC   prematurity and retinal detachment, and for treating and preventing
CC   scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC   scar. AAH57577 to AAH62099 represent sequences used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 6 C; 6 G; 4 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 1.3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        877 GCCAAGTTCCAGGAGCTG 894
              ||||  ||||||||||||
Db          2 GCCAGCTTCCAGGAGCTG 19
```

```
RESULT 90
AAF91219/c
ID   AAF91219 standard; DNA; 19 BP.
XX
AC   AAF91219;
XX
DT   04-MAY-2001  (first entry)
XX
DE   Human multi drug resistance-1 gene related sequence SEQ ID NO: 306.
XX
KW   Human; MDR-1; multi drug resistance-1; drug uptake; disease; cancer;
KW   inflammatory disease; neuronal disease; CNS disease;
KW   cardiovascular disease; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200109183-A2.
XX
PD   08-FEB-2001.
XX
PF   28-JUL-2000; 2000WO-EP07314.
XX
PR   30-JUL-1999;   99EP-0114938.
PR   22-FEB-2000; 2000EP-0103361.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI   Brinkmann U,  Hoffmeyer S,  Eichelbaum M,  Roots I;
XX
DR   WPI; 2001-159855/16.
XX
PT   New polynucleotide encoding a molecular variant Multi Drug Resistance
PT   (MDR)-1 polypeptide is useful for diagnosing and treating diseases
PT   associated with abnormal MDR-1 expression or function, e.g. cancer -
XX
PS   Disclosure; Page 140; 154pp; English.
XX
CC   The present invention provides nucleotides encoding molecular variants of
CC   the human multi drug resistance-1 (MDR-1) protein. These can be used to
CC   identify compounds capable of treating multidrug resistance and
CC   sensitivity interfering resulting from polymorphisms in MDR-1, which can
CC   lead to difficulties in treating cancer, cardiovascular, neuronal,
CC   inflammatory and CNS diseases.
XX
SQ   Sequence 19 BP; 2 A; 5 C; 9 G; 3 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 1.3e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        577 CAGGCCCTCCGTCTGCCC 594
              |||| || ||||||||||
Db         19 CAGGGCCACCGTCTGCCC 2
```

```
RESULT 91
AAF91221
ID   AAF91221 standard; DNA; 19 BP.
XX
AC   AAF91221;
XX
DT   04-MAY-2001  (first entry)
XX
DE   Human multi drug resistance-1 gene related sequence SEQ ID NO: 308.
XX
KW   Human; MDR-1; multi drug resistance-1; drug uptake; disease; cancer;
KW   inflammatory disease; neuronal disease; CNS disease;
KW   cardiovascular disease; PCR primer; ss.
XX
OS   Homo sapiens.
XX
```

PN WO200109183-A2.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-EP07314.
XX
PR 30-JUL-1999; 99EP-0114938.
PR 22-FEB-2000; 2000EP-0103361.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Brinkmann U, Hoffmeyer S, Eichelbaum M, Roots I;
XX
DR WPI; 2001-159855/16.
XX
PT New polynucleotide encoding a molecular variant Multi Drug Resistance
PT (MDR)-1 polypeptide is useful for diagnosing and treating diseases
PT associated with abnormal MDR-1 expression or function, e.g. cancer -
XX
PS Disclosure; Page 140; 154pp; English.
XX
CC The present invention provides nucleotides encoding molecular variants of
CC the human multi drug resistance-1 (MDR-1) protein. These can be used to
CC identify compounds capable of treating multidrug resistance and
CC sensitivity interfering resulting from polymorphisms in MDR-1, which can
CC lead to difficulties in treating cancer, cardiovascular, neuronal,
CC inflammatory and CNS diseases.
XX
SQ Sequence 19 BP; 3 A; 9 C; 5 G; 2 T; 0 other;

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 577 CAGGCCCTCCGTCTGCCC 594
|||| || ||||||||||
Db 1 CAGGGCCACCGTCTGCCC 18

RESULT 92
AAQ52925/c
ID AAQ52925 standard; RNA; 20 BP.
XX
AC AAQ52925;
XX
DT 25-MAR-2003 (updated)
DT 26-MAY-1994 (first entry)
XX
DE Herpes simplex virus target sequence 3.
XX
KW RNA; enzyme; enzymatic RNA molecule; ERM; cleave; RNA; mRNA; HnRNA;
KW picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV;
KW papilloma virus; HPV; Epstein-Barr virus; EBV; TCLV;
KW T-cell leukaemia virus; hepatitis C virus; HCV; cytomegalovirus;
KW influenza virus; HSV; herpes simplex virus; vector; immune response;
KW antibody; ribozyme; viral RNA; treatment; ss.
XX
OS Synthetic.
XX
PN WO9323569-A1.
XX
PD 25-NOV-1993.
XX
PF 29-APR-1993; 93WO-US04020.
XX
PR 11-MAY-1992; 92US-0882689.
PR 14-MAY-1992; 92US-0882712.
PR 14-MAY-1992; 92US-0882713.
PR 14-MAY-1992; 92US-0882714.
PR 14-MAY-1992; 92US-0882823.
PR 14-MAY-1992; 92US-0882824.
PR 14-MAY-1992; 92US-0882886.
PR 14-MAY-1992; 92US-0882888.
PR 14-MAY-1992; 92US-0882889.
PR 14-MAY-1992; 92US-0882921.
PR 14-MAY-1992; 92US-0882922.
PR 14-MAY-1992; 92US-0883823.
PR 14-MAY-1992; 92US-0883849.
PR 14-MAY-1992; 92US-0884073.
PR 14-MAY-1992; 92US-0884074.
PR 14-MAY-1992; 92US-0884333.
PR 14-MAY-1992; 92US-0884422.
PR 14-MAY-1992; 92US-0884431.
PR 14-MAY-1992; 92US-0884436.
PR 14-MAY-1992; 92US-0884521.
PR 31-JUL-1992; 92US-0923738.
PR 26-AUG-1992; 92US-0935854.
PR 26-AUG-1992; 92US-0936086.
PR 18-SEP-1992; 92US-0948359.
PR 15-OCT-1992; 92US-0963322.
PR 07-DEC-1992; 92US-0987129.
PR 07-DEC-1992; 92US-0987130.
PR 07-DEC-1992; 92US-0987133.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Draper KG, Dudycz LW, Mcswiggen JA, Macejak DG, Holecek JJ;
PI Mamone JA;
XX
DR WPI; 1993-386599/48.
XX
PT Enzymatic RNA molecules - used to inhibit viral replication,
PT infection and gene expression
XX
PS Claim 5; Fig 15; 287pp; English.
XX
CC The sequences (AAQ52923-Q53037) are pref. herpes simplex virus target
CC sequences for enzymatic RNA molecules. The RNA molecules are
CC complementary to a substrate binding region in the specified gene
CC target. They also have enzymatic activity, in that they specifically
CC cleave RNA in the target. The ERMs interfere with viral replication and
CC therefore have anti-viral properties. They can be used to attenuate
CC viruses to be used in vaccines.
CC (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 20 BP; 1 A; 8 C; 6 G; 5 U; 0 other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 130 GGACAGGGACGCCCGCTC 147
|||||||||||| ||| ||
Db 19 GGACAGGGACGGCCGATC 2

RESULT 93
AAZ02840
ID AAZ02840 standard; DNA; 20 BP.
XX
AC AAZ02840;
XX
DT 07-OCT-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer;
KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
OS Synthetic.
OS Chlamydia trachomatis.
XX

PN WO9928475-A2.
XX
PD 10-JUN-1999.
XX
PF 27-NOV-1998; 98WO-IB01939.
XX
PR 04-NOV-1998; 98US-0107077.
PR 28-NOV-1997; 97FR-0015041.
PR 17-DEC-1997; 97FR-0016034.
XX
PA (GEST) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-371125/31.
XX
PT Genome sequence of Chlamydia trachomatis
XX
PS Disclosure; Page 1557; 1755pp; English.
XX
CC PCR primers AAZ01426-Z06209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences
CC can also be used to control growth of the microorganism. Chlamydia
CC trachomatis is responsible for a large number of diseases, e.g. eye
CC diseases such as conventional trachoma, nonendemic trachoma,
CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
CC nongonococcal uretritis, epidymitis, cervicitis, salpingitis,
CC perihepatitis, bartholinitis; pneumopathy in breast feeding infants;
CC and venereal lymphogranulomatosis. The polypeptides of the
CC invention may be of use in treating these diseases.
XX
SQ Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 406 CGGCTACTAGGGGACCTA 423
||| |||||||||| |||
Db 3 CGGTTACTAGGGGAACTA 20

RESULT 94
AAA70403/c
ID AAA70403 standard; DNA; 20 BP.
XX
AC AAA70403;
XX
DT 02-FEB-2001 (first entry)
XX
DE Plant beta-tubulin PCR primer TubB16sp./rev.
XX
KW PCR primer; plant; rice; beta-tubulin; TubB16; ss.
XX
OS Oryza sativa.
XX
PN WO200039334-A1.
XX
PD 06-JUL-2000.
XX
PF 20-DEC-1999; 99WO-IT00415.
XX
PR 23-DEC-1998; 98IT-MI02789.
XX
PA (CNDR) CONSIGLIO NAZ DELLE RICERCHE.
XX
PI Breviario D, Giani' S;
XX
DR WPI; 2000-452420/39.
XX
PT Determining and monitoring the genetic variability of vegetable
PT species, comprising identifying genetic polymorphisms in plant
PT tubulins, useful for monitoring variability between cultivated and wild
PT plants -
XX
PS Claim 12; Page 25; 34pp; English.
XX
CC The present invention relates to a process for determining and monitoring
CC the genetic variability of vegetable species comprising identifying
CC genetic polymorphisms in plant tubulins via PCR. The present sequence is
CC a PCR primer for rice beta-tubulin coding sequence (TubB16 isotype). This
CC primer is used in the process of the present invention.
XX
SQ Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 743 CGCATGTTGCTGACTTTC 760
|||||| ||||||| |||
Db 20 CGCATGATGCTGACATTC 3

RESULT 95
AAC79519/c
ID AAC79519 standard; DNA; 20 BP.
XX
AC AAC79519;
XX
DT 07-FEB-2001 (first entry)
XX
DE Human p38beta antisense oligonucleotide SEQ ID 42.
XX
KW Antisense oligonucleotide; p38 mitogen activated protein kinase; MAPK;
KW antirheumatic; antiarthritic; immunosuppressive; cardiant; heart disease;
KW antiinflammatory; autoimmune disease; rheumatoid arthritis; apoptosis;
KW phosphorothioate; ss.
XX
OS Homo sapiens.
XX
PN WO200059919-A1.
XX
PD 12-OCT-2000.
XX
PF 04-APR-2000; 2000WO-US08794.
XX
PR 06-APR-1999; 99US-0286904.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Gaarde WA, Nero PS, McKay R, Popoff I;
XX
DR WPI; 2000-664982/64.
XX
PT Antisense compound targeted to p38 mitogen activated protein kinase
PT inhibits protein kinase and is useful for diagnosing and treating
PT inflammatory, autoimmune and heart disease -
XX
PS Claim 3; Page 43; 90pp; English.
XX
CC This invention relates to antisense compounds 8-30 nucleobases in
CC length targeted to the 5'-untranslated region, translational start site,
CC translational termination region or 3'-untranslated region of a nucleic
CC acid encoding a p38 mitogen activated protein kinase (MAPK), where the
CC antisense oligonucleotides inhibit the expression of MAPK. Sequences
CC AAC79480 and AAC79501 represent human p38alpha MAPK and p38beta MAPK
CC cDNA sequences. AAC79481 - AAC79500 and AAC79553 - AAC79570 represent
CC human p38alpha antisense oligonucleotides, while AAC79502 - AAC79521 and
CC AAC79571 - AAC79580 represent human p38beta antisense oligonucleotides.
CC Also included in the invention are a p38alpha cDNA sequence AAC79523 and
CC antisense oligonucleotides AAC79523 - AAC79536 isolated from rat tissue.
CC Murine p38beta MAPK cDNA is represented in AAC79537 and antisense
CC oligonucleotides targeting the sequence are given in AAC79538 - AAC79552.

```
CC   The antisense oligonucleotides have antirheumatic; antiarthritic;
CC   immunosuppressive; cardiant and antiinflammatory activity. The antisense
CC   oligonucleotides are useful for inhibiting the expression of p38 MAPK in
CC   cells or tissues. The oligonucleotides are used for treating an animal
CC   with diseases such as inflammatory or autoimmune diseases e.g. rheumatoid
CC   arthritis, or heart disease. The oligonucleotides are also useful for
CC   inhibiting inflammation or apoptosis.
XX
SQ   Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1287 TACAGTTGCTCAGCCTGG 1304
              || || ||||||||||||
Db         19 TAGAGCTGCTCAGCCTGG 2


RESULT 96
AAA72640/c
ID   AAA72640 standard; DNA; 20 BP.
XX
AC   AAA72640;
XX
DT   01-DEC-2000  (first entry)
XX
DE   PCR primer SEQ ID #8 used for variant mtDNA amplification.
XX
KW   Human; mitochondrial DNA; mtDNA; familial nephrosis; detection;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000175689-A.
XX
PD   27-JUN-2000.
XX
PF   17-DEC-1998;   98JP-0359276.
XX
PR   17-DEC-1998;   98JP-0359276.
XX
PA   (SAKA ) OTSUKA PHARM CO LTD.
XX
DR   WPI; 2000-501190/45.
XX
PT   Genetic diagnosis of familial nephrosis comprises detection of an
PT   abnormality in human mitochondrial DNA -
XX
PS   Example 3; Page 11; 14pp; Japanese.
XX
CC   This sequence represents a PCR primer used to amplify a fragment of human
CC   mitochondrial DNA (mtDNA). The primer is used in the method of the
CC   invention for detecting an abnormality in human mtDNA, where the
CC   abnormality is related to familial nephrosis. The method involves
CC   detecting at least one mutation at one of four positions in human mtDNA:
CC   1) 15923, adenine to guanine;
CC   2) 2246, adenine to guanine;
CC   3) 14180, thymidine to cytosine, or
CC   4) 14927, adenine to guanine.
CC   The method is used in the genetic diagnosis of familial nephrosis.
XX
SQ   Sequence 20 BP; 5 A; 3 C; 6 G; 6 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         47 CTTAGCATACTCCTCAAT 64
              || || ||||||||||||
Db         20 CTCAGGATACTCCTCAAT 3


RESULT 97
AAA11329
ID   AAA11329 standard; DNA; 20 BP.
XX
AC   AAA11329;
XX
DT   08-NOV-2000  (first entry)
XX
DE   Human TRPC7 gene exon 23/intron 23 junction.
XX
KW   Transmembrane protein; TRPC7; brain; transient receptor potential; TRP;
KW   calcium channel function; human; gene therapy; periodic psychosis;
KW   mutation; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            1..10
FT                   /*tag=  a
FT                   /number= 23
FT   intron          11..20
FT                   /*tag=  b
FT                   /number= 23
XX
PN   WO200029571-A1.
XX
PD   25-MAY-2000.
XX
PF   11-NOV-1999;   99WO-JP06289.
XX
PR   12-NOV-1998;   98JP-0321200.
XX
PA   (EIKE ) EIKEN KAGAKU KK.
XX
PI   Shimizu N,  Nagamine K;
XX
DR   WPI; 2000-387784/33.
XX
PT   Nucleic acids encoding transmembrane protein TRPC7 expressed in brain
PT   and homologous to transient receptor potential protein useful in the
PT   treatment of associated diseases such as periodic psychosis  -
XX
PS   Example 7; Page 39; 77pp; Japanese.
XX
CC   The invention relates to the isolation of a nucleic acid (AAA11284)
CC   coding for a transmembrane protein TRPC7 (AAY92944) which is expressed in
CC   brain and is homologous to transient receptor potential (TRP) protein.
CC   This suggests that the TRPC7 protein may have a calcium channel
CC   function. The genomic sequence has been shown to contain 31 introns. This
CC   sequence represents an exon/intron junction from the genomic TRPC7
CC   sequence. The DNA and protein can be used in the diagnosis and treatment
CC   of disorders associated with TRPC7, especially the screening, monitoring
CC   and treatment (by gene therapy) of periodic psychosis, which appears to
CC   be associated with mutations in the TRPC7 gene.
XX
SQ   Sequence 20 BP; 4 A; 3 C; 11 G; 2 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        528 GGAGGAGCAGCTGGGTGC 545
              |||||||||| ||||| |
Db          1 GGAGGAGCAGGTGGGTCC 18


RESULT 98
AAA11141/c
ID   AAA11141 standard; DNA; 20 BP.
XX
AC   AAA11141;
XX
DT   26-SEP-2000  (first entry)
```

XX
DE Primer #2 for rat beta actin gene.
XX
KW Cytostatic; chemoprevention; cancer; 4'-bromoflavone; phase II enzyme;
KW metabolic detoxification; xenobiotic compound; mammal; tumour growth;
KW carcinoma; quinone reductase; PCR primer; ss.
XX
OS Rattus sp.
XX
PN US6046231-A.
XX
PD 04-APR-2000.
XX
PF 19-MAR-1999; 99US-0273203.
XX
PR 26-MAR-1998; 98US-0079393.
XX
PA (UNII) UNIV ILLINOIS FOUND.
XX
PI Pezzuto JM, Song LL, Moon RC, Kosmeder JW, Moriarty RM;
XX
DR WPI; 2000-282705/24.
XX
PT Methods of chemopreventing cancers sensitive to 4'-bromoflavone by
PT administration of cancer chemopreventative composition comprising
PT 4'-bromoflavone, avoids high costs -
XX
PS Disclosure; Column 10; 18pp; English.
XX
CC The invention relates to a method of chemopreventing cancers sensitive
CC to 4'-bromoflavone by administration of a sufficient amount of a cancer
CC chemopreventative composition comprising 4'-bromoflavone.
CC 4'-bromoflavone is a member of a family of compounds that induce phase II
CC enzymes involved in the metabolic detoxification of xenobiotic compounds
CC in mammals. One such phase II enzyme is quinone reductase. This enzyme
CC promotes obligatory 2 electron reductions of quinones thus preventing
CC their participation in oxidative cycling and interactions with critical
CC nucleotides. Primers AAA11138-A11139 were used to detect quinone
CC reductase mRNA expression in cells before and after treatment by
CC the method of the invention. Primers AAA11140-A11141 were used to detect
CC the rat beta-actin gene as a control for the mRNA detection step. The
CC methods are used to prevent tumour growth and to suppress the
CC initiation of cancers including carcinomas.
XX
SQ Sequence 20 BP; 4 A; 8 C; 2 G; 6 T; 0 other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 935 TGGAGAAGAGGTGTGAGC 952
||||||||||| | |||||
Db 20 TGGAGAAGAGCTATGAGC 3

RESULT 99
AAS45551/c
ID AAS45551 standard; DNA; 20 BP.
XX
AC AAS45551;
XX
DT 18-DEC-2001 (first entry)
XX
DE Tumour-specific IgV region H chain, PCR primer gamma.
XX
KW Human; B cell lymphoma; cytostatic; immunostimulator; self-antigen;
KW tumour-specific vaccine; tumour; polyclonal immune response;
KW idiotype-specific anti-lymphoma immune response; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200168682-A1.
XX
PD 20-SEP-2001.
XX
PF 13-OCT-2000; 2000WO-US28362.
XX
PR 10-MAR-2000; 2000US-0522900.
XX
PA (LARG-) LARGE SCALE BIOLOGY CORP.
PA (MCCO/) MCCORMICK A A.
PA (TUSE/) TUSE D.
XX
PI Reinl SJ, Turpen TH;
XX
DR WPI; 2001-596903/67.
XX
PT Novel polypeptide vaccine produced in plants, useful for inducing an
PT immune response to a self-antigen on the surface of certain tumour cells
PT -
XX
PS Disclosure; Page 30; 89pp; English.
XX
CC The invention relates to a novel polypeptide self-antigen (I) useful as a
CC tumour-specific vaccine in a subject with a tumour or at risk of
CC developing a tumour. (I) includes an epitope or epitopes unique to,
CC or over expressed by, cells of the tumour, thereby distinguishing the
CC tumour from all other tumours of the same or different histological type,
CC or in the subject or in another member of the subject's species. (I) is
CC epitopes in their native form. (I) is capable of inducing an immune
CC response in a mammal, when used as an individual-specific immunogenic
CC product comprising (I); and as a vaccine composition useful for inducing
CC a tumour-specific immune response, idiotype-specific anti-lymphoma immune
CC response, a polyclonal immune response to at least one idiotype of a
CC surface immunoglobulin or a polyclonal immune response to an idiotype.
CC The vaccine composition is useful for inducing a tumour-specific immune
CC antibody response in a tumour-bearing subject or a subject who had a
CC tumour e.g. B-cell lymphoma, and was treated so that no tumour is
CC clinically or radiographically evident. (I) is useful for inducing a
CC protective antitumour immune response. (I) can be produced at high
CC levels, is easy to purify and can be appropriately folded to mimic the
CC conformation of the native epitopes displayed at the tumour cell surface.
CC AAS45529-AAS45579 represent B cell lymphoma self antigen vaccine
CC linker sequences and PCR primers of the invention.
XX
SQ Sequence 20 BP; 4 A; 8 C; 6 G; 2 T; 0 other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 261 CCTGGGCTGGCTGATCAA 278
||||||||| ||| ||||
Db 19 CCTGGGCTGCCTGGTCAA 2

RESULT 100
AAF92937/c
ID AAF92937 standard; DNA; 20 BP.
XX
AC AAF92937;
XX
DT 17-MAY-2001 (first entry)
XX
DE Wild type sequence for ABC1 polymorphic site #13.
XX
KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
XX
OS Homo sapiens.
XX
PN WO200115676-A2.
XX
PD 08-MAR-2001.
XX
PF 01-SEP-2000; 2000WO-IB01492.
XX

PR 01-SEP-1999; 99US-0151977.
PR 15-MAR-2000; 2000US-0526193.
PR 23-JUN-2000; 2000US-0213958.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (XENO-) XENON GENETICS INC.
XX
PI Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;
XX
DR WPI; 2001-244356/25.
XX
PT Treating a lower than normal high density lipoprotein-cholesterol
PT (HDL-C) level, a higher than normal triglyceride level, or a
PT cardiovascular disease, by administering a compound that modulates LXR-
PT or RXR-mediated transcriptional activity -
XX
PS Disclosure; Fig 4; 317pp; English.
XX
CC The present invention relates to a method for treating a patient
CC diagnosed as having a lower than normal high density
CC lipoprotein-cholesterol (HDL-C) level, a higher than normal
CC triglyceride level, or a cardiovascular disease, involving
CC administering a compound that modulates LXR- or RXR-mediated
CC transcriptional activity or ABC1 expression or activity.
CC The LXR gene product may be used in an assay to identify
CC compounds useful for the treatment of a disease or condition selected a
CC lower than normal HDL cholesterol level, a higher than normal
CC triglyceride level, and a cardiovascular disease.
XX
SQ Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 991 TTCAGATCCGGCTTGGAC 1008
||||| ||||| ||||||
Db 20 TTCAGGTCCGGGTTGGAC 3

RESULT 101
AAD17405/c
ID AAD17405 standard; DNA; 20 BP.
XX
AC AAD17405;
XX
DT 29-NOV-2001 (first entry)
XX
DE Human sFRP2 gene specific forward RT-PCR primer.
XX
KW Secreted Frizzled-related protein; sFRP; chronic bronchitis; asthma;
KW chronic obstructive pulmonary disease; COPD; antisense therapy; human;
KW emphysema; reverse transcription PCR; RT-PCR primer; sFRP2 gene; ss.
XX
OS Homo sapiens.
XX
PN WO200164717-A1.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06579.
XX
PR 29-FEB-2000; 2000US-0514885.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI D'Armiento J, Imai K;
XX
DR WPI; 2001-557764/62.
XX
PT Inhibition of apoptosis for the treatment or prevention of obstructive
PT pulmonary disease comprises inhibiting expression of secreted
PT Frizzled-related protein gene in lung cells -
XX
PS Example 2; Page 35; 79pp; English.
XX
CC The present sequence is human secreted Frizzled-related protein 2
CC (sFRP2) gene specific reverse transcription PCR (RT-PCR) primer.
CC The invention relates to a method for treating or preventing chronic
CC obstructive pulmonary disease (COPD) such as emphysema, asthma and
CC chronic bronchitis in a subject. The method involves administering to
CC the subject, an agent effective to inhibit apoptosis by inhibiting the
CC expression of a secreted Frizzled-related protein (sFRP) gene. It is
CC also useful in antisense therapy.
XX
SQ Sequence 20 BP; 1 A; 9 C; 3 G; 7 T; 0 other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 269 GGCTGATCAAAGAGGAAG 286
||||| ||||||||||
Db 19 GGCTGGCCAAAGAGGAAG 2

RESULT 102
AAD40654
ID AAD40654 standard; DNA; 20 BP.
XX
AC AAD40654;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human hepsin antisense oligonucleotide, ISIS 107110.
XX
KW Human; antisense; hepsin; inflammation; tumour; gene therapy;
KW cytostatic; phosphorothioate backbone; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	modified_base	1..20
FT		/*tag= a
FT		/mod_base= OTHER
FT		/note= "Phosphorothioate backbone"
FT	modified_base	1..5
FT		/*tag= b
FT		/mod_base= OTHER
FT		/note= "2'methoxyethyl nucleotides"
FT	modified_base	16..20
FT		/*tag= c
FT		/mod_base= OTHER
FT		/note= "2'methoxyethyl nucleotides"
FT	modified_base	2
FT		/*tag= d
FT		/mod_base= m5c
FT	modified_base	5
FT		/*tag= e
FT		/mod_base= m5c
FT	modified_base	8
FT		/*tag= f
FT		/mod_base= m5c
FT	modified_base	12
FT		/*tag= g
FT		/mod_base= m5c
FT	modified_base	15
FT		/*tag= h
FT		/mod_base= m5c
FT	modified_base	16
FT		/*tag= i
FT		/mod_base= m5c

XX
PN WO200250248-A2.
XX

```
PD   27-JUN-2002.
XX
PF   14-DEC-2001; 2001WO-US48431.
XX
PR   20-DEC-2000; 2000US-0742703.
XX
PA   (ISIS-) ISIS PHARM INC.
PA   (ABBO ) ABBOTT LAB.
XX
PI   Marcotte PA,  Cowsert LM;
XX
DR   WPI; 2002-519883/55.
XX
PT   New antisense oligonucleotides that modulate (particularly inhibit)
PT   human hepsin, useful for treating a disease or condition associated
PT   with the expression of hepsin, e.g. inflammation or tumor growth  -
XX
PS   Example 15; Page 82; 101pp; English.
XX
CC   The invention relates to an antisense compound 8-30 nucleobases in length
CC   targetted to a nucleic acid molecule encoding human hepsin. The antisense
CC   compound specifically hybridises with and inhibits the expression of
CC   human hepsin. The antisense compound or the pharmaceutical composition is
CC   useful for treating animals and humans having a disease or condition
CC   associated with the expression of hepsin, e.g. inflammation or tumour
CC   growth. The antisense compounds are useful also for diagnostics,
CC   prophylaxis (e.g. to prevent or delay infection, inflammation or tumour
CC   formation) or as research reagents and kits. The method is useful for
CC   modulating, specifically inhibiting the expression of hepsin which may be
CC   used in research, e.g to distinguish between functions of various members
CC   of a biological pathway. The invention is used in gene therapy. The
CC   present sequence is human hepsin antisense oligonucleotide.
XX
SQ   Sequence 20 BP; 3 A; 6 C; 10 G; 1 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        721 CAGCAGCAGGGGGCCTGG 738
              ||||||| || |||||||
Db          2 CAGCAGCGGGCGGCCTGG 19


RESULT 103
AAD40836
ID   AAD40836 standard; DNA; 20 BP.
XX
AC   AAD40836;
XX
DT   30-OCT-2002  (first entry)
XX
DE   Human hepsin antisense oligonucleotide, ISIS 107110.
XX
KW   Human; hepsin; antisense compound; antisense therapy; antisense;
KW   phosphorothioate backbone; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
FT   modified_base   1..5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16..20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   2
FT                   /*tag=  d
FT                   /mod_base= m5c
FT   modified_base   5
FT                   /*tag=  e
FT                   /mod_base= m5c
FT   modified_base   8
FT                   /*tag=  f
FT                   /mod_base= m5c
FT   modified_base   12
FT                   /*tag=  g
FT                   /mod_base= m5c
FT   modified_base   15
FT                   /*tag=  h
FT                   /mod_base= m5c
FT   modified_base   16
FT                   /*tag=  i
FT                   /mod_base= m5c
XX
PN   WO200250247-A2.
XX
PD   27-JUN-2002.
XX
PF   14-DEC-2001; 2001WO-US48341.
XX
PR   20-DEC-2000; 2000US-0742482.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM;
XX
DR   WPI; 2002-519882/55.
XX
PT   Novel antisense compound targeted to nucleic acids encoding human
PT   hepsin, useful for inhibiting the expression of hepsin in human cells
PT   or tissues, and for treating humans having a disease associated with
PT   human hepsin -
XX
PS   Example 15; Page 93; 100pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of hepsin. The compositions comprise
CC   antisense compounds, particularly antisense oligonucleotides, targetted
CC   to nucleic acids encoding hepsin. The antisense compound is useful for
CC   inhibiting the expression of hepsin in human cells or tissues. It is
CC   also useful for treating an animal having a disease or condition
CC   associated with hepsin, by inhibiting expression of hepsin. It is useful
CC   for diagnostics, therapeutics, prophylaxis and as research reagents and
CC   kits. It is also used in antisense therapy. The present sequence is an
CC   antisense oligonucleotide targetted to human hepsin DNA. This sequence
CC   is used in the exemplification of the invention.
XX
SQ   Sequence 20 BP; 3 A; 6 C; 10 G; 1 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        721 CAGCAGCAGGGGGCCTGG 738
              ||||||| || |||||||
Db          2 CAGCAGCGGGCGGCCTGG 19


RESULT 104
AAD41521/c
ID   AAD41521 standard; DNA; 20 BP.
XX
AC   AAD41521;
XX
DT   30-OCT-2002  (first entry)
XX
DE   Nrf2 gene specific forward RT-PCR primer.
XX
```

```
KW   Marker; vitamin D analogue; antiproliferative; cancer; osteodystrophy;
KW   multiple sclerosis; osteoporosis; osteomalacia; hyperparathyroidism;
KW   genoprotective; epidermal wound; chemoprotective; DNA repair mechanism;
KW   cytostatic; psoriasis; neuroprotective; vulnerary; RT-PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200244403-A2.
XX
PD   06-JUN-2002.
XX
PF   28-NOV-2001; 2001WO-CA01689.
XX
PR   29-NOV-2000; 2000US-253746P.
PR   02-MAY-2001; 2001US-287729P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   White JH;
XX
DR   WPI; 2002-537458/57.
XX
PT   Novel marker for testing analogs of vitamin D expected to be effective
PT   in reducing aberrant activity of vitamin D-responsive cell, comprises
PT   gene pertinent to action of vitamin D for testing the analogs -
XX
PS   Example 2; Page 48; 89pp; English.
XX
CC   The invention relates to a marker for testing analogues of vitamin D
CC   expected to be effective in reducing aberrant activity of vitamin D-
CC   responsive cell, comprises at least one gene pertinent to the action of
CC   vitamin D for testing the analogues and determining analogues capable of
CC   regulating the gene, and is indicative of a chemopreventive or
CC   chemotherapeutic agent. The invention is useful for testing analogues of
CC   vitamin D expected to be effective in reducing aberrant activity of
CC   vitamin D-responsive cell or for testing analogues of vitamin D suspected
CC   to have antiproliferative activity. The invention is useful for reducing
CC   aberrant activity of vitamin D-responsive cell, and for treating a
CC   disorder characterised by an aberrant activity of vitamin D-responsive
CC   cell, where the disorder is selected from cancer, psoriasis, multiple
CC   sclerosis, osteoporosis, osteodystrophy, osteomalacia and
CC   hyperparathyroidism. The invention is useful for identifying regulated
CC   target genes correlated with the antiproliferative effect of vitamin D
CC   and its analogues. The invention is useful for protecting against in vivo
CC   DNA damage, for inducing in vivo DNA repair mechanisms in a mammal, or
CC   for reducing or preventing DNA damage to the skin of a mammal, preferably
CC   human. The invention is useful as a genoprotective or chemoprotective
CC   agent. The invention is useful as a marker for the activity of DNA repair
CC   mechanisms. The invention is useful for testing compounds susceptible of
CC   inhibiting an enzyme which metabolises 1,25-dihydroxyvitamin D3. The
CC   invention is useful for treating epidermal wounds. The present sequence
CC   is Nrf2 gene specific RT-PCR primer.
XX
SQ   Sequence 20 BP; 4 A; 8 C; 3 G; 5 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1014 CCTGAGATGGTGCCAAAG 1031
              |||||||||||| ||| |
Db         20 CCTGAGATGGTGACAAGG 3


RESULT 105
AAD36447
ID   AAD36447 standard; DNA; 20 BP.
XX
AC   AAD36447;
XX
DT   09-AUG-2002  (first entry)
XX
DE   Mouse L66 intron 4/exon 5 junction sequence #4.
XX
KW   Mouse; nuclear receptor; L66 protein; FXR-beta; physiological response;
KW   drug screening; ds.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   intron          1..10
FT                   /*tag=  a
FT                   /number= 4
FT                   /partial
FT   exon            11..20
FT                   /*tag=  b
FT                   /number= 5
FT                   /partial
XX
PN   WO200222817-A2.
XX
PD   21-MAR-2002.
XX
PF   07-SEP-2001; 2001WO-EP10323.
XX
PR   16-SEP-2000; 2000EP-0120370.
PR   14-MAY-2001; 2001EP-0111658.
XX
PA   (LION-) LION BIOSCIENCE AG.
XX
PI   Casari G,  Hoefer M,  Jackson D,  Kranz H,  Otte K,  Remmel B;
PI   Suckow J;
XX
DR   WPI; 2002-393967/42.
XX
PT   Novel mammalian nuclear receptor polypeptide, L66, useful for screening
PT   for agents which inhibit cellular function of the polypeptide and for
PT   construction of multiple nuclear receptor specific sequence alignments
PT   -
XX
PS   Disclosure; Fig 18A; 136pp; English.
XX
CC   The present invention relates to mammalian nuclear receptor proteins, L66
CC   (also referred as FXR-beta) and polynucleotides encoding such proteins.
CC   Sequences of the are useful for screening for agents which are capable
CC   of inhibiting the cellular function of L66. They are useful for the
CC   construction of multiple nuclear receptor specific sequence alignments
CC   and for the construction of protein sequence alignments. L66 proteins
CC   are useful for screening drugs for agonist and antagonist activity,
CC   for developing antibodies for detection of L66, for screening for drugs
CC   useful in regulating physiological responses associated with L66, in
CC   cell-free screening assays for isolating compounds which affect the
CC   activity of L66, for in silico, i.e., computer analyses, for identifying
CC   domains and new receptors and for modelling the 3-dimensional structure
CC   of L66. L66 nucleic acid sequences are useful for making vectors, for
CC   determining L66 expression levels, for transforming cells, as scientific
CC   research tools for developing nucleic acid probes and primers and for
CC   developing analytical tools for selectively inhibiting expression of the
CC   L66 gene to determine physiological responses. The present DNA sequence
CC   is an intron 4/exon 5 junction sequence of mouse L66 gene.
XX
SQ   Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        622 AGGGACCAGCTCCAGGAG 639
              | |||||||||| ||||||
Db          2 ATGGACCAGCTGCAGGAG 19


RESULT 106
ABA05916
ID   ABA05916 standard; DNA; 20 BP.
XX
```

```
AC   ABA05916;
XX
DT   05-MAR-2002  (first entry)
XX
DE   Hepatitis B virus diagnostic PCR primer SEQ ID NO 6.
XX
KW   Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;
KW   PCR primer; ss.
XX
OS   Hepatitis B virus.
XX
PN   EP1152063-A1.
XX
PD   07-NOV-2001.
XX
PF   03-MAY-2000; 2000EP-0109436.
XX
PR   03-MAY-2000; 2000EP-0109436.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Schroeder KH,  Koike K;
XX
DR   WPI; 2002-068256/10.
XX
PT   Diagnosing hepatitis B virus (HBV) infection stages and determining the
PT   risk for hepatocellular carcinoma, comprises identifying full length
PT   HBV transcripts and truncated HBV transcripts in a serum sample  -
XX
PS   Example 1; Page 6; 25pp; English.
XX
CC   The invention relates to diagnosis of hepatitis B virus (HBV) infection
CC   stages comprising identification of full length HBV transcripts (I) and
CC   truncated HBV transcripts (II) in a serum sample, where the ratio of
CC   I:II is indicative of a particular infection stage. The method is useful
CC   for diagnosing HBV infection stages and determining the risk for
CC   developing hepatocellular carcinoma. The present sequence is that of a
CC   HBV diagnostic PCR primer, useful for the invention.
XX
SQ   Sequence 20 BP; 2 A; 1 C; 2 G; 15 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTGGAAG 1161
              ||||||| ||||| ||||
Db          2 TTTTTTTTTTTTTGAAG 19


RESULT 107
AAS16509/c
ID   AAS16509 standard; DNA; 20 BP.
XX
AC   AAS16509;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Human Type II GnRH-R antisense PCR primer.
XX
KW   Human; ss; type II gonadotrophin-releasing hormone receptor;
KW   GnRH-R; contraceptive; neural development; sexual arousal; gene therapy;
KW   transgenic animal; PCR primer.
XX
OS   Homo sapiens.
XX
PN   WO200178796-A1.
XX
PD   25-OCT-2001.
XX
PF   17-APR-2001; 2001WO-GB01755.
XX
PR   15-APR-2000; 2000GB-0009269.
PR   17-JUN-2000; 2000GB-0014761.
PR   30-JUN-2000; 2000US-215232P.
XX
PA   (MEDI-) MEDICAL RES COUNCIL.
XX
PI   Millar RP,  Lowe S,  Conklin D;
XX
DR   WPI; 2002-041317/05.
XX
PT   New polypeptide, useful in gene therapy, as contraceptive or for
PT   inhibiting endogenous Type II GnRH binding to its native receptor in
PT   vivo, comprises Type II gonadotropin-releasing hormone receptor and
PT   polynucleotides encoding receptor -
XX
PS   Example; Page 29; 92pp; English.
XX
CC   The invention relates to an isolated functional Type II
CC   gonadotropin-releasing hormone receptor (Type II GnRH-R), or a peptide
CC   comprising at least a portion of exon I of Type II GnRH-R, nucleic
CC   acids encoding the receptor, an expression vector comprising the nucleic
CC   acid, a host cell transformed with the vector, a transgenic animal having
CC   the construct stably integrated into its genome, an antibody able to bind
CC   specifically to Type II GnRH-R. The Type II GnRH-R is useful in gene
CC   therapy. The Type II GnRH-R is particularly useful for inhibiting
CC   endogenous Type II GnRH binding to its native receptor in vivo or as a
CC   contraceptive. The receptor may also have roles in neural development and
CC   sexual arousal. The present sequence is a PCR primer used to
CC   amplify a nucleic acid encoding human type II GnRH-R from tissue samples.
XX
SQ   Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       483 CTGCCGAGACGGTGTGCA 500
             ||||||||| |||| |||
Db        18 CTGCCGAGAAGGTGGGCA 1


RESULT 108
ABI93685/c
ID   ABI93685 standard; DNA; 20 BP.
XX
AC   ABI93685;
XX
DT   16-FEB-2002  (first entry)
XX
DE   Capture oligonucleptide Zip ID#772 oligo #9.
XX
KW   Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW   ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW   infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW   cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW   environmental monitoring; food industry; feed industry; ss.
XX
OS   Synthetic.
XX
PN   WO200179548-A2.
XX
PD   25-OCT-2001.
XX
PF   04-APR-2001; 2001WO-US10958.
XX
PR   14-APR-2000; 2000US-197271P.
XX
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Barany F,  Zirvi M,  Gerry NP,  Favis R,  Kliman R;
XX
DR   WPI; 2002-034366/04.
XX
PT   Designing capture oligonucleotide probes for use on a support to which
```

```
PT   complementary oligonucleotides hybridize with little mismatch -
XX
PS   Example 5; Fig 29; 300pp; English.
XX
CC   The present invention describes a method (M1) for designing capture
CC   oligonucleotide probes (I) for use on a support to which complementary
CC   oligonucleotide probes (II) will hybridise with little mismatch, where
CC   (I) have melting temperatures within a narrow range. The method is useful
CC   for detecting infectious diseases caused by bacterial infectious agents
CC   e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC   infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC   Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC   Epstein-Barr virus and polio virus, and parasitic infectious agents
CC   selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC   medinesis. The method is also useful for detecting genetic diseases such
CC   as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC   Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC   involved in DNA amplification, replication, recombination or repair, the
CC   cancer is specifically associated with a gene selected from BRCA1 gene,
CC   p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC   method is also used for environmental monitoring, forensics and the food
CC   and feed industry, detecting comprises scanning (using e.g. a scanning
CC   electron microscope and infrared microscope) the support at the
CC   particular sites and identifying if ligation of the oligonucleotide probe
CC   sets occurred and correlating (using a computer) identified ligation to a
CC   presence or absence of the target nucleotide sequences. ABI82074 to
CC   ABI97546 represent oligonucleotide sequences used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        161 GCTGATCCTCAAGGTCTC 178
              |||| |||||||||||  |
Db         20 GCTGGTCCTCAAGGTCGC 3


RESULT 109
ABT34167/c
ID   ABT34167 standard; DNA; 20 BP.
XX
AC   ABT34167;
XX
DT   12-JUN-2003  (first entry)
XX
DE   Human short heterodimer partner-1 expression oligo SEQ ID No 42.
XX
KW   Antiarteriosclerotic; cardiant; vasotropic; antiinfective; cytostatic;
KW   antiinflammatory; inhibitor; antisense gene therapy; atherosclerosis;
KW   short heterodimer partner-1; abnormal; lipid; cholesterol metabolism;
KW   cardiovascular disease; infection; inflammation; tumour formation; human;
KW   antisense; ds.
XX
OS   Unidentified.
XX
PN   WO2003012033-A2.
XX
PD   13-FEB-2003.
XX
PF   17-JUL-2002; 2002WO-US23245.
XX
PR   31-JUL-2001; 2001US-0919197.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248161/24.
XX
PT   New antisense oligonucleotide targeted to a nucleic acid encoding short
PT   heterodimer partner-1, useful for treating diseases involving abnormal
PT   lipid or cholesterol metabolism, e.g atherosclerosis or cardiovascular
PT   diseases -
XX
PS   Claim 3; Page 94; 121pp; English.
XX
CC   The invention relates to a novel compound of 8 - 50 nucleobases in length
CC   targeted to a nucleic acid molecule encoding a short heterodimer
CC   partner-1. The novel compound specifically hybridizes with a nucleic acid
CC   molecule encoding the short heterodimer partner-1, and inhibits the
CC   expression of the nucleic acid molecule. The compound, and a composition
CC   comprising it are useful for treating a disease or condition associated
CC   with the short heterodimer partner-1, particularly a condition involving
CC   abnormal lipid or cholesterol metabolism such as atherosclerosis or a
CC   cardiovascular disease. They are also useful in research and diagnostics
CC   for modulating the expression of short heterodimer partner-1. They can
CC   also be useful prophylactically in preventing or delaying infection,
CC   inflammation or tumour formation. This polynucleotide sequence represents
CC   a human antisense oligo relating to the heterodimer partner-1 of the
CC   invention.
XX
SQ   Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        560 TGCACACACTGCTCCAGC 577
              || |||||  |||||||||
Db         19 TGGACACAGTGCTCCAGC 2


RESULT 110
ABX78118/c
ID   ABX78118 standard; DNA; 20 BP.
XX
AC   ABX78118;
XX
DT   16-APR-2003  (first entry)
XX
DE   Human p38-beta MAPK oligonucleotide ISIS NO 17908.
XX
KW   p38 mitogen-activated protein kinase; p38 MAPK; phosphorothioate;
KW   antisense; antiarthritic; antiinflammatory; kinase inhibitor; human;
KW   inflammatory disease; rheumatoid arthritis; gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate backbone, nucleotides 1-6
FT                          and 15-20 are 2'-methoxyethoxy (MOE)
FT                          nucleotides, nucleotides 7-14 are 2'-deoxy-
FT                          nucleotides, all C nucleotides are 5-methyl
FT                          cytosines"
XX
PN   US6448079-B1.
XX
PD   10-SEP-2002.
XX
PF   15-AUG-2000; 2000US-0640101.
XX
PR   06-APR-1999;   99US-0286904.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Gaarde WA,  Nero P,  McKay R;
XX
DR   WPI; 2003-089122/08.
XX
PT   New antisense compound, useful for preparing a composition for
```

```
PT   diagnosing, treating or preventing inflammatory diseases, e.g.
PT   rheumatoid arthritis -
XX
PS   Example 3; Column 23-24; 44pp; English.
XX
CC   This invention describes a novel antisense compound, which is 8-30
CC   nucleobases in length targeted to a nucleic acid molecule encoding
CC   p38 mitogen-activated protein kinase (MAPK). The products of the
CC   invention have antiarthritic and antiinflammatory activity, can act
CC   as act as kinase inhibitors. The antisense compound is useful for
CC   preparing a composition for diagnosing, treating or preventing
CC   inflammatory diseases, e.g. rheumatoid arthritis or for use in
CC   antisense gene therapy. This sequence represents an antisense
CC   oligonucleotide used in a method to inhibit p38 MAPK.
XX
SQ   Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1287 TACAGTTGCTCAGCCTGG 1304
              || || ||||||||||||
Db         19 TAGAGCTGCTCAGCCTGG 2


RESULT 111
AAQ75627
ID   AAQ75627 standard; DNA; 21 BP.
XX
AC   AAQ75627;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-0112515.
XX
PR   16-APR-1993;   93JP-0112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA
PT   followed by digestion with restriction enzymes
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an
CC   aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC   and a plural type of labelled reverse transcription primers
CC   (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC   template for each reverse transcription primer; (b) digesting each of
CC   the prepared aggregates of the double-stranded cDNAs with restriction
CC   enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC   seperate lanes. The method can be used to analyse gene expression
CC   rapidly and easily.
XX
SQ   Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTGGAAG 1161
              ||||||| ||||| ||||
Db          4 TTTTTTTTTTTTTTGAAG 21


RESULT 112
AAV81770
ID   AAV81770 standard; DNA; 21 BP.
XX
AC   AAV81770;
XX
DT   10-MAR-1999  (first entry)
XX
DE   Human SAD PCR primer 6644.
XX
KW   PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;
KW   type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;
KW   neurodegenerative disease; neuronal survival; Alzheimer's disease;
KW   Parkinson's disease; Huntington's disease; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9849317-A2.
XX
PD   05-NOV-1998.
XX
PF   27-APR-1998;   98WO-US08439.
XX
PR   23-OCT-1997;   97US-0063595.
PR   28-APR-1997;   97US-0044428.
PR   20-MAY-1997;   97US-0047222.
PR   11-JUN-1997;   97US-0049477.
PR   11-JUN-1997;   97US-0049756.
PR   18-JUN-1997;   97US-0049914.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   App H,  Clary D,  Courtneidge SA,  Hui TH,  Jallal B;
PI   Markby D,  Onrust S,  Peles E,  Plowman GD;
XX
DR   WPI; 1999-009434/01.
XX
PT   New nucleic acid encoding specific protein tyrosine phosphatases -
PT   useful for identifying specific modulators for treatment and
PT   prevention of cancer and neurodegenerative disease
XX
PS   Example 6; Page 88; 193pp; English.
XX
CC   The present invention describes isolated, enriched or purified nucleic
CC   acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The
CC   above proteins, other than ALK-7, are protein tyrosine phosphatases
CC   (PTPs) and are used to identify substances that modulate their activity
CC   (i.e. agonists and antagonists, including NBP) in vivo or in vitro.
CC   These substances are used to treat or prevent diseases associated with
CC   abnormal signal transduction pathways that involve the proteins,
CC   particularly cancer (e.g. leukaemia and lymphoma), while modulators of
CC   ALK-7 (which is a type I receptor serine/threonine kinase) are used to
CC   promote neuronal survival, particularly for treating Alzheimer's,
CC   Parkinson's or Huntington's diseases. Nucleic acid fragments of the
CC   polynucleotides encoding the proteins can be used as probes to identify
CC   and clone related sequences; to detect protein-encoded RNA; to generate
CC   transgenic animals and in gene therapy (optionally after mutation). Ab
CC   are used to determine the proteins. The present sequence represents a
CC   PCR primer for human SAD.
XX
SQ   Sequence 21 BP; 4 A; 10 C; 3 G; 4 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy        374 CCCAGCTTCCTCCAGAGG 391
              ||||||||||||  |||
Db          4 CCCAGCTTCCTCCCAAGG 21


RESULT 113
AAA59547/c
ID   AAA59547 standard; DNA; 21 BP.
XX
AC   AAA59547;
XX
DT   14-NOV-2000  (first entry)
XX
DE   PCR primer used to amplify DNA encoding beta-secretase enzyme.
XX
KW   Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
KW   amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
KW   inhibitor; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200047618-A2.
XX
PD   17-AUG-2000.
XX
PF   10-FEB-2000; 2000WO-US03819.
XX
PR   10-FEB-1999;   99US-0119571.
PR   15-JUN-1999;   99US-0139172.
XX
PA   (ELAN-) ELAN PHARM INC.
XX
PI   Anderson JP,  Basi G,  Doane MT,  Frigon N,  John V,  Power M;
PI   Sinha S,  Tatsuno G,  Tung J,  Wang S,  McConlogue L;
XX
DR   WPI; 2000-533011/48.
XX
PT   Purified beta-secretase protein used in assays to discover inhibitors
PT   which can be used for the treatment of amyloidogenic diseases e.g.
PT   Alzheimer's disease -
XX
PS   Example 3; Page 66; 121pp; English.
XX
CC   The specification describes a beta-secretase enzyme. The enzyme cleaves
CC   beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC   enzyme is therefore implicated in the production of amyloid plaque
CC   components which accumulate in the brains of individuals afflicted with
CC   Alzheimer's disease. Inhibitors of beta-secretase are administered to
CC   a mammalian subject e.g. with Alzheimer's disease or Alzheimer's
CC   disease-like pathology to test if they maintain or improve cognitive
CC   ability or reduce the plaque burden. The compounds are used for the
CC   treatment of amyloidogenic diseases e.g. Alzheimer's disease. PCR
CC   primers AAA59530-49 were used to amplify DNA encoding beta-secretase
CC   enzyme.
XX
SQ   Sequence 21 BP; 3 A; 9 C; 7 G; 2 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        522 CCTGCCGGAGGAGCAGCT 539
              || |||||||| ||||||
Db         20 CCGGCCGGAGGGGCAGCT 3


RESULT 114
AAZ45243/c
ID   AAZ45243 standard; DNA; 21 BP.
XX
AC   AAZ45243;
XX
DT   27-MAR-2000  (first entry)
XX
DE   Reverse PCR primer for angiogenesis-associated protein cDNA.
XX
KW   Human; angiogenesis-associated protein; plasminogen; ABP-1;
KW   kringle domain; angiostatin; plasminogen receptor;
KW   angiogenesis-related disease; tumor; diabetes; rheumatoid arthritis;
KW   inflammatory disease; psoriasis; chronic inflammation; intestine;
KW   asthma; obesity; gene therapy; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9966038-A1.
XX
PD   23-DEC-1999.
XX
PF   11-JUN-1999;   99WO-EP04109.
XX
PR   15-JUN-1998;   98SE-0002130.
PR   15-JUN-1998;   98US-0089266.
PR   17-DEC-1998;   98SE-0004372.
PR   29-DEC-1998;   98US-0114386.
XX
PA   (PHAA ) PHARMACIA & UPJOHN AB.
XX
PI   Holmgren L,  Troyanovsky B;
XX
DR   WPI; 2000-106099/09.
XX
PT   Novel human protein useful for treating angiogenesis associated
PT   diseases or disorders -
XX
PS   Disclosure; Page 18; 58pp; English.
XX
CC   PCR primers AAZ45242-43 were used to amplify cDNA encoding a human
CC   angiogenesis-associated protein which is able to bind an N-terminal
CC   fragment of plasminogen. The protein is designated ABP-1, and binds
CC   the first 4 kringle domains (K1-K4) and/or kringle 5 (K5) of
CC   plasminogen. These four kringle domains comprise angiostatin. The
CC   protein acts as a receptor for plasminogen. The angiostatin-binding
CC   domain of the ABP-1 protein is described in AAY54054. A polymorphic
CC   variant of ABP-1 is also described, in AAY54053. ABP-1 can be used to
CC   manufacture medicaments for treating angiogenesis-related diseases or
CC   disorders, such as tumor conditions, diabetes, rheumatoid arthritis,
CC   and even some inflammatory diseases such as psoriasis, chronic
CC   inflammation of the intestine, asthma, etc.. The protein may also be
CC   able to treat and cure, or prevent, obesity. The ABP-1 DNA can be
CC   used in gene therapy techniques.
XX
SQ   Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        984 AGTCCCATTCAGATCCGG 1001
              | ||||||||||||||| |
Db         20 ACTCCCATTCAGATCCTG 3


RESULT 115
AAI70244/c
ID   AAI70244 standard; DNA; 21 BP.
XX
AC   AAI70244;
XX
DT   07-JAN-2002  (first entry)
XX
DE   Interleukin-1 receptor antagonist related protein primer 2351-48.
XX
KW   Interleukin-1 receptor antagonist related protein; IL-1ra-R; human;
KW   inhibitor; antiarthritic; antirheumatic; osteopathic;
KW   antiinflammatory; neuroprotective; antidiabetic; immunosuppressive;
```

KW antileprotic; antibacterial; tuberculostatic; anorectic; metabolic;
KW antiviral; hyperglycaemic; nootropic; antiparkinsonian;
KW antidepressant; anticonvulsive; tranquillizer; vulnerary;
KW antiasthmatic; antipsoriatic; dermatological; cytostatic;
KW nephrotropic; antihaemorrhagic; vasotropic; cardiant;
KW antiatherosclerotic; antiinfertility; ophthalmological;
KW gene therapy; diagnosis; PCR primer; RACE; ss.
XX
OS Homo sapiens.
XX
PN WO200142304-A1.
XX
PD 14-JUN-2001.
XX
PF 04-DEC-2000; 2000WO-US32940.
XX
PR 10-DEC-1999; 99US-170191P.
PR 09-MAR-2000; 2000US-188053P.
PR 04-APR-2000; 2000US-194521P.
PR 10-APR-2000; 2000US-195910P.
PR 28-NOV-2000; 2000US-0170191.
XX
PA (AMGE-) AMGEN INC.
XX
PI Saris CM, Giles J, Mu SX, Xia M, Bass MB, Craveiro R;
XX
DR WPI; 2001-648140/74.
XX
PT Novel interleukin-1 receptor antagonist-related polypeptide, its
PT fragment, variant useful for treating rheumatoid arthritis, septicemia,
PT Parkinson's disease, epilepsy, cystic fibrosis, Paget's disease,
PT uveitis, eczema -
XX
PS Example 1; Page 104; 163pp; English.
XX
CC The present sequence is that of PCR primer 2351-48. The primer
CC was used in a 3'RACE, using a human foetal scalp cDNA library as
CC template, to obtain the 3' sequence of human interleukin-1 receptor
CC antagonist-related protein (IL-1ra-R) cDNA. Full-length clones
CC (see AAI70234-35) encoding human IL-1ra-R (see AAM50217-18), a
CC protein that has interleukin-1 inhibitor activity, were
CC subsequently obtained. The invention provides IL-1ra-R polypeptides
CC and nucleic acids, as well as selective binding agents, vectors,
CC host cells and methods for producing the IL-1ra-R polypeptides. It
CC also provides pharmaceutical compositions and methods for the
CC diagnosis, treatment, amelioration and/or prevention of diseases,
CC disorders and conditions associated with IL-1ra-R, such as those
CC involving immune system dysfunction, infection, weight disorders,
CC neuronal dysfunction, lung, skin, kidney, bone, vascular system,
CC tumour cells, reproductive system, and eye.
XX
SQ Sequence 21 BP; 2 A; 6 C; 7 G; 6 T; 0 other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy        597 CACCAGCCTGAAGCCTGA 614
              || |||||| ||||||||
Db         21 CAGCAGCCTCAAGCCTGA 4
```

RESULT 116
AAD19825
ID AAD19825 standard; DNA; 21 BP.
XX
AC AAD19825;
XX
DT 18-DEC-2001 (first entry)
XX
DE CmYLCV CmpC promoter variant constructing CmpMr reverse PCR primer.
XX
KW Cestrum yellow leaf curling virus; CmYLCV; transcription; PCR primer;
KW transgenic plant; CmpC promoter; ss.
XX
OS Cestrum yellow leaf curling virus.
XX
PN WO200173087-A1.
XX
PD 04-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-EP03408.
XX
PR 27-MAR-2000; 2000GB-0007427.
PR 28-APR-2000; 2000GB-0010486.
PR 26-JAN-2001; 2001EP-0101802.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Hohn T, Stavolone L, De Haan PT, Ligon HT, Kononova M;
XX
DR WPI; 2001-616524/71.
XX
PT Novel DNA sequence obtained from genome of Cestrum yellow leaf curling
PT virus for conferring constitutive expression of an associated desired
PT polynucleotide -
XX
PS Example 17; Page 34; 100pp; English.
XX
CC The invention relates to Cestrum yellow leaf curling virus (CmYLCV) novel
CC DNA sequences which functions as transcription promoters of an associated
CC polynucleotide sequence. These CmYLCV DNA molecules confers constitutive
CC expression of associated polynucleotide sequences. The invention also
CC relates to recombinant DNA sequences containing promoter sequences which
CC are used for creating transgenic plants expressing DNA of interest at all
CC times and in most tissues and organs. The present DNA sequence is a PCR
CC primer which is used for amplifying cestrum yellow leaf curling virus
CC CmpC promoter variant DNA.
XX
SQ Sequence 21 BP; 3 A; 3 C; 6 G; 9 T; 0 other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy        674 CCAGCGTGGTATTTGGGA 691
              ||| |||||||||||| |
Db          1 CCATCGTGGTATTTGGTA 18
```

RESULT 117
AAD19826/c
ID AAD19826 standard; DNA; 21 BP.
XX
AC AAD19826;
XX
DT 18-DEC-2001 (first entry)
XX
DE CmYLCV CmpC promoter variant constructing CmpMf forward PCR primer.
XX
KW Cestrum yellow leaf curling virus; CmYLCV; transcription; PCR primer;
KW transgenic plant; CmpC promoter; ss.
XX
OS Cestrum yellow leaf curling virus.
XX
PN WO200173087-A1.
XX
PD 04-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-EP03408.
XX
PR 27-MAR-2000; 2000GB-0007427.
PR 28-APR-2000; 2000GB-0010486.
PR 26-JAN-2001; 2001EP-0101802.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX
PI Hohn T, Stavolone L, De Haan PT, Ligon HT, Kononova M;
XX
DR WPI; 2001-616524/71.
XX
PT Novel DNA sequence obtained from genome of Cestrum yellow leaf curling
PT virus for conferring constitutive expression of an associated desired
PT polynucleotide -
XX
PS Example 17; Page 34; 100pp; English.
XX
CC The invention relates to Cestrum yellow leaf curling virus (CmYLCV) novel
CC DNA sequences which functions as transcription promoters of an associated
CC polynucleotide sequence. These CmYLCV DNA molecules confers constitutive
CC expression of associated polynucleotide sequences. The invention also
CC relates to recombinant DNA sequences containing promoter sequences which
CC are used for creating transgenic plants expressing DNA of interest at all
CC times and in most tissues and organs. The present DNA sequence is a PCR
CC primer which is used for amplifying cestrum yellow leaf curling virus
CC CmpC promoter variant DNA.
XX
SQ Sequence 21 BP; 9 A; 6 C; 3 G; 3 T; 0 other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 674 CCAGCGTGGTATTTGGGA 691
||| |||||||||||| |
Db 21 CCATCGTGGTATTTGGTA 4

RESULT 118
AAF85557/c
ID AAF85557 standard; DNA; 21 BP.
XX
AC AAF85557;
XX
DT 13-JUN-2001 (first entry)
XX
DE Human hNDS4-isoform related PCR primer SEQ ID NO: 4.
XX
KW Human; hNDS4 isoform; NADH dehydrogenase subunit 4; PCR primer; ss.
XX
OS Unidentified.
XX
PN CN1278001-A.
XX
PD 27-DEC-2000.
XX
PF 30-MAY-2000; 2000CN-0116224.
XX
PR 30-MAY-2000; 2000CN-0116224.
XX
PA (SCHR-) SOUTH CHINA RES CENT CHINA HUMAN GENE GR.
XX
PI Xu Z, Xiao H, Kang B;
XX
DR WPI; 2001-245681/26.
XX
PT Human dehydrogenase subunit protein isomer and its coding sequence -
XX
PS Example 1; Page 17; 20pp; Chinese.
XX
CC The present invention relates to a new human NADH dehydrogenase subunit
CC 4 (NDS4) isoform expressed in human body dendron-shaped cell and its
CC coding sequence. The present invention also relates to a preparation
CC method of said protein and nucleic acid sequence and a method of
CC detecting polypeptide of human NDS4-iso nucleic acid sequence in sample.
XX
SQ Sequence 21 BP; 4 A; 10 C; 1 G; 6 T; 0 other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 936 GGAGAAGAGGTGTGAGCG 953
||| | ||||||||||||
Db 19 GGATATGAGGTGTGAGCG 2

RESULT 119
ABK15655
ID ABK15655 standard; DNA; 21 BP.
XX
AC ABK15655;
XX
DT 21-MAY-2002 (first entry)
XX
DE Anchored oligo-dt reverse primer.
XX
KW ss; lipoxygenase; RCI-1; transgenic; plant; plant antifungal;
KW rice chemically induced cDNA; promoter; transit peptide; plastid;
KW fungal mycotoxin inhibitor; plant breeding; PCR; primer.
XX
OS Synthetic.
XX
PN WO200206490-A1.
XX
PD 24-JAN-2002.
XX
PF 12-JUL-2001; 2001WO-EP08085.
XX
PR 13-JUL-2000; 2000GB-0017275.
PR 15-SEP-2000; 2000GB-0022739.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (UYZU-) UNIV ZUERICH.
XX
PI Dudler R, Schaffrath , Lawton KA;
XX
DR WPI; 2002-188550/24.
XX
PT Novel isolated nucleic acid encoding a promoter which is capable of
PT driving chemically inducible but not wound- or pathogen-inducible
PT expression of an associated nucleotide sequence -
XX
PS Example 3; Page 30; 88pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (a promoter of
CC rice chemically induced cDNA (RCI-1), which encodes a lipoxygenase)
CC capable of driving chemically-inducible but not wound- or pathogen-
CC inducible expression of an associated nucleotide sequence. Also
CC included are the RCI-1 cDNA, its encoded protein, a 4.5kb genomic clone
CC for the lipoxygenase gene, promoter fragments, the lipoxygenase transit
CC peptide which directs expressed proteins to the plastid, a vector
CC comprising the promoter or fragments and a transgenic plant comprising
CC the vector. The promoter or fragments are useful for expressing a
CC nucleotide sequence of interest. The transit peptide is useful for
CC targeting an associated protein of interest to plastids. A nucleic acid
CC which expresses polypeptide having lipoxygenase activity is useful for
CC inhibiting fungal mycotoxins when transformed into a plant. The
CC lipoxygenase is useful for inhibiting fungal mycotoxins. The promoter is
CC useful for regulating transcription of a chemically inducible but not
CC wound or pathogen inducible gene, which involves applying a chemical
CC regulator to a plant or seed containing a chemically regulatable
CC nucleotide sequence. Transgenic plants as described above are useful for
CC breeding improved plant lines that for example increase the effectiveness
CC of conventional methods such as herbicide or pesticide treatment or allow
CC to dispense with the methods due to their modified genetic properties.
CC New crops with improved stress tolerance can be obtained that, due to
CC their optimised genetic equipment yield harvested product of better
CC quality than products that were not able to tolerate comparable adverse
CC developmental conditions. The present sequence is an anchored oligo-dt
CC reverse RT-PCR primer (reverse transcriptase PCR) used to isolate the
CC cDNA encoding rice lipoxygenase.

```
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 16 T; 1 other;

  Query Match             1.1%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 1.5e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1139 ATGCCTTTTTTTCTTTTT 1156
              |||| ||||||| |||||
Db          2 ATGCTTTTTTTTTTTTTT 19


RESULT 120
AAQ51986
ID   AAQ51986 standard; RNA; 17 BP.
XX
AC   AAQ51986;
XX
DT   25-MAR-2003  (updated)
DT   26-MAY-1994  (first entry)
XX
DE   B-cell mRNA ribozyme cleavable nucleotide 844.
XX
KW   Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
KW   resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
KW   actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
KW   adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
KW   human; chronic myelogenous leukemia; CML; follicular lymphoma;
KW   B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
KW   neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
KW   hairpin; hepatitis delta virus; group I intron; RNaseP; ss.
XX
OS   Homo sapiens.
XX
PN   WO9323057-A1.
XX
PD   25-NOV-1993.
XX
PF   13-MAY-1993;   93WO-US04573.
XX
PR   14-MAY-1992;   92US-0882822.
PR   14-MAY-1992;   92US-0882885.
PR   26-AUG-1992;   92US-0936110.
PR   26-AUG-1992;   92US-0936421.
PR   26-AUG-1992;   92US-0936422.
PR   26-AUG-1992;   92US-0936531.
PR   26-AUG-1992;   92US-0936532.
PR   07-DEC-1992;   92US-0987131.
PR   19-JAN-1993;   93US-0006122.
PR   19-JAN-1993;   93US-0008910.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Draper KG,  Thompson JD;
XX
DR   WPI; 1993-386203/48.
XX
PT   New enzymatic RNA molecules (ribozymes) - which cleave mRNA
PT   associated with tumours or mRNA expressed from gene encoding
PT   multiple drug resistance
XX
PS   Claim 3; Fig 7; 69pp; English.
XX
CC   The sequences given in AAQ51825-2266 represent areas of mRNAs which are
CC   associated with development or maintenance of chronic myelogenous
CC   leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or
CC   acute lymphocytic leukemia, follicular lymphoma, B-cell acute
CC   lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma
CC   and lung cancer.  The full length mRNAs containing these target
CC   sequences, encode aberant cellular proteins which are able to control
CC   cellular proliferation and are directly linked to a leukemic
CC   phenotype.  These target sequences are identified by the ribozyme of
CC   the invention.  The ribozymes is formed in a hammerhead motif, but may
CC   also be formed in the motif of a hairpin, hepatitis delta virus, group
CC   I intron or RNaseP-like RNA.  These ribozymes may be used to inhibit
CC   the development or expression of a transformed phenotype in man and
CC   other animals by modulating expression of the corresponding gene.
CC   Cleavage of target mRNAs expressed in pre-neoplastic and transformed
CC   cells elicits inhibition of the transformed state.  Multiple drug
CC   resistance (mdr-1) mRNA specific ribozymes remove the mechanism of
CC   drug resistance used by transformed cells and thus enhances drug
CC   therapies for tumours.  The ribozymes may also be used to study
CC   genetic drift and mutations within cells.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 17 BP; 6 A; 4 C; 6 G; 1 U; 0 other;

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.4e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        279 AGAGGAAGCAGCAGCA 294
              || |||||||||||||
Db          1 AGUGGAAGCAGCAGCA 16


RESULT 121
AAA21347
ID   AAA21347 standard; RNA; 17 BP.
XX
AC   AAA21347;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Integrin alpha 6 subunit substrate sequence SEQ ID NO:4573.
XX
KW   Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW   integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW   hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
KW   ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW   dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW   age related macular degeneration; inflammation; neovascular glaucoma;
KW   myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW   tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW   Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS   Homo sapiens.
XX
PN   WO9950403-A2.
XX
PD   07-OCT-1999.
XX
PF   24-MAR-1999;   99WO-US06507.
XX
PR   27-MAR-1998;   98US-0079678.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Pavco PA,  Roberts E,  Jarvis T,  Coeshott C,  McSwiggen JA;
XX
DR   WPI; 1999-591315/50.
XX
PT   Novel ribozymes for modulating the synthesis, expression and/or
PT   stability of an mRNA encoding an angiogenic factors  -
XX
PS   Claim 55; Page 202; 305pp; English.
XX
CC   The present invention describes enzymatic nucleic acid molecules with
CC   RNA cleaving activity, which specifically cleave RNA encoded by an aryl
CC   hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC   gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC   AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC   and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC   corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC   AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC   and AAA19155 to AAA19222 represent their corresponding target sequences;
```

CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3.
XX
SQ Sequence 17 BP; 0 A; 2 C; 3 G; 12 U; 0 other;

Query Match 1.1%; Score 14.4; DB 1; Length 17;
Best Local Similarity 18.8%; Pred. No. 1.4e+02;
Matches 3; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 1141 GCCTTTTTTTCTTTTT 1156
| |:::::::|:::::
Db 2 GGCUUUUUUUCUUUUU 17

RESULT 122
AAA21348
ID AAA21348 standard; RNA; 17 BP.
XX
AC AAA21348;
XX
DT 19-JUN-2000 (first entry)
XX
DE Integrin alpha 6 subunit substrate sequence SEQ ID NO:4574.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
PN WO9950403-A2.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US06507.
XX
PR 27-MAR-1998; 98US-0079678.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
XX
DR WPI; 1999-591315/50.
XX
PT Novel ribozymes for modulating the synthesis, expression and/or
PT stability of an mRNA encoding an angiogenic factors -
XX
PS Claim 55; Page 202; 305pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules with
CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3.
XX
SQ Sequence 17 BP; 0 A; 3 C; 2 G; 12 U; 0 other;

Query Match 1.1%; Score 14.4; DB 1; Length 17;
Best Local Similarity 18.8%; Pred. No. 1.4e+02;
Matches 3; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 1141 GCCTTTTTTTCTTTTT 1156
| |:::::::|:::::
Db 1 GGCUUUUUUUCUUUUU 16

RESULT 123
AAA25575/c
ID AAA25575 standard; DNA; 17 BP.
XX
AC AAA25575;
XX
DT 19-JUL-2000 (first entry)
XX
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2073.
XX
KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9954459-A2.
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-US08547.
XX
PR 20-APR-1998; 98US-0082404.
PR 23-JUN-1998; 98US-0103636.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;
PI Matulic-Adamic J;
XX
DR WPI; 2000-013248/01.
XX
PT New nucleic acids that interact, and optionally cleave, target
PT sequences, used to treat cancer -
XX
PS Claim 77; Page 83; 148pp; English.
XX
CC The present invention describes nucleic acids (A) that interact stably

CC with a target sequence and contain at least one phosphoro(di)thioate
CC link, having endonuclease activity. (A), and more generally any
CC catalytic nucleic acid (A') that modulates expression of the oestrogen
CC receptor gene, are used to treat cancer (particularly of breast or
CC endometrium), in vivo or by transforming cells ex vivo and implanting
CC treated cells, or for other conditions associated with levels of
CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
CC can also be used to correlate inhibition of gene expression with
CC alterations in phenotype, particularly for identification of therapeutic
CC targets, and as research reagents (for RNA, in the same way that
CC restriction endonucleases are used with DNA). The combination of
CC modifications in (A) improves resistance to nucleases, binding affinity
CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
CC their corresponding target sequences. AAA26219 to AAA26271 represent
CC other ribozyme sequences and antisense oligonucleotides used in the
CC exemplification of the present invention.
XX
SQ Sequence 17 BP; 4 A; 3 C; 2 G; 8 T; 0 other;

Query Match 1.1%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 69 CACATAGGATGAATAA 84
||||| ||||||||||
Db 16 CACATTGGATGAATAA 1

RESULT 124
ACA07666
ID ACA07666 standard; RNA; 17 BP.
XX
AC ACA07666;
XX
DT 03-JUN-2003 (first entry)
XX
DE NFKB sub-unit modulating zinzyme substrate #65.
XX
KW Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW allergic airway inflammation; inflammatory bowel disease; infection;
KW ss.
XX
OS Homo sapiens.
XX
PN US2002177568-A1.
XX
PD 28-NOV-2002.
XX
PF 23-MAY-2001; 2001US-0864785.
XX
PR 15-AUG-1994; 94US-0291932.
PR 07-DEC-1992; 92US-0987132.
PR 18-MAY-1994; 94US-0245466.
PR 23-DEC-1996; 96US-0777916.
XX
PA (STIN/) STINCHCOMB D T.
PA (MCSW/) MCSWIGGEN J.
PA (DRAP/) DRAPER K G.
XX
PI Stinchcomb DT, Mcswiggen J, Draper KG;
XX
DR WPI; 2003-340953/32.
XX
PT Novel enzymatic nucleic acid molecules which down regulates expression
PT of a sequence encoding a subunit of nuclear factor kappa B useful for
PT treating cancer, inflammatory disorders and autoimmune diseases -
XX
PS Claim 3; Page 38; 72pp; English.
XX
CC The invention describes an enzymatic nucleic acid molecule (I) which down
CC regulates expression of a sequence encoding a subunit of nuclear factor
CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC configuration. The enzymatic nucleic acid molecule is adapted to treat
CC cancer and is useful for down-regulating REL-A activity in a cell, for
CC treating a patient having a condition associated with the level of REL-A.
CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
CC the presence of a divalent cation, especially Mg^2^+. The enzymatic and
CC antisense nucleic acid molecules are useful for treating breast, lung,
CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC multidrug resistant cancer. The method involves use of other drug
CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
CC acid molecules are also useful for treating inflammatory disease such as
CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
CC rejection, gene therapy applications, ischaemia/reperfusion injury
CC (central nervous system (CNS) and myocardial), glomerulonephritis,
CC sepsis, allergic airway inflammation, inflammatory bowel disease or
CC infection. This sequence represents the substrate of a novel
CC enzymatic nucleic acid molecule.
XX
SQ Sequence 17 BP; 3 A; 9 C; 4 G; 1 U; 0 other;

Query Match 1.1%; Score 14.4; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1066 CCCATCAGGCAGGCTC 1081
||||:||||||||| |
Db 1 CCCAUCAGGCAGGCCC 16

RESULT 125
ACA08919
ID ACA08919 standard; RNA; 17 BP.
XX
AC ACA08919;
XX
DT 03-JUN-2003 (first entry)
XX
DE NFKB sub-unit modulating amberzyme substrate #82.
XX
KW Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW allergic airway inflammation; inflammatory bowel disease; infection;
KW ss.
XX
OS Homo sapiens.
XX

PN US2002177568-A1.
XX
PD 28-NOV-2002.
XX
PF 23-MAY-2001; 2001US-0864785.
XX
PR 15-AUG-1994; 94US-0291932.
PR 07-DEC-1992; 92US-0987132.
PR 18-MAY-1994; 94US-0245466.
PR 23-DEC-1996; 96US-0777916.
XX
PA (STIN/) STINCHCOMB D T.
PA (MCSW/) MCSWIGGEN J.
PA (DRAP/) DRAPER K G.
XX
PI Stinchcomb DT, Mcswiggen J, Draper KG;
XX
DR WPI; 2003-340953/32.
XX
PT Novel enzymatic nucleic acid molecules which down regulates expression
PT of a sequence encoding a subunit of nuclear factor kappa B useful for
PT treating cancer, inflammatory disorders and autoimmune diseases -
XX
PS Claim 3; Page 51; 72pp; English.
XX
CC The invention describes an enzymatic nucleic acid molecule (I) which down
CC regulates expression of a sequence encoding a subunit of nuclear factor
CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC configuration. The enzymatic nucleic acid molecule is adapted to treat
CC cancer and is useful for down-regulating REL-A activity in a cell, for
CC treating a patient having a condition associated with the level of REL-A.
CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
CC the presence of a divalent cation, especially Mg^2^+. The enzymatic and
CC antisense nucleic acid molecules are useful for treating breast, lung,
CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC multidrug resistant cancer. The method involves use of other drug
CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
CC acid molecules are also useful for treating inflammatory disease such as
CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
CC rejection, gene therapy applications, ischaemia/reperfusion injury
CC (central nervous system (CNS) and myocardial), glomerulonephritis,
CC sepsis, allergic airway inflammation, inflammatory bowel disease or
CC infection. This sequence represents the substrate of a novel
CC enzymatic nucleic acid molecule.
XX
SQ Sequence 17 BP; 4 A; 8 C; 4 G; 1 U; 0 other;

Query Match 1.1%; Score 14.4; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1066 CCCATCAGGCAGGCTC 1081
||||:||||||||| |
Db 2 CCCAUCAGGCAGGCCC 17

RESULT 126
AAA52540/c
ID AAA52540 standard; DNA; 18 BP.
XX
AC AAA52540;
XX
DT 25-SEP-2000 (first entry)
XX
DE Human MN promoter fragment PR3 (-102/-85).
XX
KW MN protein; tumour associated cell adhesion molecule; oncoprotein;
KW proteoglycan domain; PG domain; carbonic anhydrase; CA domain;
KW abnormal expression; neoplastic disease; cancer; gene therapy;
KW promoter; ds.
XX
OS Homo sapiens.
XX
PN WO200024913-A2.
XX
PD 04-MAY-2000.
XX
PF 22-OCT-1999; 99WO-US24879.
XX
PR 23-OCT-1998; 98US-0177776.
PR 23-OCT-1998; 98US-0178115.
XX
PA (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
XX
PI Zavada J, Pastorekova S, Pastorek J;
XX
DR WPI; 2000-350752/30.
XX
PT A molecule which specifically binds to a site on MN protein
PT (oncoprotein) and prevents adhesion of vertebrate cells to the protein,
PT useful for treating preneoplastic or neoplastic diseases such as cancer
PT -
XX
PS Disclosure; Page 148; 154pp; English.
XX
CC The invention relates to the inhibition of cell adhesion mediated by
CC the MN oncoprotein (also known as the MN/CA IX isoenzyme or the MN/G250
CC protein). The MN protein is a tumour-associated adhesion molecule which
CC comprises a proteoglycan-like (PG) domain (AAB03017) which contains the
CC protein's binding site, and a carbonic anhydrase (CA) domain (AAB03018).
CC Abnormal expression of the MN protein is associated with tumorigenicity.
CC The invention encompasses molecules (e.g., proteins and peptides) which
CC which specifically bind to a site on the MN protein, thereby preventing
CC adhesion of vertebrate cells to the protein in a cell adhesion assay. It
CC also encompasses MN proteins or MN protein fragments which can be added
CC to the extracellular environment to prevent the adhesion of vertebrate
CC cells to each other. The invention also relates to the identification of
CC the binding site of the MN protein and to a method of identifying a site
CC on an MN protein to which cells adhere, comprising testing a series of
CC overlapping peptides from the protein in a cell adhesion assay. The
CC invention encompasses a vector comprising an expression control sequence
CC operatively linked to a nucleic acid encoding the variable domains of a
CC MN-specific antibody, where the domains are separated by a flexible
CC linker peptide (AAB03035) and the vector inhibits the growth of a
CC vertebrate preneoplastic or neoplastic cell that abnormally expresses MN
CC protein. The invention also encompasses a vector comprising a
CC nucleic acid encoding a cytotoxic protein or peptide operatively linked
CC to the MN gene promoter, which inhibits the growth of a vertebrate
CC preneoplastic or neoplastic cell. Also claimed is a repressor complex
CC that binds to the MN gene promoter (AAA52473). MN proteins and peptides,
CC MN-binding proteins and peptides, and expression vectors encoding such
CC proteins and peptides are useful for treating patients with
CC preneoplastic or neoplastic disease (e.g., cancers) associated with or
CC characterised by abnormal MN expression. The present sequence represents
CC a fragment of the human MN promoter (AAA52473) specified in the
CC invention.
XX
SQ Sequence 18 BP; 3 A; 6 C; 3 G; 6 T; 0 other;

Query Match 1.1%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1017 GAGATGGTGCCAAAGT 1032
||||||| ||||||||
Db 18 GAGATGGAGCCAAAGT 3

RESULT 127
ABL31110

```
ID   ABL31110 standard; DNA; 18 BP.
XX
AC   ABL31110;
XX
DT   21-MAR-2002  (first entry)
XX
DE   Human HLA genotyping oligonucleotide SEQ ID NO 599.
XX
KW   Human; human leukocyte antigen; HLA; genotype; polymorphism;
KW   immunogenetic; transplantation; genetic disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192572-A1.
XX
PD   06-DEC-2001.
XX
PF   01-JUN-2001; 2001WO-JP04662.
XX
PR   01-JUN-2000; 2000JP-0164798.
XX
PA   (NISN ) NISSHINBO IND INC.
PA   (SYST-) SYSTEM RES INC.
XX
PI   Inoko H,  Kagiya T,  Ichihara T,  Matsumura Y,  Moriya S,  Nishida M;
XX
DR   WPI; 2002-122074/16.
XX
PT   Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes
PT   of individuals e.g. by determining immunogenetic differences when
PT   transplanting between them -
XX
PS   Claim 10; Page 206; 345pp; Japanese.
XX
CC   The invention relates to a typing kit for judging human leukocyte antigen
CC   (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
CC   oligonucleotides (ABL30512-ABL31809) originating in the sequences of
CC   genes e.g. belonging to HLA class I antigens on human genome and
CC   containing gene polymorphisms as alloantigens have been immobilised as
CC   primers for amplification of cleaved nucleic acids relating to gene
CC   polymorphisms. The method is useful for judging HLA genotypes of
CC   individuals by determining immunogenetic differences before transplanting
CC   between them, providing genetic information to decide compatibility of
CC   organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
CC   pancreas, Langerhans islet in pancreas and cornea, susceptibility
CC   diagnosis of genetic diseases and identifying individuals.
XX
SQ   Sequence 18 BP; 3 A; 2 C; 6 G; 7 T; 0 other;

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1182 TCTATAGGTGAGTGTT 1197
                ||||| ||||||||||
Db          3 TCTATGGGTGAGTGTT 18


RESULT 128
ABK30214/c
ID   ABK30214 standard; DNA; 18 BP.
XX
AC   ABK30214;
XX
DT   23-APR-2002  (first entry)
XX
DE   CYP2D6 gene polymorphism detection primer #53.
XX
KW   Human; CYP2D6; primer; single nucleotide polymorphism detection; SNP;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200196604-A2.
XX
PD   20-DEC-2001.
XX
PF   11-JUN-2001; 2001WO-US18912.
XX
PR   12-JUN-2000; 2000US-210988P.
XX
PA   (GENI-) GENICON SCI CORP.
XX
PI   Bee G,  Kohne DE,  Korb L,  Peterson T,  Yguerabide J;
XX
DR   WPI; 2002-130745/17.
XX
PT   Determining the presence of a CYP2D6 target sequence in a DNA sample
PT   containing CYP2D6 nucleic acid, for detecting mutations or
PT   polymorphisms, comprises detecting the scattered light from a particle
PT   bound to the target sequence -
XX
PS   Example 2; Figure 6; 66pp; English.
XX
CC   The invention relates to a method of determining the presence or absence
CC   of a CYP2D6 target sequence in a DNA sample containing CYP2D6 nucleic
CC   acid. Determining the presence or absence of a CYP2D6 target sequence in
CC   a sample of DNA containing CYP2D6 nucleic acid comprises contacting the
CC   nucleic acid with a probe under stringent binding conditions, and
CC   detecting the presence or absence of the target sequence bound with the
CC   probe with a scattered light detectable particle, by observing light
CC   scattered from the particle which indicates the presence of the target
CC   sequence. The method is useful for determining the presence or
CC   absence of particular single nucleotide polymorphisms or alleles in
CC   genomic nucleic acid, especially in a pharmacogenetically relevant gene
CC   or genes in a DNA sample, and to detect and measure one or more target
CC   sequences in a sample. The method may also be used to detect specific
CC   mutations to identify the phenotypic classification of an individual.
CC   ABK30162-ABK30230 represent CYP2D6 target sequence-specific primers
CC   of the invention.
XX
SQ   Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 other;

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 1.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        562 CACACACTGCTCCAGC 577
                ||| ||||||||||||
Db         16 CACCCACTGCTCCAGC 1


RESULT 129
AAF91220/c
ID   AAF91220 standard; DNA; 19 BP.
XX
AC   AAF91220;
XX
DT   04-MAY-2001  (first entry)
XX
DE   Human multi drug resistance-1 gene related sequence SEQ ID NO: 307.
XX
KW   Human; MDR-1; multi drug resistance-1; drug uptake; disease; cancer;
KW   inflammatory disease; neuronal disease; CNS disease;
KW   cardiovascular disease; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200109183-A2.
XX
PD   08-FEB-2001.
XX
PF   28-JUL-2000; 2000WO-EP07314.
XX
PR   30-JUL-1999;   99EP-0114938.
```

PR 22-FEB-2000; 2000EP-0103361.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Brinkmann U, Hoffmeyer S, Eichelbaum M, Roots I;
XX
DR WPI; 2001-159855/16.
XX
PT New polynucleotide encoding a molecular variant Multi Drug Resistance
PT (MDR)-1 polypeptide is useful for diagnosing and treating diseases
PT associated with abnormal MDR-1 expression or function, e.g. cancer -
XX
PS Disclosure; Page 140; 154pp; English.
XX
CC The present invention provides nucleotides encoding molecular variants of
CC the human multi drug resistance-1 (MDR-1) protein. These can be used to
CC identify compounds capable of treating multidrug resistance and
CC sensitivity interfering resulting from polymorphisms in MDR-1, which can
CC lead to difficulties in treating cancer, cardiovascular, neuronal,
CC inflammatory and CNS diseases.
XX
SQ Sequence 19 BP; 2 A; 5 C; 8 G; 3 T; 1 other;

Query Match 1.1%; Score 14.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 577 CAGGCCCTCCGTCTGCCC 594
|||| || |:||||||||
Db 19 CAGGGCCACYGTCTGCCC 2

RESULT 130
AAF91222
ID AAF91222 standard; DNA; 19 BP.
XX
AC AAF91222;
XX
DT 04-MAY-2001 (first entry)
XX
DE Human multi drug resistance-1 gene related sequence SEQ ID NO: 309.
XX
KW Human; MDR-1; multi drug resistance-1; drug uptake; disease; cancer;
KW inflammatory disease; neuronal disease; CNS disease;
KW cardiovascular disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200109183-A2.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-EP07314.
XX
PR 30-JUL-1999; 99EP-0114938.
PR 22-FEB-2000; 2000EP-0103361.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Brinkmann U, Hoffmeyer S, Eichelbaum M, Roots I;
XX
DR WPI; 2001-159855/16.
XX
PT New polynucleotide encoding a molecular variant Multi Drug Resistance
PT (MDR)-1 polypeptide is useful for diagnosing and treating diseases
PT associated with abnormal MDR-1 expression or function, e.g. cancer -
XX
PS Disclosure; Page 140; 154pp; English.
XX
CC The present invention provides nucleotides encoding molecular variants of
CC the human multi drug resistance-1 (MDR-1) protein. These can be used to
CC identify compounds capable of treating multidrug resistance and
CC sensitivity interfering resulting from polymorphisms in MDR-1, which can
CC lead to difficulties in treating cancer, cardiovascular, neuronal,
CC inflammatory and CNS diseases.
XX
SQ Sequence 19 BP; 3 A; 8 C; 5 G; 2 T; 1 other;

Query Match 1.1%; Score 14.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 577 CAGGCCCTCCGTCTGCCC 594
|||| || |:||||||||
Db 1 CAGGGCCACYGTCTGCCC 18

RESULT 131
AAD34212
ID AAD34212 standard; DNA; 19 BP.
XX
AC AAD34212;
XX
DT 16-JUL-2002 (first entry)
XX
DE Erwinia rhapontici sucrose isomerase DNA amplifying reverse PCR primer.
XX
KW Isomaltulose synthase; enzyme; sucrose isomerase; PCR; primer; ss.
XX
OS Erwinia rhapontici.
XX
PN WO200218603-A1.
XX
PD 07-MAR-2002.
XX
PF 29-AUG-2001; 2001WO-AU01084.
XX
PR 29-AUG-2000; 2000AU-0009768.
XX
PA (UYQU) UNIV QUEENSLAND.
XX
PI Birch RG;
XX
DR WPI; 2002-329777/36.
XX
PT Novel isomaltulose synthase polypeptide isolated from Erwinia
PT rhapontici and a bacterial isolate 68J, useful for producing
PT isomaltulose from sucrose on contact with sucrose or sucrose-containing
PT substrate -
XX
PS Example 1; Page 73; 143pp; English.
XX
CC The invention relates to an isolated isomaltulose synthase polypeptide,
CC having full-length sucrose isomerase polypeptide from Erwinia rhapontici
CC and full-length sucrose isomerase polypeptide from bacterial isolate 68J.
CC The invention or its fragment, variant or derivative is useful for
CC producing isomaltulose from sucrose, where the polypeptide or host cell
CC is contacted with a sucrose or a sucrose-containing substrate. Antigen-
CC binding molecule is useful for detecting a sucrose isomerase in a sample.
CC A differentiated plant is useful for producing isomaltulose, where the
CC plant is cultivated and the isomaltulose from the cultivated plant is
CC harvested. The present sequence is Erwinia rhapontici sucrose isomerase
CC DNA amplifying PCR primer.
XX
SQ Sequence 19 BP; 2 A; 6 C; 5 G; 5 T; 1 other;

Query Match 1.1%; Score 14.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 986 TCCCATTCAGATCCGGCT 1003
||||| | ||:|||||||
Db 1 TCCCAGTTAGRTCCGGCT 18

RESULT 132

```
ACA10200/c
ID   ACA10200 standard; DNA; 19 BP.
XX
AC   ACA10200;
XX
DT   02-JUN-2003  (first entry)
XX
DE   Human NOVX DNA probe #15.
XX
KW   Human; NOVX; ss; metabolic disorder; diabetes; infectious disease;
KW   obesity; anorexia; cancer; cardiovascular disorder; asthma; neurogenesis;
KW   neurodegenerative disorder; epilepsy; immune disorder; osteoarthritis;
KW   haematopoietic disorder; inflammatory skin disorder; dyslipidemia;
KW   haematopoiesis; wound healing; angiogenesis; bacterial infection; probe;
KW   viral infection; fungal infection; helminthic infection; atherosclerosis;
KW   protozoal infection; hypertension.
XX
OS   Homo sapiens.
XX
PN   WO200290504-A2.
XX
PD   14-NOV-2002.
XX
PF   02-MAY-2002; 2002WO-US14342.
XX
PR   03-MAY-2001; 2001US-288395P.
PR   04-MAY-2001; 2001US-288900P.
PR   07-MAY-2001; 2001US-289087P.
PR   14-MAY-2001; 2001US-290753P.
PR   15-MAY-2001; 2001US-291189P.
PR   16-MAY-2001; 2001US-291243P.
PR   18-MAY-2001; 2001US-292001P.
PR   21-MAY-2001; 2001US-292374P.
PR   22-MAY-2001; 2001US-292587P.
PR   23-MAY-2001; 2001US-293107P.
PR   29-MAY-2001; 2001US-294110P.
PR   30-MAY-2001; 2001US-294434P.
PR   31-MAY-2001; 2001US-294827P.
PR   18-JUN-2001; 2001US-298988P.
PR   31-JUL-2001; 2001US-308901P.
PR   17-AUG-2001; 2001US-313388P.
PR   21-AUG-2001; 2001US-313851P.
PR   21-AUG-2001; 2001US-313937P.
PR   17-SEP-2001; 2001US-322701P.
PR   17-SEP-2001; 2001US-322802P.
PR   25-SEP-2001; 2001US-324757P.
PR   27-SEP-2001; 2001US-325314P.
PR   27-SEP-2001; 2001US-325682P.
PR   21-NOV-2001; 2001US-332129P.
PR   03-DEC-2001; 2001US-336882P.
PR   14-DEC-2001; 2001US-340305P.
PR   01-MAY-2002; 2002US-0138588.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Alsobrook JP,  Anderson DW,  Boldog FL,  Burgess CE,  Casman SJ;
PI   Chapoval A,  Edinger S,  Gerlach V,  Gorman L,  Gunther E,  Guo X;
PI   Kekuda R,  Lepley DM,  Li L,  Liu X,  Malyankar UM,  Miller CE;
PI   Millet I,  Padigaru M,  Patturajan M,  Pena CEA,  Rieger DK;
PI   Shenoy SG,  Shimkets RA,  Spytek KA,  Taupier RJ,  Vernet CAM;
PI   Voss EZ,  Zerhusen BD;
XX
DR   WPI; 2003-103512/09.
XX
PT   New isolated NOVX polypeptides and polynucleotides, useful for
PT   preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT   osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT   asthma, or infections -
XX
PS   Examples; Page 218; 340pp; English.
XX
CC   The invention relates to human NOVX polypeptides and the polynucleotides
CC   encoding them. The polypeptides, polynucleotides and antibodies that bind
CC   immunospecifically to the polypeptides are useful in the manufacture of a
CC   medicament for treating a syndrome associated with a human disease,
CC   preferably a NOVX-associated disorder. The sequences are useful for
CC   treating, preventing or diagnosing diseases such as metabolic disorders,
CC   diabetes, obesity, infectious diseases (viral, bacterial, fungal,
CC   helminthic, and protozoal), anorexia, cancer, cardiovascular disorders
CC   (e.g. hypertension, atherosclerosis), neurodegenerative disorders (e.g.
CC   Alzheimer's disease, Parkinson's disease), epilepsy, immune disorders,
CC   osteoarthritis, haematopoietic disorders, inflammatory skin disorders,
CC   asthma and various dyslipidemias. The nucleic acids and polypeptides may
CC   also be used as targets for the identification of small molecules that
CC   modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC   proliferation, haematopoiesis, wound healing and angiogenesis, and in the
CC   generation of antibodies that bind immunospecifically to NOVX substances
CC   for use in therapeutic or diagnostic methods. The nucleic acids are
CC   further used as hybridisation probes, and in chromosome mapping, tissue
CC   typing, preventive medicine and pharmacogenomics. This sequence
CC   represents a probe for a human NOVX polynucleotide of the invention.
XX
SQ   Sequence 19 BP; 1 A; 8 C; 6 G; 4 T; 0 other;

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        128 CGGGACAGGGACGCCC 143
              ||||||||||||| ||
Db         17 CGGGACAGGGACGGCC 2


RESULT 133
ABX56454/c
ID   ABX56454 standard; DNA; 19 BP.
XX
AC   ABX56454;
XX
DT   19-FEB-2003  (first entry)
XX
DE   Human NOV25a, NOV25b and NOV25c detecting probe Ag343 SEQ ID 240.
XX
KW   NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
KW   metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
KW   antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
KW   cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
KW   anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;
KW   Parkinson's disease; haematopoietic disorder; metabolic disturbance;
KW   metabolic syndrome X; wasting disease; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200281625-A2.
XX
PD   17-OCT-2002.
XX
PF   03-APR-2002; 2002WO-US10366.
XX
PR   03-APR-2001; 2001US-281086P.
PR   05-APR-2001; 2001US-281906P.
PR   06-APR-2001; 2001US-282020P.
PR   10-APR-2001; 2001US-282930P.
PR   12-APR-2001; 2001US-283444P.
PR   12-APR-2001; 2001US-283512P.
PR   13-APR-2001; 2001US-283657P.
PR   13-APR-2001; 2001US-283678P.
PR   13-APR-2001; 2001US-283710P.
PR   17-APR-2001; 2001US-284234P.
PR   19-APR-2001; 2001US-285325P.
PR   20-APR-2001; 2001US-285381P.
PR   24-APR-2001; 2001US-286068P.
PR   25-APR-2001; 2001US-286292P.
PR   07-JUN-2001; 2001US-296692P.
PR   26-JUN-2001; 2001US-300883P.
PR   08-AUG-2001; 2001US-311003P.
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PR 13-AUG-2001; 2001US-311973P.
PR 16-AUG-2001; 2001US-312901P.
PR 14-SEP-2001; 2001US-322283P.
PR 05-OCT-2001; 2001US-327448P.
PR 31-DEC-2001; 2001US-345734P.
PR 03-JAN-2002; 2002US-345755P.
PR 04-FEB-2002; 2002US-354391P.
PR 02-APR-2002; 2002US-0114153.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Padigaru M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD, Smithson G;
PI Guo X, Gerlach V, Casman SJ, Boldog FL, Li L, Zerhusen BD;
PI Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA, Malyankar UM;
PI Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J, Peyman JA;
PI Catterton E, MacDougall JR, Edinger SR, Stone DJ, Mazur A;
XX
DR WPI; 2003-046862/04.
XX
PT New isolated NOVX polypeptide useful for treating cardiomyopathy,
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
PT cancer -
XX
PS Example C; Page 379; 425pp; English.
XX
CC This invention describes novel polypeptides, termed NOVX which have
CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
CC neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,
CC cardiant and immunomodulatory activity. The polypeptide and any
CC antibodies generated from it are useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease
CC selected from a pathology associated with the NOVX polypeptide. Fragments
CC and portions of the polynucleotides encoding NOVX polypeptides are useful
CC to map the location of NOVX genes on a chromosome, to identify
CC individuals from minute biological samples, as DNA markers for
CC restriction fragment length polymorphism (RFLP), and are useful to
CC prepare polymerase chain reaction primers. The products of the invention
CC can be used in gene therapy and for treating cardiomyopathy, metabolic
CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
CC disease, immune disorders, haematopoietic disorders, and various
CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
CC syndrome X and wasting disorders associated with chronic diseases and
CC various cancers. ABX56307-ABX56465 represent PCR primers and probes used
CC in the amplification and detection of the NOVX polynucleotides
CC represented in ABX56261-ABX56306.
XX
SQ Sequence 19 BP; 1 A; 8 C; 6 G; 4 T; 0 other;

Query Match 1.1%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 128 CGGGACAGGGACGCCC 143
||||||||||||| ||
Db 17 CGGGACAGGGACGGCC 2

RESULT 134
AAT41134
ID AAT41134 standard; DNA; 20 BP.
XX
AC AAT41134;
XX
DT 03-DEC-1996 (first entry)
XX
DE Human gene signature HUMGS01489-derived anti-sense primer.
XX
KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW human; cloning; mapping; non-biased library; diagnosis; detection;
KW cell typing; abnormal cell function; primer; PCR; amplification;
KW polymerase chain reaction; ss.
XX
OS Synthetic.
XX
PN WO9514772-A1.
XX
PD 01-JUN-1995.
XX
PF 11-NOV-1994; 94WO-JP01916.
XX
PR 12-NOV-1993; 93JP-0355504.
XX
PA (MATS/) MATSUBARA K.
PA (OKUB/) OKUBO K.
XX
PI Matsubara K, Okubo K;
XX
DR WPI; 1995-206931/27.
XX
PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human
PT tissues
XX
PS Example 7; Fig 7; 2245pp; Japanese.
XX
CC Primers T41001-T41382 are derived from novel human gene signature (GS)
CC sequences which did not match with sequences deposited in Genbank release
CC 76. The GS sequences (T19001-T26837) were obtained from 3'-directed cDNA
CC libraries prepared from various human tissues; synthesis of cDNA was
CC initiated from the 3'-end of mRNA by using poly(T) as the sole primer.
CC Each library is constructed so as to reflect accurately the relative
CC abundance of different mRNAs in the particular tissue from which it was
CC derived. The appearance frequency of a given GS in a cDNA library can be
CC determined (esp. using primers and probes derived from the GS sequences)
CC as a means of diagnosing abnormal cell function or for recognising
CC different cell types. The primers T41133-4 amplify clone pm0559 which
CC comprises the GS HUMGS001489 (T20489), located on chromosome 11.
XX
SQ Sequence 20 BP; 9 A; 4 C; 1 G; 6 T; 0 other;

Query Match 1.1%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 20 ATTAAACCAAACCCAG 35
||||||||||| ||||
Db 3 ATTAAACCAAATCCAG 18

RESULT 135
AAQ75560
ID AAQ75560 standard; DNA; 20 BP.
XX
AC AAQ75560;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC seperate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 other;

Query Match 1.1%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1144 TTTTTTTCTTTTGGA 1159
||||||| ||||||||
Db 5 TTTTTTTTTTTTGGA 20

RESULT 136
AAV06457
ID AAV06457 standard; DNA; 20 BP.
XX
AC AAV06457;
XX
DT 06-MAY-1998 (first entry)
XX
DE Avian sex determination using Tsex sequence based primer 1.
XX
KW Avian; sex determination; Tsex; probe; Z chromosome; W chromosome;
KW hybridisation; bird; PCR primer; ss.
XX
OS Synthetic.
OS Meleagris gallopavo.
XX
PN US5707809-A.
XX
PD 13-JAN-1998.
XX
PF 12-APR-1996; 96US-0634331.
XX
PR 12-APR-1996; 96US-0634331.
PR 21-SEP-1990; 90US-0585915.
PR 17-SEP-1992; 92US-0947100.
PR 09-FEB-1994; 94US-0194131.
XX
PA (PEKE) PERKIN-ELMER CORP.
XX
PI Dvorak J, Halverson J;
XX
DR WPI; 1998-109344/10.
XX
PT Avian nucleic acid amplification primers and probes - hybridise to Z
PT and/or W chromosomes; used for sex determination
XX
PS Claim 1; Columns 29-30; 20pp; English.
XX
CC This sequence is based on a Tsex sequence obtained from a cDNA library
CC prepared from a turkey embryonic poly(A)+ mRNA. This can be used as a
CC primer. The Tsex sequence or its complementary sequence or a sequence of
CC at least eighteen contiguous nucleotides of one of these sequences can
CC be used for the identification of sex in avian species. These sequences
CC can be used for the production of a variety of nucleic acid hybridisation
CC probes and amplification primers. This primer can be used in combination
CC with an Osex or an Esex sequence. The primers and probes can hybridise
CC to both Z and W sex chromosomes allowing for differentiation between the
CC two chromosomes based on length polymorphisms. Alternatively, they may
CC hybridise to one of the chromosomes, permitting gender identification on
CC the basis of sex-specific hybridisation intensity. The combinations of
CC primers from different sequences allows amplification of fragments from
CC a specific chromosome. This primer sequence is exemplary of an intron
CC sequence that is specific to the W chromosome of many avian species. The
CC primers/probes are used to determine the sex of birds (e.g. poultry or
CC emus) before development of obvious external sexual differences.
XX
SQ Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 other;

Query Match 1.1%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 670 TTGGCCAGCGTGGTAT 685
| |||||||||||||||
Db 3 TAGGCCAGCGTGGTAT 18

RESULT 137
AAT99084/c
ID AAT99084 standard; DNA; 20 BP.
XX
AC AAT99084;
XX
DT 24-MAR-1998 (first entry)
XX
DE Primer alphaEN-S2 for alphaENAC coding sequence.
XX
KW Alpha epithelial sodium channel; alphaENACa; alphaENACb; binding assay;
KW amiloride-sensitive salt channel alpha subunit; membrane-transport;
KW salt substitute; salty taste blocker; PCR primer; amplify; ss.
XX
OS Synthetic.
OS Rattus rattus.
XX
PN US5693756-A.
XX
PD 02-DEC-1997.
XX
PF 23-JAN-1995; 95US-0376362.
XX
PR 23-JAN-1995; 95US-0376362.
PR 28-FEB-1994; 94US-0202654.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Blackshaw S, Li X, Snyder SH;
XX
DR WPI; 1998-031814/03.
XX
PT Alternatively spliced epithelial sodium channel alpha subunit
PT proteins - useful in screening assays for salty taste enhancers or
PT blockers
XX
PS Disclosure; Column 9; 33pp; English.
XX
CC This sequence represents a primer for the coding sequence for the alpha
CC epithelial sodium channel a (alphaENACa). AlphaENACa (see AAW34529) and
CC alphaENACb (see AAW34530) represent the sequences of the invention. The
CC two sodium channels are alternatively spliced forms of the
CC amiloride-sensitive salt channel alpha subunit and can be used in
CC membrane-transport or binding assays to identify substances that enhance
CC or block perception of a salty taste. Enhancers could be used as salt
CC substitutes and blockers could be used to mask salty tastes in foods and
CC pharmaceuticals.
XX
SQ Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 other;

```
  Query Match             1.1%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        629 AGCTCCAGGAGCTCTG 644
              ||| ||||||||||||
Db         16 AGCCCCAGGAGCTCTG 1


RESULT 138
AAZ37518/c
ID   AAZ37518 standard; DNA; 20 BP.
XX
AC   AAZ37518;
XX
DT   07-JAN-2000  (first entry)
XX
DE   Human mdm2 phosphorothioate oligodeoxynucleotide #48.
XX
KW   Human mdm2 gene; proliferation; tumour; phosphorothioate; p53;
KW   cancer; antisense; modulation; oligonucleotide; expression;
KW   inhibition; hyperproliferation; blood cancer; brain cancer;
KW   breast cancer; lung cancer; soft tissue cancer; psoriasis; fibrosis;
KW   atherosclerosis; restenosis; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9949065-A1.
XX
PD   30-SEP-1999.
XX
PF   26-MAR-1999;   99WO-US06702.
XX
PR   26-MAR-1998;   98US-0048810.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Miraglia LJ,  Nero P,  Graham MJ,  Monia BP,  Cowsert LM;
XX
DR   WPI; 1999-610754/52.
XX
PT   New antisense compounds used to treat eg. hyperproliferative conditions
PT   -
XX
PS   Example 9; Page 48; 157pp; English.
XX
CC   AAZ37473-Z37738 represent human mdm2 phosphorothioate oligonucleotides.
CC   AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the
CC   exemplification of the present invention. The present invention
CC   describes novel nucleotide antisense compounds, targetted to the 5'
CC   untranslated, translation termination codon, or 3' untranslated region
CC   of a nucleic acid encoding human mdm2, that modulates expression of
CC   human mdm2. The oligonucleotides mediate their effect by antisense
CC   inhibition of hyperproliferative gene expression. The antisense compound
CC   is used to treat an animal having a disease or condition associated
CC   with mdm2, particularly a hyperproliferative condition, more
CC   particularly cancer, especially of the blood, brain, breast, lung or soft
CC   tissue, or psoriasis, fibrosis, atherosclerosis or restenosis.
XX
SQ   Sequence 20 BP; 2 A; 7 C; 8 G; 3 T; 0 other;

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        788 CCAGTGCCCTGGCTCG 803
              |||||||||||||  ||
Db         20 CCAGTGCCCTGGCCCG 5


RESULT 139
AAZ09195/c
ID   AAZ09195 standard; DNA; 20 BP.
XX
AC   AAZ09195;
XX
DT   19-OCT-1999  (first entry)
XX
DE   Oligonucleotide 7 for DNA analysis.
XX
KW   Primer; DNA analysis; amplification; hybridisation; ss.
XX
OS   Synthetic.
XX
PN   JP11196874-A.
XX
PD   27-JUL-1999.
XX
PF   14-JAN-1998;   98JP-0005399.
XX
PR   14-JAN-1998;   98JP-0005399.
XX
PA   (HITA ) HITACHI LTD.
XX
DR   WPI; 1999-496652/42.
XX
PT   Analysis of DNA fragment - comprises addition of known common
PT   oligonucleotide, amplification of resultant DNA fragment and
PT   analysis and labelling of amplified DNA
XX
PS   Example 1; Page 12; 17pp; Japanese.
XX
CC   This invention descibes a novel method for the analysis of a DNA
CC   fragment which comprises: (i) addition of a known common oligonucleotide
CC   sequence to at least one terminal of each DNA fragment, (ii)
CC   amplification of the resultant DNA fragment as a primer using a first
CC   common primer containing a complementary nucleotide sequence to the above
CC   mentioned known common oligonucleotide sequence, a second common primer
CC   containing a complementary nucleotide sequence to the prepared known
CC   common oligonucleotide sequence optionally having been introduced with
CC   complementary nucleotide sequence at a terminal, and a specific primer
CC   capable of hybridisation with a DNA fragment containing whole or
CC   part of the gene having known sequence, to give amplified DNA, (iii)
CC   analysis of the amplified DNA to find the information of the DNA
CC   fragment, in which the specific primer is designed to prepare fragments
CC   of the common first and second primers and to give short fragment of
CC   amplified DNA and (iv) labelling them to make their differentiation.
CC   Differentiation of informations of known and unknown genes readily
CC   provides information of unknown gene and simultaneous monitoring of
CC   signals derived from minor genes.  Furthermore, labelling of DNAs
CC   according to functions of known genes can be performed. AAZ09189-Z09201
CC   represent oligonucleotide primers used to illustrate the method
CC   of the invention.
XX
SQ   Sequence 20 BP; 15 A; 3 C; 0 G; 2 T; 0 other;

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1144 TTTTTTTCTTTTTGGA 1159
              ||||||| ||||||||
Db         18 TTTTTTTTTTTTTGGA 3


RESULT 140
AAX26904
ID   AAX26904 standard; DNA; 20 BP.
XX
AC   AAX26904;
XX
DT   23-JUN-1999  (first entry)
XX
DE   Primer used for STS-PCR mapping of RIGUI nucleic acids.
XX
```

KW RIGUI; Drosophila circadian rhythm period gene; circadian clock gene;
KW Drosophila Timeless ortholog; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9912952-A1.
XX
PD 18-MAR-1999.
XX
PF 09-SEP-1998; 98WO-US18755.
XX
PR 04-NOV-1997; 97US-0065957.
PR 09-SEP-1997; 97US-0058256.
XX
PA (RERE-) RES DEV FOUND.
XX
PI Albrecht U, Eichele G, Lee C, Sun ZS;
XX
DR WPI; 1999-229221/19.
XX
PT New isolated mammalian circadian rhythm genes
XX
PS Example 1; Page 30; 73pp; English.
XX
CC Primers AAX26903-04 were used for STS-PCR mapping of RIGUI nucleic
CC acids. RIGUI is a gene corresponding to the Drosophila circadian
CC rhythm period gene. The specification describes both mouse and
CC human genes. The RIGUI polypeptides act as regulators of circadian
CC rhythms. The identification of RIGUI as a putative circadian clock
CC gene provides a useful tool to explore the molecular mechanism of
CC the mammalian circadian machinery. Using interaction screening
CC approaches, it should be possible to find interacting proteins,
CC perhaps in the form of a Drosophila Timeless ortholog. Furthermore,
CC promoter analyses of the RIGUI gene should uncover how light cues
CC and possibly other environmental stimuli, regulate the expression of
CC this gene. Targeted disruption of the m-rigui gene using stem cell
CC technology, may provide a valuable model system to study the various
CC physiological and pathological aspects of disrupting circadian
CC rhythms.
XX
SQ Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 other;

Query Match 1.1%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 624 GGACCAGCTCCAGGAG 639
||||||| |||||||||
Db 1 GGACCATCTCCAGGAG 16

RESULT 141
AAA48521/c
ID AAA48521 standard; DNA; 20 BP.
XX
AC AAA48521;
XX
DT 19-DEC-2000 (first entry)
XX
DE Murine villin gene regulatory region PCR primer #2.
XX
KW Mouse; villin; regulatory region; digestive tract;
KW colorectal cancer mouse model; PCR primer; ss.
XX
OS Mus sp.
XX
PN WO200034492-A1.
XX
PD 15-JUN-2000.
XX
PF 09-DEC-1998; 98WO-EP08009.
XX
PR 09-DEC-1998; 98WO-EP08009.
XX
PA (CNRS) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
XX
PI Pinto D, Robine S, Jaisser F, Louvard D;
XX
DR WPI; 2000-423433/36.
XX
PT Novel nucleotide sequence derived from mouse villin gene for targeted
PT expression of transgenes in immature and differentiated epithelial
PT cells of intestine or urogenital tracts -
XX
PS Disclosure; Page 17; 54pp; English.
XX
CC The present sequence is a PCR primer which was used in the RT-PCR
CC analysis of a plasmid containing the murine villin gene regulatory
CC region. It has been shown that this region directs the expression of the
CC villin gene in the intestine and uro-genital tracts, and thus could be
CC used in a fusion gene to direct expression of exogenous genes in these
CC areas. This could be used, for example, to create a mouse model for
CC colorectal cancer.
XX
SQ Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 other;

Query Match 1.1%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1288 ACAGTTGCTCAGCCTG 1303
|||||||| |||||||
Db 19 ACAGTTGCGCAGCCTG 4

RESULT 142
AAA49259/c
ID AAA49259 standard; DNA; 20 BP.
XX
AC AAA49259;
XX
DT 19-DEC-2000 (first entry)
XX
DE Mouse villin gene PCR primer #2.
XX
KW Mouse; villin; intestinal epithelial cell;
KW uro-genital tract epithelial cell; tumour; PCR primer; ss.
XX
OS Mus sp.
XX
PN WO200034493-A2.
XX
PD 15-JUN-2000.
XX
PF 09-DEC-1999; 99WO-EP09782.
XX
PR 09-DEC-1998; 98WO-EP08009.
XX
PA (CNRS) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
XX
PI Pinto D, Robine S, Jaisser F, Louvard D, Niewoehner J;
XX
DR WPI; 2000-423434/36.
XX
PT Novel nucleotide sequence derived from mouse villin gene for targeted
PT expression of transgenes in immature and differentiated epithelial
PT cells of intestine or urogenital tracts -
XX
PS Example 1; Page 16; 52pp; English.
XX
CC The present sequence is a PCR primer used to amplify the murine villin
CC gene. The villin gene is expressed in the epithelial cells of the
CC intestine and uro-genital tracts. Its promoter sequence can be used in
CC the targeted expression of exogenous genes in these places, which may,

```
CC   for example, be useful in the treatment of tumours.
XX
SQ   Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 other;

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1288 ACAGTTGCTCAGCCTG 1303
              ||||||| |||||||
Db         19 ACAGTTGCGCAGCCTG 4


RESULT 143
AAS45819
ID   AAS45819 standard; DNA; 20 BP.
XX
AC   AAS45819;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Mouse PARP-2 antisense inhibitor ISIS #110285.
XX
KW   Mouse; ss; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide;
KW   cytostatic; nootropic; neuroprotective; antiinflammatory; antidiabetic;
KW   immunosuppressant; hyperproliferative disorder; cancer; cellular injury;
KW   oxidative stress; neurological disorder; parkinsonism; apoptosis;
KW   meningitis-associated intracranial complication; ischaemia; probe;
KW   inflammatory disorder; autoimmune disorder; arthritis; diabetes.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
FT   modified_base   1..20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "All cytidine residues are 5-methyl cytidine"
FT   modified_base   1..5
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl nucleotides"
FT   modified_base   16..20
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "2' methoxyethyl nucleotides"
XX
PN   WO200164955-A1.
XX
PD   07-SEP-2001.
XX
PF   01-MAR-2001; 2001WO-US06572.
XX
PR   02-MAR-2000; 2000US-0517467.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Popoff I,  Cowsert LM;
XX
DR   WPI; 2001-602570/68.
XX
PT   Antisense compound useful for treating hyperproliferative,
PT   neurological, inflammatory and autoimmune disorders and diabetes
PT   inhibits human PARP -
XX
PS   Example 17; Page 89; 168pp; English.
XX
CC   The invention relates to antisense oligonucleotides targeted to human
CC   PARP nucleic acid and inhibiting expression of human PARP. PARP
CC   (Poly (ADP-ribose) polymerase plays an important role in chromatin
CC   decondensation, DNA replication, DNA repair, gene expression, malignant
CC   transformation, cellular differentiation and apoptosis. The antisense
CC   oligonucleotide inhibitors are useful for inhibiting the expression of
CC   PARP in human cells or tissues.  They are also useful for treating a
CC   human with a disease associated with PARP especially hyperproliferative
CC   disorders (e.g. cancer), cellular injury resulting from oxidative stress,
CC   neurological (e.g parkinsonism, meningitis-associated intracranial
CC   complications and ischaemia) , inflammatory and autoimmune disorders (e.g
CC   arthritis) and diabetes. The present sequence is an antisense
CC   oligonucleotide of the invention.
XX
SQ   Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 other;

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1289 CAGTTGCTCAGCCTGG 1304
              ||||| ||||||||||
Db          2 CAGTTACTCAGCCTGG 17


RESULT 144
AAS29287/c
ID   AAS29287 standard; DNA; 20 BP.
XX
AC   AAS29287;
XX
DT   21-NOV-2001  (first entry)
XX
DE   Human mdm2 antisense oligonucleotide 31397.
XX
KW   Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW   atherosclerosis; tumour; cytostatic; anti psoriatic;
KW   anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= All phosphorothioate linkages,
FT                          additionally bases 1-6 and bases 15-20 are
FT                          2'-O-methoxyethyl bases, and bases 7-14 are
FT                          deoxynucleotides"
XX
PN   US2001016575-A1.
XX
PD   23-AUG-2001.
XX
PF   02-JAN-2001; 2001US-0752983.
XX
PR   26-MAR-1999;   99US-0280805.
PR   26-MAR-1998;   98US-0048810.
XX
PA   (MIRA/) MIRAGLIA L J.
PA   (NERO/) NERO P.
PA   (GRAH/) GRAHAM M J.
PA   (MONI/) MONIA B P.
PA   (COWS/) COWSERT L M.
XX
PI   Miraglia LJ,  Nero P,  Graham MJ,  Monia BP,  Cowsert LM;
XX
DR   WPI; 2001-535565/59.
XX
PT   An antisense compound, useful for treating e.g. cancer, comprises
PT   nucleobases targeted a region (e.g. translation termination codon
PT   region) of a nucleic acid encoding human mdm2 -
XX
PS   Example 9; Page 15; 81pp; English.
XX
CC   The present invention relates to antisense compounds, 8-30 nucleobases
```

CC in length targeted to the 5' untranslated region, translation
CC termination codon region, 3' untranslated region, coding region or
CC translation start site of a nucleic acid encoding human mdm2, where
CC the antisense compound modulates the expression of human mdm2. The
CC antisense oligonucleotides of the invention are useful for encoding
CC human mdm2 and for inhibiting the expression of human mdm2. They may be
CC used for treating an animal having a disease or condition associated
CC with amplification of mdm2 gene or overexpression of mdm2 e.g. a
CC hyperproliferative disorder such as cancer (blood, brain, breast, lung,
CC or a soft tissue cancer) and psoriasis, fibrosis, atherosclerosis or
CC restenosis, tumours, colorectal carcinoma and chronic myelogenous
CC leukemia. The antisense compound may be administered with a
CC chemotherapeutic agent to overcome drug resistance. The antisense
CC compound reduces hyperproliferation of human cells. The method, which
CC involves the use of the antisense compound, is also useful for detecting
CC the role of mdm2 expression in various cell functions and physiological
CC processes and useful in both clinical research and diagnostic tools.
CC AAS29242-AAS29507 represent the human mdm2 antisense oligonucleotides
CC of the present invention.
XX
SQ Sequence 20 BP; 2 A; 7 C; 8 G; 3 T; 0 other;

Query Match 1.1%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 788 CCAGTGCCCTGGCTCG 803
||||||||||||| ||
Db 20 CCAGTGCCCTGGCCCG 5

RESULT 145
AAF80672/c
ID AAF80672 standard; DNA; 20 BP.
XX
AC AAF80672;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #46.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
OS Homo sapiens.
XX
PN US6184212-B1.
XX
PD 06-FEB-2001.
XX
PF 26-MAR-1999; 99US-0280805.
XX
PR 26-MAR-1998; 98US-0048810.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsert LM;
XX
DR WPI; 2001-190948/19.
XX
PT Novel antisense compound 8-30 nucleobases in length targeted to a
PT nucleic acid molecule encoding human mdm-2 useful for modulating the
PT expression of human mdm-2 and reducing hyperproliferation of human
PT cells -
XX
PS Example 9; Column 27; 77pp; English.
XX
CC The present invention relates to an antisense compound 8-30
CC nucleobases in length targeted to nucleobases 1-308 of the
CC 5' untranslated region, 1776-1806 of the translation termination
CC codon region or 1818-2370 of the 3' untranslated region of a
CC nucleic acid molecule encoding human mdm-2. The invention is
CC useful for reducing hyperproliferation of human cells,
CC modulating the expression of mdm2 in human cells or tissues
CC or in vitro. The hyperproliferative disorder includes cancer or
CC psoriasis.
XX
SQ Sequence 20 BP; 2 A; 7 C; 8 G; 3 T; 0 other;

Query Match 1.1%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 788 CCAGTGCCCTGGCTCG 803
||||||||||||| ||
Db 20 CCAGTGCCCTGGCCCG 5

RESULT 146
ABT32305/c
ID ABT32305 standard; DNA; 20 BP.
XX
AC ABT32305;
XX
DT 08-MAY-2003 (first entry)
XX
DE Neuroblastoma-related oligonucleotide #82.
XX
KW Neuroblastoma; prognosis; spontaneous regression; primer; probe; ds;
KW high malignancy.
XX
OS Unidentified.
XX
PN WO200297093-A1.
XX
PD 05-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-JP05294.
XX
PR 30-MAY-2001; 2001JP-0162775.
PR 24-AUG-2001; 2001JP-0255226.
XX
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
XX
PI Nakagawara A;
XX
DR WPI; 2003-140476/13.
XX
PT Nucleic acids having higher expression in human neuroblastoma with poor
PT prognosis for diagnostic prediction of neuroblastoma prognosis -
XX
PS Example 5; Page 26; 111pp; Japanese.
XX
CC The invention comprises nucleic acids that show increased expression in
CC human neuroblastomas with poor prognosis over those with a good
CC prognosis. The nucleic acids of the invention are useful as a tool for
CC distinguishing neuroblastomas with a favourable prognosis (spontaneous
CC regression) from neuroblastomas with a poor prognosis (high malignancy).
CC The DNA sequences ABT32224 - ABT32571 represent oligonucleotides used in
CC an example of the invention.
XX
SQ Sequence 20 BP; 5 A; 4 C; 7 G; 4 T; 0 other;

Query Match 1.1%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 222 AGCTCCTCAGCCTCAG 237
||||||||||| ||||
Db 16 AGCTCCTCAGCATCAG 1

RESULT 147
ABZ76936/c
ID ABZ76936 standard; DNA; 20 BP.
XX

```
AC   ABZ76936;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Bovine DGAT BAC-DNA sequencing primer #9.
XX
KW   Acyl CoA:diacylglycerol transferase; DGAT; enzyme; chromosome 14;
KW   bovine; milk; meat marbling; low fat; polymorphic; SNP;
KW   single nucleotide polymorphism; PCR primer; ss.
XX
OS   Bos taurus.
OS   Synthetic.
XX
PN   WO2003004630-A2.
XX
PD   16-JAN-2003.
XX
PF   05-JUL-2002; 2002WO-EP07520.
XX
PR   06-JUL-2001; 2001EP-0116412.
PR   13-MAY-2002; 2002US-379412P.
XX
PA   (ARBE-) ARBEITSGEMEINSCHAFT DEUT RINDERZUECHTER.
XX
PI   Fries H,  Winter A;
XX
DR   WPI; 2003-239205/23.
XX
PT   New nucleic acid molecule comprising a sequence of an allele of a
PT   polymorphic bovine acyl CoA-diacylglycerol transferase gene useful for
PT   testing a mammal for its predisposition for fat content of milk and for
PT   meat marbling  -
XX
PS   Example 1; Page 35; 91pp; English.
XX
CC   The present invention describes a nucleic acid molecule (NA) (I) encoding
CC   a bovine acyl CoA-diacylglycerol transferase (DGAT) contributing to or
CC   indicative for low fat content of milk and to low meat marbling
CC   (intramuscular fat content). Human DGAT is located to chromosome 8, and
CC   bovine DGAT is located to chromosome 14. (I) is useful for testing a
CC   mammal for its predisposition for fat content of milk and/or its
CC   predisposition for meat marbling. The method comprises analysing the
CC   gene encoding DGAT for nucleotide polymorphisms (e.g. single nucleotide
CC   polymorphisms (SNPs)) which are connected with the predisposition. The
CC   nucleotide polymorphisms are located in the coding region of the DGAT
CC   gene and result in substitution, deletion and/or addition of an amino
CC   acid sequence of the polypeptide which is encoded by the gene. The
CC   nucleic acid molecule has at the position 10433 and 10434 of the DGAT
CC   gene a guanine and a cytosine residue, at position 3343 a cytosine or
CC   guanine, 11030 a guanine, 11048 a cytosine or thymine and 11093 a
CC   thymine, which correlate with a predisposition for low fat content of
CC   milk and low meat marbling. The nucleic acid molecule has at the position
CC   corresponding to position 10433 and 10434 of the DGAT gene two adenine
CC   residues which correlate with a predisposition for high content of milk
CC   and high meat marbling. The nucleotide polymorphisms are located in a
CC   region which is responsible for the regulation of the expression of the
CC   product of the gene encoding DGAT. ABZ76924 to ABZ77045 and ABP96035 to
CC   ABP96046 represent sequences used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 20 BP; 7 A; 7 C; 5 G; 1 T; 0 other;

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        296 TGTCTGCTGTGGGGGC 311
              ||||| ||||||||||
Db         18 TGTCTACTGTGGGGGC 3


RESULT 148
ABZ77002/c
ID   ABZ77002 standard; DNA; 20 BP.
XX
AC   ABZ77002;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Bovine DGAT PCR primer #38.
XX
KW   Acyl CoA:diacylglycerol transferase; DGAT; enzyme; chromosome 14;
KW   bovine; milk; meat marbling; low fat; polymorphic; SNP;
KW   single nucleotide polymorphism; PCR primer; ss.
XX
OS   Bos taurus.
OS   Synthetic.
XX
PN   WO2003004630-A2.
XX
PD   16-JAN-2003.
XX
PF   05-JUL-2002; 2002WO-EP07520.
XX
PR   06-JUL-2001; 2001EP-0116412.
PR   13-MAY-2002; 2002US-379412P.
XX
PA   (ARBE-) ARBEITSGEMEINSCHAFT DEUT RINDERZUECHTER.
XX
PI   Fries H,  Winter A;
XX
DR   WPI; 2003-239205/23.
XX
PT   New nucleic acid molecule comprising a sequence of an allele of a
PT   polymorphic bovine acyl CoA-diacylglycerol transferase gene useful for
PT   testing a mammal for its predisposition for fat content of milk and for
PT   meat marbling  -
XX
PS   Example 1; Page 36; 91pp; English.
XX
CC   The present invention describes a nucleic acid molecule (NA) (I) encoding
CC   a bovine acyl CoA-diacylglycerol transferase (DGAT) contributing to or
CC   indicative for low fat content of milk and to low meat marbling
CC   (intramuscular fat content). Human DGAT is located to chromosome 8, and
CC   bovine DGAT is located to chromosome 14. (I) is useful for testing a
CC   mammal for its predisposition for fat content of milk and/or its
CC   predisposition for meat marbling. The method comprises analysing the
CC   gene encoding DGAT for nucleotide polymorphisms (e.g. single nucleotide
CC   polymorphisms (SNPs)) which are connected with the predisposition. The
CC   nucleotide polymorphisms are located in the coding region of the DGAT
CC   gene and result in substitution, deletion and/or addition of an amino
CC   acid sequence of the polypeptide which is encoded by the gene. The
CC   nucleic acid molecule has at the position 10433 and 10434 of the DGAT
CC   gene a guanine and a cytosine residue, at position 3343 a cytosine or
CC   guanine, 11030 a guanine, 11048 a cytosine or thymine and 11093 a
CC   thymine, which correlate with a predisposition for low fat content of
CC   milk and low meat marbling. The nucleic acid molecule has at the position
CC   corresponding to position 10433 and 10434 of the DGAT gene two adenine
CC   residues which correlate with a predisposition for high content of milk
CC   and high meat marbling. The nucleotide polymorphisms are located in a
CC   region which is responsible for the regulation of the expression of the
CC   product of the gene encoding DGAT. ABZ76924 to ABZ77045 and ABP96035 to
CC   ABP96046 represent sequences used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 20 BP; 7 A; 7 C; 5 G; 1 T; 0 other;

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        296 TGTCTGCTGTGGGGGC 311
              ||||| ||||||||||
Db         18 TGTCTACTGTGGGGGC 3
```

```
RESULT 149
AAD51819
ID   AAD51819 standard; DNA; 20 BP.
XX
AC   AAD51819;
XX
DT   02-MAY-2003  (first entry)
XX
DE   DNA fragment #1 used to construct beta-galactosidase enzyme acceptors.
XX
KW   Antibiotic; screening; therapy; ds.
XX
OS   Unidentified.
XX
PN   WO200290593-A1.
XX
PD   14-NOV-2002.
XX
PF   03-MAY-2002; 2002WO-US14081.
XX
PR   09-MAY-2001; 2001US-289911P.
PR   15-FEB-2002; 2002US-357355P.
XX
PA   (DISC-) DISCOVERX INC.
XX
PI   Rouhani R,  Vainshtein I;
XX
DR   WPI; 2003-140221/13.
XX
PT   Screening for enzyme inhibitors, by combining candidate compound,
PT   enzyme donor-conjugate and acceptor having indicator enzyme, target
PT   enzyme and substrate, and measuring rate of product formation/substrate
PT   depletion  -
XX
PS   Example 7; Page 44; 61pp; English.
XX
CC   The invention relates to a method of screening a candidate compound for
CC   inhibition of a target enzyme. The method involves combining candidate
CC   compound, an enzyme donor-conjugate and an enzyme acceptor comprising
CC   inactive portions of an indicator enzyme, target enzyme and a substrate
CC   for indicator enzyme under binding conditions, where substrate reacts
CC   to form a product, and substrate or product provides a detectable
CC   signal, and determining the signal. The method is useful for screening
CC   a candidate compound for effective inhibition of a target enzyme, where
CC   the target enzyme includes plural target enzymes selected from lyases,
CC   hydrolases, oxidoreductases, transferases, ligases, isomerases and
CC   kinases and the target enzyme is derived from an organism selected from
CC   viruses, bacteria, fungi, protozoans, and multicellular human parasites.
CC   It is useful for identifying inhibitors that function as antibiotics.
CC   Inhibitors identified are useful as lead compounds for effective drugs
CC   with increased potency and fewer side effects, for treating human
CC   disease and improving human health. The present sequence is a DNA
CC   fragment used to construct beta-galactosidase enzyme acceptors. This
CC   sequence is used in the exemplification of the invention.
XX
SQ   Sequence 20 BP; 6 A; 6 C; 5 G; 3 T; 0 other;

  Query Match             1.1%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1288 ACAGTTGCTCAGCCTG 1303
              ||||||||  |||||||
Db          3 ACAGTTGCGCAGCCTG 18


RESULT 150
AAD04572
ID   AAD04572 standard; DNA; 19 BP.
XX
AC   AAD04572;
XX
DT   04-JUL-2001  (first entry)
XX
DE   Human insulinoma-associated antigen, IA-1 cDNA sequencing primer #5.
XX
KW   Human; insulinoma-associated antigen; IA-1; regulatory factor;
KW   tumour marker; therapy; neuroendocrine tumour; cancer; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6225049-B1.
XX
PD   01-MAY-2001.
XX
PF   19-MAY-1994;   94US-0246489.
XX
PR   17-JUN-1992;   92US-0901715.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Lan MS,  Notkins AL;
XX
DR   WPI; 2001-299371/31.
XX
PT   Novel insulinoma-associated neuroendocrine tumor-associated cDNA,
PT   useful for diagnosing and identifying insulinoma, neuroendocrine tumors
PT   and cancers -
XX
PS   Example 5; Column 25; 26pp; English.
XX
CC   The present sequence is a sequencing primer which is used for
CC   sequencing the human insulinoma-associated antigen, IA-1 cDNA clone.
CC   The IA-1 function as a regulatory factor in islet cell transformation.
CC   The IA-1 is used as a tumour marker for diagnosis and identification
CC   of insulinoma and neuroendocrine tumours. It is also used for
CC   identifying cancers. Correct identification of insulinomas and cancers
CC   is possible. The IA-1 fragments may be used to immunise animals for the
CC   generation of polyclonal and monoclonal antibodies.
XX
SQ   Sequence 19 BP; 5 A; 6 C; 5 G; 3 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 1.7e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        521 ACCTGCCGGAGGAGCAGCT 539
              ||||||  ||||||  ||  ||
Db          1 ACCTGCAGGAGGATCACCT 19


RESULT 151
ABT13587/c
ID   ABT13587 standard; DNA; 19 BP.
XX
AC   ABT13587;
XX
DT   07-FEB-2003  (first entry)
XX
DE   Liver regeneration-related gene panel PCR primer #115.
XX
KW   PCR; primer; ss; liver regeneration; gene panel; expression profile;
KW   drug screening; drug development; hepatitis; liver transplantation.
XX
OS   Unidentified.
XX
PN   WO200277222-A1.
XX
PD   03-OCT-2002.
XX
PF   13-MAR-2002; 2002WO-JP02372.
XX
PR   13-MAR-2001; 2001JP-0070940.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
```

PI Yokoya F, Okutsu T, Mori M, Takahara Y, Fukuda H, Aburatani H;
PI Sonaka I;
XX
DR WPI; 2003-018922/01.
XX
PT Gene panel participating in liver regeneration, applicable in providing
PT expression data, diagnosis and development of drugs for promoting liver
PT regeneration e.g. after transplantation or removal of liver during
PT cancer -
XX
PS Claim 19; Page 76; 101pp; Japanese.
XX
CC The invention comprises a gene panel constructed from the expression
CC profile of known genes which show a change in expression level between
CC normal liver cells and liver cells under regeneration. The gene panel is
CC useful for providing expression data and screening/development of drugs
CC for liver regeneration (e.g. when treating hepatitis, after
CC transplantation or removal of the liver during cancer or hepatitis
CC therapy). The present DNA sequence represents a PCR primer used in the
CC invention.
XX
SQ Sequence 19 BP; 4 A; 7 C; 2 G; 6 T; 0 other;

Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 924 GATGGCAGATCTGGAGAAG 942
||| ||||| ||||||| |
Db 19 GATTGCAGAACTGGAGATG 1

RESULT 152
AAQ82417
ID AAQ82417 standard; DNA; 20 BP.
XX
AC AAQ82417;
XX
DT 25-MAR-2003 (updated)
DT 11-SEP-1995 (first entry)
XX
DE Chromosome 11 (locus D11S1195) STS primer cSRL-5f4-tA.
XX
KW sequence sampled mapping; genomic analysis; complex genome mapping;
KW cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
XX
OS Synthetic.
XX
PN WO9429486-A1.
XX
PD 22-DEC-1994.
XX
PF 15-JUN-1994; 94WO-US06810.
XX
PR 15-JUN-1993; 93US-0078471.
PR 07-SEP-1993; 93US-0117952.
XX
PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Evans GA, Smith MW;
XX
DR WPI; 1995-036508/05.
XX
PT Sequencing complex genomes, present as fragments in a cosmid
PT library - by sequencing end-specific nucleotides of each clone
PT then correlating with spatial relationship of cosmid, esp. for
PT mammalian chromosomes.
XX
PS Example 4; Page 80; 128pp; English.
XX
CC Sequences were determined from the ends of chromosome 11-specific
CC cosmids by automated sequencing without intermediate subcloning.
CC A sample of 371 DNA sequence fragments were determined and of
CC these, 277 were suitable for STS primer prediction by computer
CC analysis (using the "Primer" program available from E.Lander, MIT).
CC The STSs and cosmids were mapped by in situ hybridisation, somatic
CC cell hybrid analysis or both. Using this method, 370 STSs specific
CC for human chromosome 11 were generated and most of them were
CC regionally mapped. This procedure illustrates a novel method for
CC sequencing complex genomes, designated "sequence sampled mapping".
CC The sequence sampled mapping method is useful for the completion of
CC high density sequence-based maps, and ultimately, for the complete
CC sequencing of genomic DNA directly from cosmid clones.
CC See AAQ82001-Q82706 for STS primers. (Also see AAQ91325-58).
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 BP; 11 A; 4 C; 4 G; 1 T; 0 other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1159 AAGTAAAGCAGCTAAAACA 1177
||||||||| || ||| ||
Db 1 AAGTAAAGCCGCAAAAGCA 19

RESULT 153
AAT17134
ID AAT17134 standard; DNA; 20 BP.
XX
AC AAT17134;
XX
DT 25-MAR-2003 (updated)
DT 03-JUL-1996 (first entry)
XX
DE Primer for cGMP-phosphodiesterase beta-subunit gene amplification.
XX
KW Primer; human; cGMP-phosphodiesterase; beta-subunit; mutation; PCR;
KW polymerase chain reaction; eye; rod; retina; photoreceptor;
KW retinitis pigmentosa; diagnostic; prenatal diagnosis; ss.
XX
OS Synthetic.
XX
PN US5498521-A.
XX
PD 12-MAR-1996.
XX
PF 11-MAR-1993; 93US-0033081.
XX
PR 11-MAR-1993; 93US-0033081.
PR 24-JAN-1990; 90US-0469215.
PR 11-DEC-1991; 91US-0805123.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Berson EL, Dryja TP;
XX
DR WPI; 1996-159684/16.
XX
PT Diagnosis of hereditary retinal degenerative diseases e.g. retinitis
PT pigmentosa, - caused by a human photoreceptor protein mutation, by
PT detection of the mutation by PCR amplification or hybridisation
PT methods
XX
PS Example 9; Column 15; 71pp; English.
XX
CC This antisense primer is derived from exon-13 of the human retinal
CC rod cGMP-phosphodiesterase beta-subunit (PDE-beta) gene, and may be
CC used for PCR amplification and sequencing of normal and mutant
CC forms of the PDE-beta gene. The primer may be used along with
CC sense primer AAT17133 to detect a variant with a C-to-T transition
CC at position 19876 in exon-13, resulting in a missense mutation
CC (His557Tyr) (e.g. in patient AR67) linked with autosomal recessive
CC retinitis pigmentosa. Mutations in the rhodopsin and retinal
CC degradation slow protein genes are also implicated in retinitis

```
CC   pigmentosa.  Detection of any of these mutations in a foetus or
CC   patient may be used in diagnosis.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        324 CCTGCATCATCCTGGTGAT 342
              ||||||  | |||||||||
Db          2 CCTGCACAACCCTGGTGAT 20


RESULT 154
AAT92490/c
ID   AAT92490 standard; DNA; 20 BP.
XX
AC   AAT92490;
XX
DT   04-FEB-1998  (first entry)
XX
DE   BRCA2 cancer susceptibility gene exon 9 PCR primer F for SSCP.
XX
KW   BRCA2 cancer susceptibility gene; breast cancer; ovarian cancer;
KW   gene therapy; prostate cancer; colorectal cancer; ocular melanoma;
KW   leukaemia; human; single stranded conformation polymorphism test;
KW   SSCP; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   GB2307477-A.
XX
PD   28-MAY-1997.
XX
PF   25-NOV-1996;   96GB-0024453.
XX
PR   28-AUG-1996;   96GB-0017961.
PR   23-NOV-1995;   95GB-0023959.
PR   14-DEC-1995;   95GB-0025555.
XX
PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
PA   (UYDU-) UNIV DUKE.
XX
PI   Ashworth A,  Futreal PA,  Stratton MR,  Wooster RF;
XX
DR   WPI; 1997-261854/24.
XX
PT   Nucleic acid molecules comprising part or all of the BRCA2 cancer
PT   susceptibility gene - useful for diagnosis, prognosis or therapeutic
PT   treatment of cancer
XX
PS   Example 1; Fig 8; 124pp; English.
XX
CC   The present sequence represents a PCR primer for single stranded
CC   conformation polymorphism testing of the BRCA2 cancer susceptibility
CC   gene. The nucleic acid molecule can be used to construct probes for
CC   screening cDNA or genomic libraries, sequencing positive clones
CC   obtained, and assembling the full length BRCA2 sequence. The BRCA2
CC   nucleic acid molecules and proteins are useful in a method of medical
CC   treatment, preferably gene therapy, especially for treating cancer,
CC   where the cancer is female or male breast cancer, ovarian, prostate or
CC   colorectal cancer, ocular melanoma or leukaemia. In particular
CC   antisense oligonucleotides capable of hybridising to the BRCA2 nucleic
CC   acid, pre-mRNA or mature mRNA are used so that the expression of the
CC   BRCA2 nucleic acid is reduced or prevented. The nucleic acid molecules
CC   are also useful in a method for diagnosing susceptibility or
CC   predisposition to cancer in a patient. The nucleic acid molecules are
CC   used to design probes or primers for PCR to determine or detect the
CC   presence of mutations in a sample of nucleic acid from a patient. The
CC   BRCA2 promoter region is useful for screening for substances which
CC   modulate the expression of nucleic acid under control of the promoter.
CC   Antibodies are used to determine the presence, amount or location in a
CC   cell of a BRCA2 polypeptide or its mutant forms. The polypeptides are
CC   used to screen for binding partners, these are useful to screen for
CC   substances which mimic the activity of BRCA2 polypeptide, which can be
CC   used as cancer therapeutics.
XX
SQ   Sequence 20 BP; 8 A; 4 C; 4 G; 4 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1110 AGTTTTCTGTTTAATTGAA 1128
              |||  |||||||| |||||
Db         20 AGTCCTCTGTTTAGTTGAA 2


RESULT 155
AAT73292
ID   AAT73292 standard; DNA; 20 BP.
XX
AC   AAT73292;
XX
DT   12-DEC-1997  (first entry)
XX
DE   Primer 2 for pUC19 DNA amplification.
XX
KW   primer; PCR; polymerase chain reaction; sequencing; walking;
KW   complementary extension reaction; low redundancy; universal primer; ss.
XX
OS   Synthetic.
XX
PN   EP767240-A2.
XX
PD   09-APR-1997.
XX
PF   17-SEP-1996;   96EP-0114907.
XX
PR   30-JAN-1996;   96JP-0013634.
PR   18-SEP-1995;   95JP-0238141.
XX
PA   (HITA ) HITACHI LTD.
XX
PI   Kambara H,  Okano K;
XX
DR   WPI; 1997-205424/19.
XX
PT   Efficient sequencing of long DNA by fragment walking  - with
PT   simultaneous sequencing of restriction enzyme fragment and adjacent
PT   region of intact DNA, avoids the need for cloning and requires fewer
PT   primers
XX
PS   Example 1; Page 11; 50pp; English.
XX
CC   A method for DNA analysis based on a complementary extension reaction
CC   using a DNA polymerase, comprises a combination of fragment walking and
CC   DNA sequencing. DNA fragments are formed by digestion of DNA with a
CC   restriction enzyme and the targeted DNA sequence can be determined
CC   directly from the digested DNA fragments.  By exploring the overlapping
CC   sequence of the determined base sequence, the overall base sequence of a
CC   lengthy DNA can be determined with low redundancy without cloning or
CC   subcloning. In addition, the method can be done with commercially
CC   available universal primers or with fewer primers than required in
CC   existing methods. AAT73291-92 are primers used in determination of the
CC   pUC19 sequence. Primer extension was carried out using 16 primers
CC   AAT73293.
XX
SQ   Sequence 20 BP; 1 A; 1 C; 3 G; 15 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy       1144 TTTTTTTCTTTTTGGAAGT 1162
              ||||||| |||||| | ||
Db          2 TTTTTTTTTTTTTGCAGGT 20


RESULT 156
AAV57183/c
ID   AAV57183 standard; DNA; 20 BP.
XX
AC   AAV57183;
XX
DT   25-MAR-2003  (updated)
DT   06-JAN-1999  (first entry)
XX
DE   Human Notch-3 mutant gene primer #20.
XX
KW   Human; Notch3; transmembrane receptor; lateral inhibition; regulation;
KW   developmental cascade; neurogenic gene; mutant; neurological disorder;
KW   cerebral autosomal dominant arteriopathy; subcortical infarct; CADASIL;
KW   leukoencephalopathy; therapy; PCR; primer; amplification; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   FR2751985-A1.
XX
PD   06-FEB-1998.
XX
PF   01-AUG-1996;   96FR-0009733.
XX
PR   01-AUG-1996;   96FR-0009733.
XX
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI   Tournier LE,  Joutel A,  Bousser MG,  Bach JF;
XX
DR   WPI; 1998-133137/13.
XX
PT   Human Notch3 nucleic acids - and methods for identifying
PT   pre-disposition to cerebral autosomal dominant arteriopathy with
PT   sub-cortical infarcts and leukoencephalopathy
XX
PS   Example 3; Page 21; 42pp; French.
XX
CC   Primers AAV57164-V57197 are used to detect mutations in a partial human
CC   Notch-3 gene (AAV57163).  Primers AAV57182-V57183 amplify a fragment
CC   from exon N12.
CC   Notch3 is a transmembrane receptor protein involved in lateral
CC   inhibition and regulating developmental cascades of neurogenic genes.
CC   Mutated Notch3 proteins are thought to be involved in neurological
CC   disorders, especially of the cerebral autosomal dominant arteriopathy
CC   with subcortical infarcts and leukoencephalopathy (CADASIL) type.
CC   Blocking expression of a mutated Notch3 gene or by substitution therapy
CC   with non-mutated Notch3 gene or protein can be used to treat CADASIL or
CC   related disorders.
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 20 BP; 5 A; 2 C; 10 G; 3 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1208 ACCTCCCCTTCCCTGTACA 1226
              ||||| |||||||| | ||
Db         20 ACCTCACCTTCCCTCTGCA 2


RESULT 157
AAV57102/c
ID   AAV57102 standard; DNA; 20 BP.
XX
AC   AAV57102;
XX
DT   25-MAR-2003  (updated)
DT   21-DEC-1998  (first entry)
XX
DE   Human Notch3 mutant gene primer N6R.
XX
KW   Human; Notch3; transmembrane receptor; lateral inhibition; regulation;
KW   developmental cascade; neurogenic gene; mutant; neurological disorder;
KW   cerebral autosomal dominant arteriopathy; subcortical infarct; CADASIL;
KW   leukoencephalopathy; therapy; PCR; primer; amplification; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   FR2751986-A1.
XX
PD   06-FEB-1998.
XX
PF   16-APR-1997;   97FR-0004680.
XX
PR   01-AUG-1996;   96FR-0009733.
XX
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI   Tournier LE,  Joutel A,  Bousser MG,  Bach JF;
XX
DR   WPI; 1998-133138/13.
XX
PT   Human Notch3 nucleic acids - and methods for identifying
PT   pre-disposition to cerebral autosomal dominant arteriopathy with
PT   sub-cortical infarcts and leukoencephalopathy
XX
PS   Example 3; Page 24; 45pp; French.
XX
CC   Primers AAV57066-V57162 are used to detect mutations in the human Notch3
CC   gene (AAV57001).  Primers AAV57101-V57102 amplify a 207 bp fragment from
CC   the EGF18-19 domain sequences found in exon 14.
CC   Notch3 is a transmembrane receptor protein involved in lateral
CC   inhibition and regulating developmental cascades of neurogenic genes.
CC   Mutated Notch3 proteins are thought to be involved in neurological
CC   disorders, especially of the cerebral autosomal dominant arteriopathy
CC   with subcortical infarcts and leukoencephalopathy (CADASIL) type.
CC   Blocking expression of a mutated Notch3 gene or by substitution therapy
CC   with non-mutated Notch3 gene or protein can be used to treat CADASIL or
CC   related disorders.
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 20 BP; 5 A; 2 C; 10 G; 3 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1208 ACCTCCCCTTCCCTGTACA 1226
              ||||| |||||||| | ||
Db         20 ACCTCACCTTCCCTCTGCA 2


RESULT 158
AAV38813/c
ID   AAV38813 standard; DNA; 20 BP.
XX
AC   AAV38813;
XX
DT   25-MAR-2003  (updated)
DT   09-OCT-1998  (first entry)
XX
DE   PCR primer used to amplify a durum wheat glutenin gene.
XX
KW   Glutenin gene; durum wheat; low-molecular-weight;
KW   transgenic durum wheat; PCR primer; ss.
XX
```

OS Synthetic.
OS Triticum durum.
XX
PN FR2757538-A1.
XX
PD 26-JUN-1998.
XX
PF 18-DEC-1997; 97FR-0016059.
XX
PR 19-DEC-1996; 96IT-MI02663.
XX
PA (ITUY-) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.
XX
PI D Ovidio R, Porceddu E, Marchitelli C, Cardelli LE;
XX
DR WPI; 1998-365055/32.
XX
PT Durum wheat glutenin gene - coding for glutenin protein of low
PT molecular weight
XX
PS Example 1; Page 6; 18pp; French.
XX
CC PCR primers AAV38812-13 were used to amplify the glutenin gene of
CC Triticum durum L. The gene codes for a low-molecular-weight glutenin
CC protein and can be used to produce transgenic durum wheat plants
CC with "better quality characteristics" [no details given].
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 20 BP; 4 A; 7 C; 6 G; 3 T; 0 other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1011 GCACCTGAGATGGTGCCAA 1029
||||| ||| ||||||| |
Db 20 GCACCGGAGTTGGTGCCTA 2

RESULT 159
AAZ32721/c
ID AAZ32721 standard; DNA; 20 BP.
XX
AC AAZ32721;
XX
DT 31-JAN-2000 (first entry)
XX
DE Human chemokine receptor CXCR3b-specific RT-PCR primer SCM54.
XX
KW Chemokine receptor; CXCR3b; splice variant; N-terminus; CXCR3a;
KW seven transmembrane; G-protein coupled; CXC; IP10; Mig; T-lymphocyte;
KW recruitment; selective; activated; T-cell; neutrophil; inflammation;
KW tissue distribution; therapy; rheumatoid arthritis; psoriasis;
KW multiple sclerosis; transplantation; atherosclerosis; restenosis;
KW cytokine; delayed type hypersensitivity reaction; RT-PCR; expression;
KW reverse transcriptase-PCR; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9950299-A1.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-SE00501.
XX
PR 30-MAR-1998; 98SE-0001098.
XX
PA (ASTR) ASTRA PHARM LTD.
PA (ASTR) ASTRA AB.
XX
PI Delaney S;
XX
DR WPI; 1999-633638/54.
XX
PT New polynucleotide encoding a variant chemokine receptor -
XX
PS Example 2; Page 6; 18pp; English.
XX
CC This sequence represents human chemokine receptor CXCR3b-specific
CC reverse transcriptase-PCR (RT-PCR) primer SCM54, used with primer SCM56
CC (AAZ32722) to amplify human chemokine receptor CXCR3b cDNA for expression
CC studies. The template cDNA was prepared via reverse transcription from
CC T-cells and human tissues. The human chemokine receptor CXCR3 has two
CC differentially spliced forms, CXCR3a and CXCR3b (AAY50129). Expression
CC of both forms was detected in human Th1 and Th2 cells and also faintly
CC in spleen. Chemokines are a family of small cytokines which bring about
CC the recruitment of leukocytes during inflammation. The CXC chemokines
CC mostly attract neutrophils, while the CC chemokines are less selective.
CC All chemokine receptors are seven transmembrane G-protein coupled
CC receptors and most are receptors for a number of chemokines, CXCR3a
CC being a receptor for the CXC chemokines IP10 and Mig. CXCR3a is
CC expressed in activated, but not in resting T-lymphocytes, and may
CC therefore play an important role in the selective recruitment of
CC T-cells which occurs in T-cell mediated inflammatory conditions.
CC CXCR3b may have an altered pattern of tissue distribution and
CC function in the inflammatory process. Cells expressing the active
CC CXCR3b are useful for identifying ligands, especially agonists and
CC antagonists, of a chemokine receptor. In addition, the receptor
CC facilitates identification of chemokines responsible for mediating
CC inflammation reactions via interaction with CXCR3b. The modulation
CC of inflammatory responses is of therapeutic benefit in many conditions
CC such as rheumatoid arthritis, psoriasis, multiple sclerosis,
CC transplantation, delayed type hypersensitivity reactions,
CC atherosclerosis and restenosis.
XX
SQ Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1054 AGCCCTGGCCTTCCCATCA 1072
||||||||| ||||| | |
Db 20 AGCCCTGGCATTCCCCTGA 2

RESULT 160
AAZ03892
ID AAZ03892 standard; DNA; 20 BP.
XX
AC AAZ03892;
XX
DT 07-OCT-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer;
KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
OS Synthetic.
OS Chlamydia trachomatis.
XX
PN WO9928475-A2.
XX
PD 10-JUN-1999.
XX
PF 27-NOV-1998; 98WO-IB01939.
XX
PR 04-NOV-1998; 98US-0107077.
PR 28-NOV-1997; 97FR-0015041.
PR 17-DEC-1997; 97FR-0016034.
XX
PA (GEST) GENSET.

XX
PI Griffais R;
XX
DR WPI; 1999-371125/31.
XX
PT Genome sequence of Chlamydia trachomatis
XX
PS Disclosure; Page 1644; 1755pp; English.
XX
CC PCR primers AAZ01426-Z06209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences
CC can also be used to control growth of the microorganism. Chlamydia
CC trachomatis is responsible for a large number of diseases, e.g. eye
CC diseases such as conventional trachoma, nonendemic trachoma,
CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
CC nongonococcal uretritis, epidymitis, cervicitis, salpingitis,
CC perihepatitis, bartholinitis; pneumopathy in breast feeding infants;
CC and venereal lymphogranulomatosis. The polypeptides of the
CC invention may be of use in treating these diseases.
XX
SQ Sequence 20 BP; 3 A; 9 C; 2 G; 6 T; 0 other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1042 TCTTCCCACGACAGCCCTG 1060
||||||||| || |||||
Db 1 TCTTCCCACAACGTCCCTG 19

RESULT 161
AAX29423
ID AAX29423 standard; DNA; 20 BP.
XX
AC AAX29423;
XX
DT 10-JUN-1999 (first entry)
XX
DE Rat JNK1-specific oligo ISIS No: 21869.
XX
KW Antisense oligonucleotide; Jun N-terminal kinase; JNK; hybridise; JNK1;
KW JNK2; JNK3; cell cycle progression; phosphorylation; tumour; probe; rat;
KW hyperproliferative; stress-activated protein kinase; p54; SAP; ss.
XX
OS Synthetic.
OS Rattus norvegicus.
XX
PN WO9909214-A1.
XX
PD 25-FEB-1999.
XX
PF 07-AUG-1998; 98WO-US16488.
XX
PR 13-AUG-1997; 97US-0910629.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dean N, Gaarde WA, Mckay R, Monia BP, Nero PS;
XX
DR WPI; 1999-181060/15.
XX
PT New antisense oligonucleotides that detect and modulate the
PT expression of Jun N-terminal kinase proteins - useful for treating
PT hyperproliferative diseases and inhibiting tumor growth in animals,
PT and for modulating protein phosphorylation by these proteins
XX
PS Example 7; Page 114; 190pp; English.
XX
CC The invention relates to antisense oligonucleotides that detect and
CC modulate the expression of Jun N-terminal kinase (JNK) proteins. The
CC oligonucleotides specifically hybridize to a nucleic acid encoding a
CC JNK1, JNK2 or JNK3 protein, and which modulate expression of these
CC proteins. The oligonucleotides are useful for modulating JNK protein
CC expression and cell cycle progression in cultured cells or animal cells.
CC The oligonucleotides are also useful for modulating the phosphorylation
CC of a protein that has been phosphorylated by a JNK protein, and the
CC expression of a cellular protein that promotes one or more metastatic
CC events. The oligonucleotides also form pharmaceutical compositions for
CC treating animals with a hyperproliferative disease, and for inhibiting
CC tumor growth in an animal. The invention also provides sequences that can
CC specifically hybridise to nucleic acids encoding rat stress activated
CC protein kinase (SAP) or p54, a homologue of human JNK protein.
XX
SQ Sequence 20 BP; 6 A; 5 C; 7 G; 2 T; 0 other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 910 CTGGTCCTAAAGGAGATGG 928
||| |||||||||| ||
Db 2 CTGCACCTAAAGGAGACGG 20

RESULT 162
AAZ71860/c
ID AAZ71860 standard; DNA; 20 BP.
XX
AC AAZ71860;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:6216.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX
PS Claim 9; Page 1556; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side

```
CC   effects from pharmaceutical agents acting on a disease as well as other
CC   treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC   and 3367, are not actually given a sequence in the Sequence Listing
CC   from the present invention.
XX
SQ   Sequence 20 BP; 5 A; 2 C; 9 G; 4 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1205 CACACCTCCCCTTCCCTGT 1223
              || |||||  |||||||||
Db         19 CAGACCTCAACTTCCCTGT 1

RESULT 163
AAZ77262/c
ID   AAZ77262 standard; DNA; 20 BP.
XX
AC   AAZ77262;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human biallelic marker downstream amplification primer SEQ ID NO:11618.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   amplification; single nucleotide polymorphism; SNP; PCR primer;
KW   diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB00822.
XX
PR   21-APR-1998;   98US-0082614.
PR   23-NOV-1998;   98US-0109732.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome  -
XX
PS   Claim 9; Page 2707; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the
CC   invention have a variety of uses: they can be used for high density
CC   mapping of the human genome, and in complex association studies and
CC   haplotyping studies which are useful in determining the genetic basis
CC   for disease states. Compositions and methods of the invention can also
CC   be useful for the identification of the targets for the development of
CC   pharmaceutical agents and diagnostic methods, as well as the
CC   characterisation of the differential efficacious responses to and side
CC   effects from pharmaceutical agents acting on a disease as well as other
CC   treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC   and 3367, are not actually given a sequence in the Sequence Listing
CC   from the present invention.
XX
SQ   Sequence 20 BP; 7 A; 9 C; 2 G; 2 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1232 CTTTGGTGCTGGACGTGGC 1250
              ||||||| |||| | |||
Db         20 CTTTGGTGTTGGAAGGGGC 2

RESULT 164
AAC93165/c
ID   AAC93165 standard; DNA; 20 BP.
XX
AC   AAC93165;
XX
DT   15-FEB-2001  (first entry)
XX
DE   Human STAT3 phosphorothioate antisense oligonucleotide SEQ ID NO:16.
XX
KW   Human; mouse; STAT3; phosphorothioate; antisense oligonucleotide;
KW   modulation; signal transducer and activator of transcription;
KW   DNA-binding protein; signal transduction; inhibition; apoptosis;
KW   inflammatory disease; cancer; antiinflammatory; antirheumatic;
KW   cytostatic; immunostimulatory; rheumatoid arthritis; leukaemia;
KW   myeloma; melanoma; lymphoma; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061602-A1.
XX
PD   19-OCT-2000.
XX
PF   06-APR-2000; 2000WO-US09054.
XX
PR   08-APR-1999;   99US-0288461.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Karras JG;
XX
DR   WPI; 2000-619223/59.
XX
PT   New antisense compound for inhibiting the expression of signal
PT   transducer and activator of transcription 3 (STAT3) in cells or tissues
PT   and treating diseases or condition associated with STAT3, such as
PT   rheumatoid arthritis and cancer -
XX
PS   Example 2; Page 46; 104pp; English.
XX
CC   The present invention describes an antisense compound (I), 8 to 30
CC   nucleobases in length, that is targeted to a nucleic acid molecule
CC   encoding STAT3 (Signal Transducer and Activator of Transcription) and
CC   which inhibits the expression of it. (I) has antiinflammatory,
CC   antirheumatic, cytostatic and immunostimulatory activities. (I) is used
CC   for inhibiting the expression of STAT3 in cells or tissues, treating
CC   an animal having a disease or condition associated with STAT3 or a
CC   human having a disease or condition characterised by a reduction in
CC   apoptosis, and inducing apoptosis in a cell. Diseases or conditions
CC   that are treated are rheumatoid arthritis, cancer of the breast,
CC   prostate, brain, head and/or neck, leukaemia, myeloma, melanoma or
CC   lymphoma. (I) can also be used for diagnostic methods in detecting and
CC   determining the role of STAT3 in various cell functions, physiological
CC   processes and conditions and for diagnosing the conditions associated
CC   with expression of STAT3. (I) can be used alone or with other drugs as
CC   an immunostimulator. (I) is used in sandwich and colourimetric assays,
CC   involving enzyme conjugation and radiolabeling and is used in
CC   diagnostic kits. AAC93150 encodes human STAT3 and AAC93231 encodes mouse
CC   STAT3 as given in the exemplification of the present invention. AAC93151
CC   to AAC93230 and AAC93232 to AAC93299 represent STAT3 phosphorothioate
CC   antisense oligonucleotides, and AAC93300 represents a mismatch control
CC   oligonucleotide which are used in example from the present invention.
XX
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SQ   Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        628 CAGCTCCAGGAGCTCTGCA 646
              ||||||||  ||||||  ||
Db         20 CAGCTCCATCAGCTCTACA 2


RESULT 165
AAC93217/c
ID   AAC93217 standard; DNA; 20 BP.
XX
AC   AAC93217;
XX
DT   15-FEB-2001  (first entry)
XX
DE   Human STAT3 phosphorothioate antisense oligonucleotide SEQ ID NO:68.
XX
KW   Human; mouse; STAT3; phosphorothioate; antisense oligonucleotide;
KW   modulation; signal transducer and activator of transcription;
KW   DNA-binding protein; signal transduction; inhibition; apoptosis;
KW   inflammatory disease; cancer; antiinflammatory; antirheumatic;
KW   cytostatic; immunostimulatory; rheumatoid arthritis; leukaemia;
KW   myeloma; melanoma; lymphoma; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061602-A1.
XX
PD   19-OCT-2000.
XX
PF   06-APR-2000; 2000WO-US09054.
XX
PR   08-APR-1999;   99US-0288461.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Karras JG;
XX
DR   WPI; 2000-619223/59.
XX
PT   New antisense compound for inhibiting the expression of signal
PT   transducer and activator of transcription 3 (STAT3) in cells or tissues
PT   and treating diseases or condition associated with STAT3, such as
PT   rheumatoid arthritis and cancer -
XX
PS   Example 2; Page 47; 104pp; English.
XX
CC   The present invention describes an antisense compound (I), 8 to 30
CC   nucleobases in length, that is targeted to a nucleic acid molecule
CC   encoding STAT3 (Signal Transducer and Activator of Transcription) and
CC   which inhibits the expression of it. (I) has antiinflammatory,
CC   antirheumatic, cytostatic and immunostimulatory activities. (I) is used
CC   for inhibiting the expression of STAT3 in cells or tissues, treating
CC   an animal having a disease or condition associated with STAT3 or a
CC   human having a disease or condition characterised by a reduction in
CC   apoptosis, and inducing apoptosis in a cell. Diseases or conditions
CC   that are treated are rheumatoid arthritis, cancer of the breast,
CC   prostate, brain, head and/or neck, leukaemia, myeloma, melanoma or
CC   lymphoma. (I) can also be used for diagnostic methods in detecting and
CC   determining the role of STAT3 in various cell functions, physiological
CC   processes and conditions and for diagnosing the conditions associated
CC   with expression of STAT3. (I) can be used alone or with other drugs as
CC   an immunostimulator. (I) is used in sandwich and colourimetric assays,
CC   involving enzyme conjugation and radiolabeling and is used in
CC   diagnostic kits. AAC93150 encodes human STAT3 and AAC93231 encodes mouse
CC   STAT3 as given in the exemplification of the present invention. AAC93151
CC   to AAC93230 and AAC93232 to AAC93299 represent STAT3 phosphorothioate
CC   antisense oligonucleotides, and AAC93300 represents a mismatch control
CC   oligonucleotide which are used in example from the present invention.
XX
SQ   Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1256 GAGGCCAGGTTGAGGCCCT 1274
              ||||  |||  |||||  ||||
Db         20 GAGGGCAGTTTGAGTCCCT 2


RESULT 166
AAC62966
ID   AAC62966 standard; DNA; 20 BP.
XX
AC   AAC62966;
XX
DT   06-FEB-2001  (first entry)
XX
DE   JNK antisense oligonucleotide ISIS #21869.
XX
KW   Antisense; gene therapy; JNK2 protein; apoptosis; cancer;
KW   cellular hyperproliferation; Alzheimer's; Parkinson's disease;
KW   amylotrophic lateral sclerosis; retinitis; pigmentosa; epilepsy;
KW   myocardial infarction; stroke; obstructive jaundice; polycystic kidney;
KW   diabetes; Jun N-terminal kinase; ss.
XX
OS   Homo sapiens.
XX
PN   WO200059549-A1.
XX
PD   12-OCT-2000.
XX
PF   04-APR-2000; 2000WO-US08880.
XX
PR   07-APR-1999;   99US-0287796.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Mckay R,  Dean NM,  Monia BP,  Nero PS,  Gaarde WA;
XX
DR   WPI; 2000-638427/61.
XX
PT   Novel methods for reducing apoptosis comprising contacting cells with
PT   antisense oligonucleotides, useful for treating apoptotic disorders,
PT   e.g. cancer -
XX
PS   Example 8; Page 151; 160pp; English.
XX
CC   The present invention relates to antisense oligonucleotides
CC   (AAC62844-C63000, AAA96093-A96099 and AAA07993) that hybridise
CC   specifically to a nucleotide encoding a Jun N-terminal kinase (JNK2)
CC   protein, resulting in decrease of JNK2 expression and leading to
CC   induction of apoptosis. The present sequence is one such antisense
CC   oligonucleotide. The oligonucleotides of the present invention are useful
CC   for treating diseases or conditions with reduced apoptosis, e.g. cancer
CC   and cellular hyperproliferation. The oligonucleotides may also be used to
CC   increase the stimulation of apoptotic proteins, e.g. for treating
CC   Alzheimer's or Parkinson's disease, amylotrophic lateral sclerosis,
CC   retinitis, pigmentosa, epilepsy, myocardial infarction, stroke,
CC   obstructive jaundice, polycystic kidney and diabetes. The present
CC   sequence may have a phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 6 A; 5 C; 7 G; 2 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        910 CTGGTCCTAAAGGAGATGG 928
              |||  ||||||||||| ||
Db          2 CTGCACCTAAAGGAGACGG 20
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```
RESULT 167
AAA99073/c
ID   AAA99073 standard; DNA; 20 BP.
XX
AC   AAA99073;
XX
DT   18-JAN-2001  (first entry)
XX
DE   Putative suppressor phyB-4 mutation detection PCR primer SEQ ID NO:4.
XX
KW   Arabidopsis thaliana; bas1; promoter; cytochrome P450; CYP72B1; plant;
KW   brassinosteroid signalling; brassinosteroid synthesis; brassinolide;
KW   suppressor; phyB-4 mutation; detection; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200055302-A2.
XX
PD   21-SEP-2000.
XX
PF   16-MAR-2000; 2000WO-US06915.
XX
PR   16-MAR-1999;   99US-0124570.
PR   14-DEC-1999;   99US-0170931.
PR   20-DEC-1999;   99US-0172832.
XX
PA   (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI   Neff MM,  Chory J;
XX
DR   WPI; 2000-638195/61.
XX
PT   Transgenic plants having modulated brassinolide synthesis resulting in
PT   insect resistance, dwarfism and darker-green foliage compared with
PT   wild-type plants, have nucleic acid encoding BAS1 polypeptide in its
PT   genome  -
XX
PS   Example 1; Page 75; 104pp; English.
XX
CC   The present invention describes a genetically modified plant (I)
CC   comprising at least one exogenous nucleic acid sequence encoding a BAS1
CC   polypeptide, homologue or functional fragment, in its genome or at least
CC   one regulatory sequence that modified expression of endogenous bas1
CC   gene, homologue or functional fragment, and which is characterised as
CC   having modulated brassinolide activity or synthesis. The bas1 gene
CC   encodes a cytochrome P450 (CYP72B1), which has a role in brassinosteroid
CC   signalling or synthesis. Overexpression of the bas1 gene in plants
CC   causes a dark green, dwarf phenotype which mimics plants that have low
CC   levels of the plant hormone, brassinolide. Overexpression of the bas1
CC   gene also increases resistance to insects in plants. The present
CC   sequence represents a PCR primer used in the analysis of putative
CC   suppressors, having shorter hypocotyls than phyB-4, for the phyB-4
CC   mutation.
XX
SQ   Sequence 20 BP; 4 A; 2 C; 9 G; 5 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1037 CTGACTCTTCCCACGACAG 1055
              || || ||| |||||||||
Db         19 CTCACACTTTCCACGACAG 1


RESULT 168
AAA99178
ID   AAA99178 standard; DNA; 20 BP.
XX
AC   AAA99178;
XX
DT   22-JAN-2001  (first entry)
XX
DE   Bovine cytochrome b sense PCR primer SEQ ID NO:1.
XX
KW   Bovine; sheep; cytochrome b; PCR primer; identification; meat; ss.
XX
OS   Bos taurus.
XX
PN   JP2000210085-A.
XX
PD   02-AUG-2000.
XX
PF   25-JAN-1999;   99JP-0015617.
XX
PR   25-JAN-1999;   99JP-0015617.
XX
PA   (NIKA-) ZH NIPPON KAGAKU SENI KENSA KYOKAI.
XX
DR   WPI; 2000-604609/58.
XX
PT   Identification of animal meat with DNA comprising carrying out PCR by
PT   using the DNA extracted from the animal meat and at least one
PT   species-specific primer  -
XX
PS   Claim 1; Page 3; 6pp; Japanese.
XX
CC   The present invention describes a method for the identification of
CC   animal meat in which at least one animal meat is selected from bovine
CC   and sheep species. The method comprises carrying out PCR by using the
CC   DNA extracted from the animal meat and at least one species-specific
CC   primer designed from the cytochrome b base sequence to amplify the DNA
CC   and then analysing the amplified product. The method can be used for
CC   the identification of animal meat in high precision. The present
CC   sequence represents a specifically claimed bovine cytochrome b PCR
CC   primer for use in the method of the invention.
XX
SQ   Sequence 20 BP; 3 A; 8 C; 1 G; 8 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         52 CATACTCCTCAATTACCCA 70
              ||| ||||||  |||||||
Db          1 CATTCTCCTCTGTTACCCA 19


RESULT 169
AAA99182
ID   AAA99182 standard; DNA; 20 BP.
XX
AC   AAA99182;
XX
DT   22-JAN-2001  (first entry)
XX
DE   Bovine cytochrome b sense PCR primer SEQ ID NO:1.
XX
KW   Bovine; sheep; camel; goat; cytochrome b; identification; fiber; ss.
XX
OS   Bos taurus.
XX
PN   JP2000210084-A.
XX
PD   02-AUG-2000.
XX
PF   25-JAN-1999;   99JP-0015616.
XX
PR   25-JAN-1999;   99JP-0015616.
XX
PA   (NIKA-) ZH NIPPON KAGAKU SENI KENSA KYOKAI.
XX
DR   WPI; 2000-604608/58.
XX
```

```
PT   Identification of animal fiber using DNA extracted from animal fiber
PT   sample and at least one species-specific primer -
XX
PS   Claim 1; Page 3; 9pp; Japanese.
XX
CC   The present invention describes a method for the identification of
CC   animal fiber in which at least one animal fiber is selected from bovine,
CC   camel, goat and sheep species. The method comprises carrying out PCR by
CC   using the DNA extracted from the animal fiber and at least one species-
CC   specific primer designed from the cytochrome b base sequence to amplify
CC   the DNA and then analysing the amplified product. The method is used for
CC   the identification of animal fiber in high precision. The present
CC   sequence represents a specifically claimed bovine cytochrome b PCR
CC   primer for use in the method of the invention.
XX
SQ   Sequence 20 BP; 3 A; 8 C; 1 G; 8 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         52 CATACTCCTCAATTACCCA 70
              ||| ||||||  |||||||
Db          1 CATTCTCCTCTGTTACCCA 19


RESULT 170
AAA72160
ID   AAA72160 standard; DNA; 20 BP.
XX
AC   AAA72160;
XX
DT   24-NOV-2000  (first entry)
XX
DE   Humanised anti-Fas antibody heavy chain primer, SEQ ID NO:90.
XX
KW   Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
KW   murine; humanised antibody; complementarity determining region; CDR;
KW   human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW   autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW   cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
KW   hepatitis; AIDS; graft rejection; heavy chain; sequencing primer; ss.
XX
OS   Chimeric - Mus musculus.
OS   Chimeric - Homo sapiens.
XX
PN   JP2000169393-A.
XX
PD   20-JUN-2000.
XX
PF   30-SEP-1999;   99JP-0278301.
XX
PR   30-SEP-1998;   98JP-0276883.
XX
PA   (SANY ) SANKYO CO LTD.
XX
DR   WPI; 2000-485645/43.
XX
PT   Preventive or treating agent for the diseases caused by an abnormality
PT   in the Fas/Fas ligand system e.g. autoimmune diseases, contains
PT   anti-Fas antibody -
XX
PS   Example 15; Page 49; 139pp; Japanese.
XX
CC   The invention relates to compositions for the prevention or treatment
CC   or diseases caused by an abnormality in the Fas/Fas ligand system
CC   containing an anti-Fas antibody as the active component. The anti-Fas
CC   antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
CC   or a humanised version of HFE7A containing identical CDRs
CC   (complementarity determining regions) to antibody HFE7A. Via its
CC   interaction with Fas, the antibody of the invention acts as a modulator
CC   of apoptosis. The compositions of the invention may therefore be used in
CC   the treatment or prevention of conditions such as autoimmune diseases,
CC   allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC   glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC   and organ graft rejection. The present sequence represents a humanised
CC   HFE7A-derived anti-Fas antibody heavy chain sequencing primer used in an
CC   exemplification of the invention.
XX
SQ   Sequence 20 BP; 5 A; 5 C; 8 G; 2 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        482 ACTGCCGAGACGGTGTGCA 500
              || |||| || ||||||||
Db          1 ACAGCCGGGAAGGTGTGCA 19


RESULT 171
AAA11598
ID   AAA11598 standard; DNA; 20 BP.
XX
AC   AAA11598;
XX
DT   08-AUG-2000  (first entry)
XX
DE   Humanised HFE7A designed heavy chain DNA primer #1.
XX
KW   Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW   anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;
KW   dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW   nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW   hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW   Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW   Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW   Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW   multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW   insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW   cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection;
KW   primer; ss.
XX
OS   Synthetic.
XX
PN   EP990663-A2.
XX
PD   05-APR-2000.
XX
PF   29-SEP-1999;   99EP-0307711.
XX
PR   30-SEP-1998;   98JP-0276881.
PR   30-SEP-1998;   98JP-0276882.
XX
PA   (SANY ) SANKYO CO LTD.
XX
PI   Serizawa N,  Haruyama H,  Nakahara K,  Tamaki I,  Takahashi T;
XX
DR   WPI; 2000-258930/23.
XX
PT   New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT   inflammatory or autoimmune disease, induces apoptosis selectively in
PT   cells with abnormal Fas-Fas ligand systems -
XX
PS   Example reference 15; Page 136; 263pp; English.
XX
CC   This invention describes a novel humanized anti-Fas antibody-like
CC   molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC   ligand system, by binding to Fas on the cell surface, and prevents
CC   apoptosis in cells with a normal system, by inhibiting binding between
CC   Fas and its ligand. The products of the invention have anti-inflammatory,
CC   anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
CC   immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC   antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC   antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC   apoptosis by binding to cell surface Fas or inhibit it by competitive
```

CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC primer used in the construction of a humanised anti-Fas antibody HFE7A
CC designed heavy chain which is used in the method described in the
CC invention.
XX
SQ Sequence 20 BP; 5 A; 5 C; 8 G; 2 T; 0 other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 482 ACTGCCGAGACGGTGTGCA 500
|| |||| || ||||||||
Db 1 ACAGCCGGGAAGGTGTGCA 19

RESULT 172
AAA40718/c
ID AAA40718 standard; DNA; 20 BP.
XX
AC AAA40718;
XX
DT 15-AUG-2000 (first entry)
XX
DE Mouse fibrinogen-like protein primer SEQ ID NO:155.
XX
KW Human; rat; CD36; SHR; spontaneous hypertensive rat; diagnosis;
KW therapy; screening; polymorphism; variant; detection; mutant;
KW blood; mutation; insulin; glucose metabolism; fatty acid metabolism;
KW catecholamine; malaria; infection; parasite; antiparasitic;
KW antidiabetic; primer; ss.
XX
OS Mus sp.
XX
PN WO200019883-A2.
XX
PD 13-APR-2000.
XX
PF 07-OCT-1999; 99WO-US23418.
XX
PR 07-OCT-1998; 98US-0167750.
PR 28-DEC-1998; 98US-0221222.
PR 17-MAR-1999; 99US-0270542.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
PA (SCIO-) SCIOS INC.
PA (AITM/) AITMAN T J.
PA (SCOT/) SCOTT J.
PA (STAN/) STANTON L W.
XX
PI Aitman TJ, Scott J, Stanton LW;
XX
DR WPI; 2000-303596/26.
XX
PT Nucleic acids encoding mutant CD36 proteins useful for preventing,
PT diagnosing and treating parasitic infections, especially malaria -
XX
PS Example 1; Page 125; 167pp; English.
XX

CC The present invention describes isolated nucleic acid molecules (A)
CC encoding mutant CD36 proteins (B). Parasites such as Plasmodium
CC falciparum (the major cause of malaria) are unable to utilise the
CC mutated proteins to gain entry to, and infect cells. The mutant CD36
CC proteins do not function correctly preventing parasites utilising them
CC to infect cells. The nucleic acids may be used for the recombinant
CC production of mutant CD36 proteins according to standard methodologies.
CC They may be used in this way to prevent and treat parasitic infections
CC that utilise the CD36 protein to infect cells, such as P. falciparum,
CC the major cause of malaria. For example, the protein may be used to
CC identify modulators of CD36 expression and activity or a patient's CD36
CC DNA may be screened to determine whether there are any mutations present
CC that may confer resistance to parasitic infections. The proteins and
CC nucleic acids may also be used to prevent, diagnose and treat diseases
CC associated with defects in insulin action and/or glucose metabolism
CC and/or fatty acid metabolism and/or catecholamine action in subjects
CC possessing mutations in the CD36 genes. AAA40606 to AAA40759, and
CC AAB02515 to AAB02564, represent nucleotide and amino acid sequences
CC respectively which are used in the exemplification of the present
CC invention.
XX
SQ Sequence 20 BP; 1 A; 7 C; 5 G; 7 T; 0 other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 622 AGGGACCAGCTCCAGGAGC 640
| ||||||| |||||| ||
Db 19 AAGGACCAGATCCAGGGGC 1

RESULT 173
AAA35414/c
ID AAA35414 standard; DNA; 20 BP.
XX
AC AAA35414;
XX
DT 25-JUL-2000 (first entry)
XX
DE Myrtaceae microsatellite scu051TT detection PCR primer.
XX
KW Myrtaceae; microsatellite; isolation; genotyping; plant; tea tree;
KW breeding; Melaleuca alternifolia; broad-spectrum germicidal oil;
KW pharmaceutical; cosmetic; identification; detection; PCR primer; ss.
XX
OS Myrtaceae sp.
XX
PN WO200017341-A1.
XX
PD 30-MAR-2000.
XX
PF 23-SEP-1999; 99WO-AU00820.
XX
PR 23-SEP-1998; 98AU-0006099.
PR 16-FEB-1999; 99AU-0008718.
XX
PA (BUSI-) BUSINESS & RES MANAGEMENT PTY LTD.
XX
PI Rossetto M, McLauchlan A, Harriss FCL, Henry RJ, Baverstock PR;
PI Lee LS, Maguire TL, Edwards KJ;
XX
DR WPI; 2000-292840/25.
XX
PT Isolating microsatellites from Myrtaceae, useful for genotyping,
PT particularly in breeding programs for tea tree, by reacting plant
PT nucleic acid with immobilized oligonucleotides -
XX
PS Claim 10; Page 36; 100pp; English.
XX
CC A method has been developed of isolating a microsatellite (MS) from
CC nucleic acid extract of a plant of Myrtaceae family. The method
CC comprises: (i) treating the extract with one or more immobilised,

CC single-stranded oligonucleotides (ON) having a consensus MS repeat
CC sequence (MSRS) or its complement; (ii) washing under specified
CC stringency conditions; (iii) eluting nucleic acid bound to ON; and
CC (iv) sequencing the eluted nucleic acids to identify those containing
CC an MSRS. Microsatellites (MS) isolated by the method, specifically
CC from Melaleuca alternifolia (the tea tree, a source of a broad-spectrum
CC germicidal oil, useful in pharmaceuticals and cosmetics), are useful as
CC genotyping markers, particularly for breeding plants that produce the
CC oil in higher yield or of better quality. Primers based on MS are
CC useful for both inter- and intra-species genotyping. The selected
CC washing conditions improve efficiency of recovery of microsatellites
CC (MS) and reduce the number of washing stages required. Particularly
CC about 86% of recovered sequence contain an MS repeat sequence,
CC compared with 50-70% when the conventional washing procedure is
CC followed. AAA35313 to AAA35357, and AAA35562 to AAA35575 represent
CC nucleotide sequences from the present invention which contain
CC microsatellite sequences. AAA35358 to AAA35561 represent oligonucleotide
CC PCR primers used for identifying Myrtaceae microsatellite sequences.
XX
SQ Sequence 20 BP; 11 A; 6 C; 3 G; 0 U; 0 other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1140 TGCCTTTTTTTCTTTTTGG 1158
||||||||| ||||| ||
Db 19 TGCCTTTTGTCTTTGGGG 1

RESULT 174
AAZ40588/c
ID AAZ40588 standard; DNA; 20 BP.
XX
AC AAZ40588;
XX
DT 29-FEB-2000 (first entry)
XX
DE NPTII gene forward target primer for detection in E.coli.
XX
KW Reporter; quencher; probe; assay; internal control agent; primer; PCR;
KW detection; measurement; amplification; blocking sequence; copy-number;
KW quantitation; allele; discrimination; polymorphism; pathogen; NPTII; ss.
XX
OS Synthetic.
XX
PN US5952202-A.
XX
PD 14-SEP-1999.
XX
PF 26-MAR-1998; 98US-0048880.
XX
PR 26-MAR-1998; 98US-0048880.
XX
PA (PEKE) PERKIN-ELMER CORP.
XX
PI Aoyagi K, Livak KJ;
XX
DR WPI; 2000-011874/01.
XX
PT Methods using exogenous, internal controls and analogue blocks
PT during nucleic acid amplification -
XX
PS Example 4; Column 21; 29pp; English.
XX
CC The invention relates to methods of rendering reporter-quencher probe
CC assays more meaningful by the addition of internal control agents.
CC Primers for a target and an internal control sequence are labelled with
CC a detectable marker which allows concurrent detection and measurement
CC of target and control nucleic acid amplification. The reaction may also
CC contain a non-extendable oligonucleotide (i.e. a blocking sequence)
CC complementary to the internal control sequence, which functions as a
CC negative control. The method can be used for quantitating nucleic acid
CC amplification of control DNA in the presence of, and concurrently with,
CC nucleic acid amplification of known or unknown target DNA. Suggested
CC uses include tracking of target sample extraction, isolation and
CC purification, for amplification of low copy number genes, for allelic
CC discrimination of polymorphic samples or pathogen detection.
CC Primers AAZ40588-Z40590 are used to detect NPTII RNA in transgenic
CC E.coli by the method of the invention. Primers AAZ40588-Z40589 were
CC used for amplifying the NPTII target sequence.
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 620 TCAGGGACCAGCTCCAGGA 638
||||| ||| | |||||||
Db 20 TCAGGAACCTGGTCCAGGA 2

RESULT 175
AAI66616/c
ID AAI66616 standard; DNA; 20 BP.
XX
AC AAI66616;
XX
DT 07-JAN-2002 (first entry)
XX
DE Rat leukotriene B4 receptor JULF2 DNA amplifying PCR primer.
XX
KW Leukotriene receptor; leukotriene B4; inflammatory disease; rat;
KW JULF2; bronchitis; dermatitis; psoriasis; ulcerative colitis;
KW rheumatoid arthritis; edema; PCR primer; ss.
XX
OS Rattus norvegicus.
XX
PN WO200170815-A1.
XX
PD 27-SEP-2001.
XX
PF 15-MAR-2001; 2001WO-JP02060.
XX
PR 21-MAR-2000; 2000JP-0078992.
PR 22-JUN-2000; 2000JP-0187978.
XX
PA (YAMA) YAMANOUCHI PHARM CO LTD.
XX
PI Kamohara M, Matsumoto M, Takasaki J, Saito T, Ohishi T;
XX
DR WPI; 2001-611487/70.
XX
PT New polypeptide for screening for compounds which treat inflammatory
PT diseases such as bronchitis, dermatitis, psoriasis, ulcerative colitis,
PT rheumatoid arthritis, and edema comprises the leukotriene B4 receptor -
XX
PS Example 10; Page 47; 55pp; Japanese.
XX
CC The invention provides a leukotriene receptor, which binds leukotriene B4
CC and polynucleotides encoding the leukotriene B4 receptor. The receptor
CC can be expressed by standard recombinant methodology. Pharmaceutical
CC compositions containing materials which modify the receptor activity,
CC other than 4-octyloxybenzene carboximidoamide are used for treating and
CC preventing inflammatory disease. The materials detected by screening the
CC receptor (JULF2) are useful for treating diseases such as bronchitis,
CC dermatitis, psoriasis, ulcerative colitis, rheumatoid arthritis, and
CC edema. Sequences AAI66614-19 represent PCR primers for amplifying a
CC rat leukotriene B4 receptor JULF2 DNA.
XX
SQ Sequence 20 BP; 5 A; 11 C; 4 G; 0 U; 0 other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy        723 GCAGCAGGGGGCCTGGCTG 741
              || || ||||| |||||||
Db         20 GCTGCTGGGGGTCTGGCTG 2


RESULT 176
AAS08740/c
ID   AAS08740 standard; DNA; 20 BP.
XX
AC   AAS08740;
XX
DT   26-SEP-2001  (first entry)
XX
DE   Human PD-ABC form 1 DNA exon 11 3' splice site.
XX
KW   PD-ATP-binding cassette; PD-ABC; chromosome 19p13.3; spleen; thymus; ds;
KW   peripheral blood leukocyte; bone marrow; lymph node; dyslipidaemia;
KW   cardiovascular disorder; inflammatory disorder; abnormal calcium flux;
KW   epilepsy; coronary artery disease; Tangier's disease; atherosclerosis;
KW   familial high-density lipoprotein deficiency; fatty liver disease;
KW   atherosclerosis; diabetes; insulin resistance; obesity; drug screening;
KW   alcoholism; retinal degeneration; hypertension; vascular disease.
XX
OS   Homo sapiens.
XX
PN   WO200153490-A1.
XX
PD   26-JUL-2001.
XX
PF   23-JAN-2001; 2001WO-US02191.
XX
PR   24-JAN-2000; 2000US-0177889.
PR   30-JUN-2000; 2000US-0215405.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Johns MA,  Tafuri SR,  Wang M;
XX
DR   WPI; 2001-442259/47.
XX
PT   New Human PD-ABC DNA molecules and proteins for diagnosis and treatment
PT   of dyslipidaemia, epilepsy and diseases related to abnormal calcium flux
PT   -
XX
PS   Disclosure; Page 37; 77pp; English.
XX
CC   The sequence represents a splice site within a DNA molecule encoding
CC   human PD-ATP-binding cassette (PD-ABC) protein. PD-ABC maps to chromosome
CC   19p13.3 and is expressed in various tissues including spleen, thymus,
CC   peripheral blood leukocytes, bone marrow and lymph nodes. The PD-ABC DNA
CC   molecules and proteins are used to diagnose and treat cardiovascular
CC   disorders, inflammatory disorders, dyslipidaemia, epilepsy, diseases
CC   related to abnormal calcium flux, coronary artery disease, Tangier's
CC   disease, familial high-density lipoprotein deficiency, atherosclerosis,
CC   diabetes, fatty liver disease, insulin resistance, obesity, alcoholism,
CC   retinal degeneration, hypertension and vascular disease. The sequences
CC   are also used in drug screening assays.
XX
SQ   Sequence 20 BP; 5 A; 3 C; 11 G; 1 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        971 CCCTCACTTGACCAGTCCC 989
              ||||| | ||||| |||||
Db         20 CCCTCGCCTGACCTGTCCC 2


RESULT 177
AAS08831/c
ID   AAS08831 standard; DNA; 20 BP.
XX
AC   AAS08831;
XX
DT   26-SEP-2001  (first entry)
XX
DE   Human PD-ABC form 2 DNA exon 11 3' splice site.
XX
KW   PD-ATP-binding cassette; PD-ABC; chromosome 19p13.3; spleen; thymus; ds;
KW   peripheral blood leukocyte; bone marrow; lymph node; dyslipidaemia;
KW   cardiovascular disorder; inflammatory disorder; abnormal calcium flux;
KW   epilepsy; coronary artery disease; Tangier's disease; atherosclerosis;
KW   familial high-density lipoprotein deficiency; fatty liver disease;
KW   atherosclerosis; diabetes; insulin resistance; obesity; drug screening;
KW   alcoholism; retinal degeneration; hypertension; vascular disease.
XX
OS   Homo sapiens.
XX
PN   WO200153490-A1.
XX
PD   26-JUL-2001.
XX
PF   23-JAN-2001; 2001WO-US02191.
XX
PR   24-JAN-2000; 2000US-0177889.
PR   30-JUN-2000; 2000US-0215405.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Johns MA,  Tafuri SR,  Wang M;
XX
DR   WPI; 2001-442259/47.
XX
PT   New Human PD-ABC DNA molecules and proteins for diagnosis and treatment
PT   of dyslipidaemia, epilepsy and diseases related to abnormal calcium flux
PT   -
XX
PS   Disclosure; Page 39; 77pp; English.
XX
CC   The sequence represents a splice site within a DNA molecule encoding
CC   human PD-ATP-binding cassette (PD-ABC) protein. PD-ABC maps to chromosome
CC   19p13.3 and is expressed in various tissues including spleen, thymus,
CC   peripheral blood leukocytes, bone marrow and lymph nodes. The PD-ABC DNA
CC   molecules and proteins are used to diagnose and treat cardiovascular
CC   disorders, inflammatory disorders, dyslipidaemia, epilepsy, diseases
CC   related to abnormal calcium flux, coronary artery disease, Tangier's
CC   disease, familial high-density lipoprotein deficiency, atherosclerosis,
CC   diabetes, fatty liver disease, insulin resistance, obesity, alcoholism,
CC   retinal degeneration, hypertension and vascular disease. The sequences
CC   are also used in drug screening assays.
XX
SQ   Sequence 20 BP; 5 A; 3 C; 11 G; 1 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        971 CCCTCACTTGACCAGTCCC 989
              ||||| | ||||| |||||
Db         20 CCCTCGCCTGACCTGTCCC 2


RESULT 178
AAH57078
ID   AAH57078 standard; DNA; 20 BP.
XX
AC   AAH57078;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human oestrogen receptor alpha probe oligonucleotide 23.
XX
KW   Ligand dependent transcriptional factor; oestrogen receptor; ER;
KW   glucocorticoid receptor protein; GR; mineralocorticoid receptor protein;
```

KW MR; peroxisome proliferator-activated receptor protein; PPAR;
KW progesterone receptor protein; PR; pregnane X receptor protein; PXR;
KW thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR;
KW transactivation; ERalpha; breast cancer; PCR primer; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200142307-A1.
XX
PD 14-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-JP08553.
XX
PR 07-DEC-1999; 99JP-0348022.
PR 27-DEC-1999; 99JP-0370667.
PR 07-JUL-2000; 2000JP-0207011.
PR 21-JUL-2000; 2000JP-0220508.
PR 02-AUG-2000; 2000JP-0234053.
PR 03-AUG-2000; 2000JP-0235460.
PR 03-AUG-2000; 2000JP-0235461.
PR 03-AUG-2000; 2000JP-0235463.
XX
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
PI Saito K, Ohe N, Satoh H;
XX
DR WPI; 2001-367866/38.
XX
PT Ligand dependent transcriptional factors, nucleic acids encoding them
PT and cells comprising them and a specified reporter gene, useful for
PT screening agents for the treatment of breast cancer -
XX
PS Disclosure; Page 241; 276pp; English.
XX
CC The present invention relates to ligand dependent transcriptional factors
CC including oestrogen receptor (ER) alpha and beta protein, glucocorticoid
CC receptor protein (GR), mineralocorticoid receptor protein (MR),
CC peroxisome proliferator-activated receptor protein (PPAR), progesterone
CC receptor protein (PR), pregnane X receptor protein (PXR), thyroid hormone
CC receptor protein (TR) and vitamin D receptor protein (VDR), the nucleic
CC acids encoding them and cells comprising them and a specified reporter
CC gene for the ligand dependent transcriptional factor. These proteins are
CC useful in the modulation of ligand dependent transcriptional factor
CC activity. The cells, mutant ERalpha and the polynucleotide encoding it
CC may be used in assays for qualitatively analysing an activity for
CC transactivation of a reporter gene by a test ERalpha, for screening
CC mutant ligand dependent transcriptional factors, for evaluating an
CC activity for transactivation of a reporter gene by a test ERalpha and/or
CC for screening a compound useful for treating a disorder of a mutant
CC ERalpha, especially breast cancer.
XX
SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1002 CTTGGACAGGCACCTGAGA 1020
||||||||||.|||.|.||
Db 2 CTTGGACAGGAACCAGGGA 20

RESULT 179
AAH57086/c
ID AAH57086 standard; DNA; 20 BP.
XX
AC AAH57086;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human oestrogen receptor alpha probe oligonucleotide 31.
XX
KW Ligand dependent transcriptional factor; oestrogen receptor; ER;
KW glucocorticoid receptor protein; GR; mineralocorticoid receptor protein;
KW MR; peroxisome proliferator-activated receptor protein; PPAR;
KW progesterone receptor protein; PR; pregnane X receptor protein; PXR;
KW thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR;
KW transactivation; ERalpha; breast cancer; PCR primer; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200142307-A1.
XX
PD 14-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-JP08553.
XX
PR 07-DEC-1999; 99JP-0348022.
PR 27-DEC-1999; 99JP-0370667.
PR 07-JUL-2000; 2000JP-0207011.
PR 21-JUL-2000; 2000JP-0220508.
PR 02-AUG-2000; 2000JP-0234053.
PR 03-AUG-2000; 2000JP-0235460.
PR 03-AUG-2000; 2000JP-0235461.
PR 03-AUG-2000; 2000JP-0235463.
XX
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
PI Saito K, Ohe N, Satoh H;
XX
DR WPI; 2001-367866/38.
XX
PT Ligand dependent transcriptional factors, nucleic acids encoding them
PT and cells comprising them and a specified reporter gene, useful for
PT screening agents for the treatment of breast cancer -
XX
PS Disclosure; Page 243; 276pp; English.
XX
CC The present invention relates to ligand dependent transcriptional factors
CC including oestrogen receptor (ER) alpha and beta protein, glucocorticoid
CC receptor protein (GR), mineralocorticoid receptor protein (MR),
CC peroxisome proliferator-activated receptor protein (PPAR), progesterone
CC receptor protein (PR), pregnane X receptor protein (PXR), thyroid hormone
CC receptor protein (TR) and vitamin D receptor protein (VDR), the nucleic
CC acids encoding them and cells comprising them and a specified reporter
CC gene for the ligand dependent transcriptional factor. These proteins are
CC useful in the modulation of ligand dependent transcriptional factor
CC activity. The cells, mutant ERalpha and the polynucleotide encoding it
CC may be used in assays for qualitatively analysing an activity for
CC transactivation of a reporter gene by a test ERalpha, for screening
CC mutant ligand dependent transcriptional factors, for evaluating an
CC activity for transactivation of a reporter gene by a test ERalpha and/or
CC for screening a compound useful for treating a disorder of a mutant
CC ERalpha, especially breast cancer.
XX
SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 469 CTGCAGGGGGAGGACTGCC 487
||||||| ||| |||||
Db 20 CTGCAGGGTCAGGCCTGCC 2

RESULT 180
AAF62896/c
ID AAF62896 standard; DNA; 20 BP.
XX
AC AAF62896;
XX
DT 08-MAY-2001 (first entry)
XX
DE Human PEPCK-cytosolic antisense oligonucleotide ISIS 108064.
XX

KW Human; antiinflammatory; cytostatic; antisense gene therapy;
KW phosphoenol pyruvate carboxykinase-cytosolic; PEPCK-cytosolic;
KW infection; inflammation; tumour formation; phosphorothioate; ss.
XX
OS Homo sapiens.
XX
PN US6187545-B1.
XX
PD 13-FEB-2001.
XX
PF 21-JAN-2000; 2000US-0488671.
XX
PR 21-JAN-2000; 2000US-0488671.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI McKay R, Butler MM, Wyatt J, Cowsert LM;
XX
DR WPI; 2001-190979/19.
XX
PT Antisense compound capable of modulating the expression of phosphoenol
PT pyruvate carboxykinase-cytosolic, useful for preventing or delaying
PT infection, inflammation or tumor formation -
XX
PS Claim 1; Column 43; 64pp; English.
XX
CC The present sequence is one of a number of antisense compounds of up to
CC 30 nucleobases in length that are capable of inhibiting the expression of
CC phosphoenol pyruvate carboxykinase-cytosolic (PEPCK-cytosolic). The
CC antisense compounds are useful for inhibiting the expression of
CC PEPCK-cytosolic in cells or tissues. They are commonly used as research
CC reagents and in diagnostics, e.g. to elucidate the function of particular
CC genes. They are also useful for distinguishing between functions of
CC various members of a biological pathway and for research use. The
CC antisense compounds are also useful prophylactically, e.g. to prevent or
CC delay infection, inflammation or tumour formation. The present sequence
CC is a chimeric phosphorothioate oligonucleotide with 2'-MOE wings and a
CC deoxy gap.
XX
SQ Sequence 20 BP; 4 A; 3 C; 10 G; 3 T; 0 other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 512 TCAGCGCCAACCTGCCGGA 530
||| |||| ||||||| ||
Db 20 TCATCGCCCACCTGCCTGA 2

RESULT 181
AAA91053
ID AAA91053 standard; DNA; 20 BP.
XX
AC AAA91053;
XX
DT 05-APR-2001 (first entry)
XX
DE PCR primer for Human secreted protein PRO6496 coding sequence.
XX
KW Secreted protein; human; PRO protein; neoplastic cell growth; tumour;
KW proliferation; leukaemia; lymphoid malignancy; inflammatory disorder;
KW angiogenic disorder; immunologic disorder; PRO6496; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200075317-A2.
XX
PD 14-DEC-2000.
XX
PF 15-MAY-2000; 2000WO-US13358.
XX
PR 09-JUN-1999; 99US-0138385.
PR 20-JUL-1999; 99US-0144790.
PR 03-AUG-1999; 99US-0146843.
PR 10-AUG-1999; 99US-0148188.
PR 17-AUG-1999; 99US-0149320.
PR 17-AUG-1999; 99US-0149327.
PR 17-AUG-1999; 99US-0149396.
PR 20-AUG-1999; 99US-0150114.
PR 31-AUG-1999; 99US-0151700.
PR 31-AUG-1999; 99US-0151734.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein DA, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX
DR WPI; 2001-071075/08.
XX
PT Antibodies against PRO polypeptides, useful for diagnosing and treating
PT tumours are associated with gene amplification, neoplastic cell growth
PT and proliferation in mammals -
XX
PS Example 11; Page 95; 143pp; English.
XX
CC This sequence represents a PCR primer used to isolate DNA encoding
CC human PRO5800 protein of the invention. The PRO proteins are secreted
CC proteins. Antagonists or antibodies of PRO polypeptides are useful for
CC diagnosing and treating tumours are associated with gene amplification,
CC neoplastic cell growth and proliferation in mammals, and those conditions
CC characterised by overexpression and/or activation of the amplified genes.
CC Such conditions include benign or malignant tumours (e.g. renal, liver,
CC kidney, bladder, breast, gastric, ovarian, colorectal, prostate,
CC pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas,
CC glioblastomas and various head and neck tumours); leukaemias and lymphoid
CC malignancies; neuronal, glial, astrocytal, hypothalamic, and other
CC glandular, macrophageal, epithelial, stromal and blastocoelic disorders;
CC and inflammatory, angiogenic and immunologic disorders. These may further
CC be used to qualitatively or quantitatively detect the expression of
CC proteins encoded by the amplified genes, and in tumour diagnostics or
CC prognostics. The PRO polypeptide or its antagonist may be used for the
CC preparation of a medicament in the treatment of a condition, which is
CC responsive to the PRO polypeptide, its antagonist or anti-PRO antibody.
XX
SQ Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 611 CTGACACCTTCAGGGACCA 629
|||||| ||||||| |||
Db 2 CTGACAACTTCAGGTTCCA 20

RESULT 182
AAH89204
ID AAH89204 standard; DNA; 20 BP.
XX
AC AAH89204;
XX
DT 27-FEB-2002 (first entry)
XX
DE Human polymorphic oligonucleotide U85199 fragment #2.
XX
KW Human; single nucleotide polymorphic; SNP; forensic science;
KW paternity testing; phenotypic trait; genetic mapping; animal breeding;
KW plant breeding; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(10,c)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX

PN WO200134840-A2.
XX
PD 17-MAY-2001.
XX
PF 10-NOV-2000; 2000WO-US30766.
XX
PR 10-NOV-1999; 99US-0164596.
XX
PA (GLAX) GLAXO GROUP LTD.
PA (AFFY-) AFFYMETRIX INC.
XX
PI Au K, Chen J, Patil N, Thomas D;
XX
DR WPI; 2001-335945/35.
XX
PT New polymorphic sites derived from the human genome are useful to
PT determine sites correlating with phenotypic traits, particularly
PT disease, and also in forensics and paternity testing -
XX
PS Claim 95; Page 16; 43pp; English.
XX
CC The present invention relates to human oligonucleotides comprising a
CC single nucleotide polymorphic site (SNP: AAH88797-AAH89219). The present
CC sequence is one such oligonucleotide. The oligonucleotides can be used in
CC forensics, paternity testing, correlation of polymorphisms with
CC phenotypic traits, genetic mapping of phenotypic traits and marker
CC assisted breeding of animals and crop plants.
XX
SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 220 CGAGCTCCTCAGCCTCAGG 238
| ||||||| || ||||||
Db 2 CTAGCTCCTGAGGCTCAGG 20

RESULT 183
ABQ81623
ID ABQ81623 standard; DNA; 20 BP.
XX
AC ABQ81623;
XX
DT 12-DEC-2002 (first entry)
XX
DE CYP2E1 sense primer.
XX
KW Transgenic animal; drug; fetotoxicity; teratogenicity; antidiabetic;
KW neuroprotective; cerebroprotective; nootropic; cytostatic; cardiant;
KW nephrotropic; osteopathic; antiallergic; antiarteriosclerotic;
KW anti-microbial; diabetes; infection; dementia; cytochrome P; PCR;
KW primer; ss.
XX
OS Homo sapiens.
XX
PN WO200266635-A1.
XX
PD 29-AUG-2002.
XX
PF 21-FEB-2002; 2002WO-JP01555.
XX
PR 23-FEB-2001; 2001JP-0047735.
XX
PA (GENC-) GENCOM CORP.
XX
PI Katsuki M, Kamataki T, Teranishi Y, Ishida M, Kato M;
XX
DR WPI; 2002-674938/72.
XX
PT Transgenic animals having drug metabolism enzyme genes, useful in
PT testing fetotoxicity and/or teratogenicity and applicable to drug
PT development for diseases including diabetes, infections and dementia -
XX
PS Example 2; Page 27; 60pp; Japanese.
XX
CC The invention relates to a recombinant gene that comprises, a gene
CC encoding human P450 or its variant, the human EF1alpha promoter, chick
CC beta globin insulator sequence or a part of it, and the SV40
CC polyA-attached signal. The activity of the gene of the invention may be
CC described as, antidiabetic, neuroprotective, cerebroprotective,
CC nootropic, cytostatic, cardiant, nephrotropic, osteopathic, antiallergic,
CC antiarteriosclerotic and anti-microbial. The intention of this invention
CC is to provide a transgenic animal. The animal is useful in testing
CC fetotoxicity and/or teratogenicity, and is applicable to drug development
CC for diseases including diabetes, infections and dementia. The current
CC sequence represents a primer designated CYP2E1 sense primer, which is
CC used in an example from the invention in the amplification of cytochrome
CC P from total RNA from human liver.
XX
SQ Sequence 20 BP; 2 A; 8 C; 7 G; 3 T; 0 other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 381 TCCTCCAGAGGTGGCAGCA 399
|||||| | | ||||||||
Db 2 TCCTCCCGGGCTGGCAGCA 20

RESULT 184
AAL49010
ID AAL49010 standard; DNA; 20 BP.
XX
AC AAL49010;
XX
DT 29-OCT-2002 (first entry)
XX
DE Murine IL-13 coding sequence PCR primer #2.
XX
KW Mouse; immune response; IL-13; NK-T cell; cancer; metastasis; PCR;
KW interleukin-13; neurokinin-T; antitumour; virucide; cytostatic; anti-HIV;
KW hepatotropic; immunostimulant; antiinflammatory; primer; ss.
XX
OS Mus sp.
XX
PN WO200255100-A2.
XX
PD 18-JUL-2002.
XX
PF 22-OCT-2001; 2001WO-US51339.
XX
PR 20-OCT-2000; 2000US-0693600.
PR 07-SEP-2001; 2001US-318185P.
XX
PA (GEMY) GENETICS INST LLC.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Berzofsky JA, Terabe M, Donaldson DD, Matsui S, Noben-Trauth N;
PI Paul WE;
XX
DR WPI; 2002-636505/68.
XX
PT Tumor growth inhibition by administration of interleukin-13 or
PT neurokinin-T cell inhibitors -
XX
PS Example 1; Page 11; 34pp; English.
XX
CC The present invention relates to the inhibition of tumour growth. It
CC involves administration of an inhibitor of interleukin-13 (IL-13)
CC comprising an IL-13 ligand, or a neurokinin-T (NK-T) cell inhibitor. The
CC method can be used to inhibit tumour and virus growth and chronic
CC infection and for enhancing an immune response in mammals (preferably
CC humans). The present sequence is a PCR primer used to amplify the murine

```
CC   IL-13 coding sequence in the exemplification of the invention.
XX
SQ   Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        290 CAGCAATGTCTGCTGTGGG 308
              |||||| ||||| |||| |
Db          2 CAGCAAAGTCTGATGTGAG 20


RESULT 185
AAL47998/c
ID   AAL47998 standard; DNA; 20 BP.
XX
AC   AAL47998;
XX
DT   26-SEP-2002  (first entry)
XX
DE   Human homeodomain-interacting protein kinase HIPK2 cDNA PCR primer #1.
XX
KW   Human; homeodomain-interacting protein kinase 2; HIPK2; cancer; enzyme;
KW   cell proliferation; cell growth; cytostatic; vulnerary; wound healing;
KW   PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200257433-A2.
XX
PD   25-JUL-2002.
XX
PF   21-JAN-2002; 2002WO-EP00557.
XX
PR   22-JAN-2001; 2001DE-1002797.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Hofmann T,  Schmitz L,  Droege W,  Moeller A,  Will H,  Hueseyin S;
XX
DR   WPI; 2002-538471/57.
XX
PT   Use of homeodomain-interacting protein kinase for modifying cell
PT   behavior, treatment or diagnosis of proliferative diseases and in drug
PT   screening -
XX
PS   Example 1; Page 15; 44pp; German.
XX
CC   The present invention relates to the use of homeodomain-interacting
CC   protein kinase HIPK2 to modulate cell differentiation and proliferation
CC   and to diagnose and treat associated diseases, including cancers,
CC   particularly lymphoma and carcinoma (of breast, liver, stomach,
CC   intestines, lung, ovary or cervix), and to promote wound healing. The
CC   present sequence is a PCR primer used to isolate the human HIPK2 coding
CC   sequence.
XX
SQ   Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1244 ACGTGGCCATGTGAGGCCA 1262
              || ||  ||||||||||||
Db         20 ACTTGCACATGTGAGGCCA 2


RESULT 186
AAD37217/c
ID   AAD37217 standard; DNA; 20 BP.
XX
AC   AAD37217;
XX
DT   21-AUG-2002  (first entry)
XX
DE   Human MEKK4 antisense oligonucleotide, ISIS #123152.
XX
KW   Human; MEKK4 modulation; mitogen-activated protein kinase kinase 4; MTK1;
KW   MAP3K4; MAP three kinase 1; MAP/ERK kinase kinase 4; MAPKKK4; cytostatic;
KW   prophylaxis; immunological; hyperproliferative disorder; cancer; therapy;
KW   antisense; inflammatory; phosphorothioate backbone; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1..20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone"
FT   modified_base    1..5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-methoxyethyl nucleotides"
FT   modified_base    16..20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-methoxyethyl nucleotides"
FT   modified_base    5
FT                    /*tag=  d
FT                    /mod_base= m5c
FT   modified_base    12
FT                    /*tag=  e
FT                    /mod_base= m5c
FT   modified_base    16
FT                    /*tag=  f
FT                    /mod_base= m5c
FT   modified_base    20
FT                    /*tag=  g
FT                    /mod_base= m5c
XX
PN   WO200227033-A1.
XX
PD   04-APR-2002.
XX
PF   28-SEP-2001; 2001WO-US30549.
XX
PR   29-SEP-2000; 2000US-0676436.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ward DT,  Gaarde WA,  Monia BP,  Wyatt JR;
XX
DR   WPI; 2002-416486/44.
XX
PT   New antisense compound targeted to nucleic acid encoding
PT   mitogen-activated protein kinase 4, useful for treating immunologic
PT   disorder, inflammatory disorder or cancer  -
XX
PS   Claim 3; Page 93; 132pp; English.
XX
CC   The present invention relates to antisense compounds, compositions and
CC   methods for modulating the expression of MEKK4 (also referred as mitogen-
CC   activated protein kinase kinase 4; MAP3K4; MAP three kinase 1; MAP/ERK
CC   kinase kinase 4; MAPKKK4; MTK1). The antisense oligos are useful for
CC   inhibiting the expression of MEKK4 in cells or tissues. They are also
CC   useful for treating an animal having a disease or condition associated
CC   with MEKK4 such as immunological, inflammatory, hyperproliferative
CC   disorder or cancer. Sequences of the invention are also useful for
CC   diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC   They are also useful in antisense therapy. The present sequence is an
CC   antisense oligonucleotide targetted to human MEKK4 DNA. This sequence
CC   is used in the exemplification of the invention.
XX
SQ   Sequence 20 BP; 2 A; 4 C; 10 G; 4 T; 0 other;
```

```
  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        215 GCCAGCGAGCTCCTCAGCC 233
              |||||| ||||||||  ||
Db         20 GCCAGCCAGCTCCTCGACC 2


RESULT 187
ABK15887
ID   ABK15887 standard; DNA; 20 BP.
XX
AC   AEK15887;
XX
DT   21-MAY-2002  (first entry)
XX
DE   HES-1 (hairy-enhancer of split-1) forward PCR primer DNA sequence.
XX
KW   Hairy-enhancer of split-1; HES-1; real-time PCR; primer; ss;
KW   multiple sclerosis; rheumatoid arthritis; diabetes; organ transplant;
KW   asthma; allergy; autoimmunity; graft rejection; tumour; cytostatic;
KW   Notch signal modulator; T-cell mediated disease; infectious disease;
KW   human immunodeficiency virus; HIV; virucide; hepatotropic; protozoacide;
KW   neuroprotective; cancer.
XX
OS   Unidentified.
XX
PN   WO200212890-A2.
XX
PD   14-FEB-2002.
XX
PF   03-AUG-2001; 2001WO-GB03503.
XX
PR   04-AUG-2000; 2000GB-0019242.
XX
PA   (LORA-) LORANTIS LTD.
XX
PI   Lamb JR,  Hoyne GF,  Dallman MJ,  Champion BR;
XX
DR   WPI; 2002-217232/27.
XX
PT   Monitoring the immune system for prevention and/or treatment of T-cell
PT   mediated diseases e.g. allergy, autoimmunity or cancer, involves
PT   detecting modulation of Notch signalling  -
XX
PS   Disclosure; Fig 13; 75pp; English.
XX
CC   The present invention relates to a new method for monitoring the immune
CC   system that involves detecting modulation of Notch signalling. The method
CC   of the invention can be used for monitoring the immune system such as
CC   detecting or monitoring T-cell activation or inactivation, immunological
CC   tolerance or activity, monitoring the efficacy of immunotherapy and for
CC   detecting or monitoring the reactivity of a T-cell to an antigen e.g. for
CC   detecting increased or decreased reactivity of a T-cell to an antigen and
CC   detecting tolerisation of a T-cell to an antigen, and for detecting
CC   whether the antigen is self or foreign antigen. The method is used in the
CC   prevention and/or treatment of T-cell mediated diseases such as asthma,
CC   allergy, autoimmunity, graft rejection, tumour induced aberrations to the
CC   T-cell system, and infectious diseases caused by e.g. Cytomegalovirus,
CC   Pseudomonas, Toxoplasma, Microfilariae, Helminths, Mycobacteria, human
CC   immunodeficiency virus (HIV), plasmodium species, Echinococcus,
CC   Haemophilus influenza type B, measles, Hepatitis C or Toxicara. The
CC   method is also used for the treatment of multiple sclerosis, rheumatoid
CC   arthritis, diabetes and for organ transplantation. The present assay
CC   method provides a much more objective measure of the effectiveness of
CC   therapy than the rather subjective symptoms-based measures which are
CC   often used at present. The ability to detect an immune response could be
CC   used in identifying the cause of an allergic reaction by monitoring the
CC   activity of the immune system in the presence of different potential
CC   allergens. The assay could be used to check for successful immunisation
CC   against a given disease antigen. The present nucleic acid sequence
CC   represents the human HES-1 (hairy-enhancer of split-1) forward PCR primer
CC   that was used in the invention with the HES-1 reverse PCR primer
CC   (ABK15888) and the HES-1 probe (ABK09925) for real-time PCR of the
CC   HES-1 gene.
XX
SQ   Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1081 CTTCAGTGAGTGTTTGAAC 1099
              |||||| |||||  |||||
Db          2 CTTCAGCGAGTGCATGAAC 20


RESULT 188
ABL45977
ID   ABL45977 standard; DNA; 20 BP.
XX
AC   ABL45977;
XX
DT   26-APR-2002  (first entry)
XX
DE   Humanised anti-Fas antibody related PCR primer SEQ ID NO 153.
XX
KW   Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
KW   light chain subunit; apoptosis; immunosuppressive; antiallergic;
KW   autoimmune disease; allergy; atopic; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   JP2001342148-A.
XX
PD   11-DEC-2001.
XX
PF   28-MAR-2001; 2001JP-0093106.
XX
PR   29-MAR-2000; 2000JP-0090918.
XX
PA   (SANY ) SANKYO CO LTD.
XX
DR   WPI; 2002-145113/19.
XX
PT   Drug containing humanised anti-Fas antibody, used for preventing and
PT   treating autoimmune diseases, allergy, and atopy -
XX
PS   Example 3; Page 65; 194pp; Japanese.
XX
CC   The invention relates to a preventive or treating agent for diseases
CC   caused by abnormality in Fas/Fas ligand system containing as the active
CC   component an antibody having as the light chain subunit a polypeptide
CC   containing residues 1-218 of one of 3, 239 residue amino acid sequences,
CC   or residues 1-451 of one of 3, 470 residue amino acid sequences, all
CC   fully defined in the specification and having an activity of combining
CC   specifically with mammalian Fas and an activity of inducing apoptosis
CC   in a cell expressing Fas. The agent has immunosuppressive and
CC   antiallergic activity and is used for preventing and treating autoimmune
CC   diseases, allergy, atopy and others. The present sequence is that of a
CC   PCR primer, useful to the invention.
XX
SQ   Sequence 20 BP; 5 A; 5 C; 8 G; 2 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        482 ACTGCCGAGACGGTGTGCA 500
              || |||| || ||||||||
Db          1 ACAGCCGGGAAGGTGTGCA 19


RESULT 189
```

```
ABL48720
ID   ABL48720 standard; DNA; 20 BP.
XX
AC   ABL48720;
XX
DT   30-APR-2002  (first entry)
XX
DE   Humanised anti-Fas antibody related PCR primer SEQ ID NO 58.
XX
KW   Human; mouse; Fas/Fas ligand system; Fas; antibody; light chain;
KW   heavy chain; apoptosis; antiallergic; immunosuppressive; apoptotic;
KW   autoimmune disease; allergy; atopy; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   JP2001342149-A.
XX
PD   11-DEC-2001.
XX
PF   28-MAR-2001; 2001JP-0093243.
XX
PR   29-MAR-2000; 2000JP-0091144.
XX
PA   (SANY ) SANKYO CO LTD.
XX
DR   WPI; 2002-145114/19.
XX
PT   Drug for preventing or treating e.g. autoimmune disease or allergy,
PT   comprises humanised anti-Fas antibody  -
XX
PS   Example 14 (preparatory); Page 32; 154pp; Japanese.
XX
CC   The invention relates to a preventive or treating agent for diseases
CC   caused by abnormality in the Fas/Fas ligand system containing, as the
CC   active component, an antibody having a light chain subunit and a heavy
CC   chain subunit and an activity of combining specifically with mammalian
CC   Fas and an activity of inducing apoptosis in a cell expressing Fas. The
CC   agent has antiallergic, immunosuppressive and apoptotic activity and is
CC   used for preventing and treating autoimmune diseases, allergy, atopy and
CC   others. The present sequence is that of a PCR primer useful in the
CC   construction of anti-Fas antibodies of the invention.
XX
SQ   Sequence 20 BP; 5 A; 5 C; 8 G; 2 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        482 ACTGCCGAGACGGTGTGCA 500
              || |||| || ||||||||
Db          1 ACAGCCGGGAAGGTGTGCA 19


RESULT 190
AAS97928
ID   AAS97928 standard; DNA; 20 BP.
XX
AC   AAS97928;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Murine SAC1 gene-specific oligonucleotide PCR primer #481.
XX
KW   Human; mouse; SAC1; carbohydrate; sweetener; ethanol; alcoholism; ss;
KW   obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;
KW   blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
KW   protein replacement therapy.
XX
OS   Mus sp.
XX
PN   WO200183749-A2.
XX
PD   08-NOV-2001.
XX
PF   25-APR-2001; 2001WO-US13387.
XX
PR   28-APR-2000; 2000US-200794P.
PR   28-JUL-2000; 2000US-221419P.
PR   10-NOV-2000; 2000US-247443P.
XX
PA   (WARN ) WARNER LAMBERT CO.
PA   (MONE-) MONELL CHEM SENSES CENT.
XX
PI   Bachmanov AA,  Beauchamp GK,  Chatterjee A,  De Jong PJ,  Li S,  Li X;
PI   Ohmen JD,  Reed DR,  Ross D,  Tordoff MG;
XX
DR   WPI; 2002-075162/10.
XX
PT   Novel isolated polypeptide comprising variant form of mouse or human
PT   SAC1 polypeptide, and is associated with altered preference for
PT   carbohydrates or other sweeteners, useful for preventing obesity,
PT   diabetes, alcoholism  -
XX
PS   Claim 14; Page 93; 239pp; English.
XX
CC   The invention relates to an isolated polypeptide, comprising a variant
CC   form of mouse or human SAC1 polypeptide. The variant form is associated
CC   with altered preference for carbohydrates, other sweeteners or ethanol.
CC   The polypeptide and its associated DNA sequence can be produced by
CC   recombinant techniques and is useful for preventing obesity, diabetes or
CC   alcoholism associated with SAC1 expression. The sequences are useful in
CC   screening for drugs and sweeteners. Recombinant cell lines and transgenic
CC   embryos may be used in screening for and identifying agents that induce
CC   or repress function of SAC1. Predisposition to diabetes, obesity or
CC   alcoholism can be ascertained by testing any fluid or tissue of a human
CC   (such as blood, pancreas or tongue) for sequence variations of the SAC1
CC   gene. A sequence variation of the SAC1 locus may indicate a
CC   predisposition to diabetes, obesity and/or alcoholism and may provide a
CC   diagnostic mark. The polynucleotide can be detected in a biological
CC   sample by contacting the DNA with a probe to form a hybridisation complex
CC   which is then detected. The sequences represent cDNA encoding human and
CC   mouse SAC1 polypeptides and PCR primers specific for the SCA1 genes.
XX
SQ   Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        879 CAAGTTCCAGGAGCTGCGG 897
              |||||| ||||||||  ||
Db          2 CAAGTTTCAGGAGCTAGGG 20


RESULT 191
AAS96782/c
ID   AAS96782 standard; DNA; 20 BP.
XX
AC   AAS96782;
XX
DT   26-FEB-2002  (first entry)
XX
DE   Human STAT3 antisense phosphorothioate oligodeoxynucleotide #15.
XX
KW   STAT3; human; signal transducer and activator of transcription; ss; STAT;
KW   antisense gene therapy; Fas-mediated apoptosis; inflammatory disease;
KW   autoimmune disease; rheumatoid arthritis; cancer; breast; prostate; head;
KW   neck; brain; leukaemia; myeloma; melanoma; lymphoma; apoptosis;
KW   antiinflammatory; immunosuppressive; antirheumatic; antiarthritic;
KW   cytostatic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US2001029250-A1.
XX
```

PD 11-OCT-2001.
XX
PF 11-JAN-2001; 2001US-0758881.
XX
PR 08-APR-1999; 99US-0288461.
PR 06-APR-2000; 2000WO-US09054.
XX
PA (KARR/) KARRAS J G.
XX
PI Karras JG;
XX
DR WPI; 2002-009991/01.
XX
PT Novel antisense compound useful for treating and diagnosing
PT inflammatory diseases and cancers, is targeted to a nucleic acid
PT molecule encoding signal transducer and activator of transcription
PT proteins -
XX
PS Example 2; Page 13; 21pp; English.
XX
CC The invention relates to antisense compounds targeted to a nucleic acid
CC molecule encoding a signal transducer and activator of transcription
CC (STAT) protein, specifically STAT3, where the antisense compounds inhibit
CC the expression of STAT3. The antisense sequences are useful for
CC inhibiting the expression of STAT3 in cells or tissues, inducing
CC Fas-mediated apoptosis in cells, and sensitising cells to apoptosis. They
CC are also useful for treating an animal having a disease or condition
CC associated with STAT3. These disorders include inflammatory or autoimmune
CC disease, particularly rheumatoid arthritis, cancers, such as those of the
CC breast, prostate, brain and head and neck and leukaemias, myelomas,
CC melanomas and lymphomas. Also treatable are human diseases or conditions
CC characterised by a reduction in apoptosis or an insensitivity to
CC apoptotic signals. The sequences of the invention can be used in clinical
CC research, for detecting and determining the role of STAT3 in various cell
CC functions and physiological processes and for diagnosing conditions
CC associated with the expression of STAT3. The sequences represent cDNA
CC encoding human STAT3 and human STAT3 oligonucleotides.
XX
SQ Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 628 CAGCTCCAGGAGCTCTGCA 646
|||||||| |||||| ||
Db 20 CAGCTCCATCAGCTCTACA 2

RESULT 192
AAS96834/c
ID AAS96834 standard; DNA; 20 BP.
XX
AC AAS96834;
XX
DT 26-FEB-2002 (first entry)
XX
DE Human STAT3 antisense phosphorothioate oligodeoxynucleotide #67.
XX
KW STAT3; human; signal transducer and activator of transcription; ss; STAT;
KW antisense gene therapy; Fas-mediated apoptosis; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; cancer; breast; prostate; head;
KW neck; brain; leukaemia; myeloma; melanoma; lymphoma; apoptosis;
KW antiinflammatory; immunosuppressive; antirheumatic; antiarthritic;
KW cytostatic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2001029250-A1.
XX
PD 11-OCT-2001.
XX
PF 11-JAN-2001; 2001US-0758881.
XX
PR 08-APR-1999; 99US-0288461.
PR 06-APR-2000; 2000WO-US09054.
XX
PA (KARR/) KARRAS J G.
XX
PI Karras JG;
XX
DR WPI; 2002-009991/01.
XX
PT Novel antisense compound useful for treating and diagnosing
PT inflammatory diseases and cancers, is targeted to a nucleic acid
PT molecule encoding signal transducer and activator of transcription
PT proteins -
XX
PS Example 2; Page 13; 21pp; English.
XX
CC The invention relates to antisense compounds targeted to a nucleic acid
CC molecule encoding a signal transducer and activator of transcription
CC (STAT) protein, specifically STAT3, where the antisense compounds inhibit
CC the expression of STAT3. The antisense sequences are useful for
CC inhibiting the expression of STAT3 in cells or tissues, inducing
CC Fas-mediated apoptosis in cells, and sensitising cells to apoptosis. They
CC are also useful for treating an animal having a disease or condition
CC associated with STAT3. These disorders include inflammatory or autoimmune
CC disease, particularly rheumatoid arthritis, cancers, such as those of the
CC breast, prostate, brain and head and neck and leukaemias, myelomas,
CC melanomas and lymphomas. Also treatable are human diseases or conditions
CC characterised by a reduction in apoptosis or an insensitivity to
CC apoptotic signals. The sequences of the invention can be used in clinical
CC research, for detecting and determining the role of STAT3 in various cell
CC functions and physiological processes and for diagnosing conditions
CC associated with the expression of STAT3. The sequences represent cDNA
CC encoding human STAT3 and human STAT3 oligonucleotides.
XX
SQ Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1256 GAGGCCAGGTTGAGGCCCT 1274
|||| ||| ||||| ||||
Db 20 GAGGGCAGTTTGAGTCCCT 2

RESULT 193
ABI96234
ID ABI96234 standard; DNA; 20 BP.
XX
AC ABI96234;
XX
DT 16-FEB-2002 (first entry)
XX
DE Capture oligonucleptide Zip ID#3321 oligo #9.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX

```
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Barany F,  Zirvi M,  Gerry NP,  Favis R,  Kliman R;
XX
DR   WPI; 2002-034366/04.
XX
PT   Designing capture oligonucleotide probes for use on a support to which
PT   complementary oligonucleotides hybridize with little mismatch -
XX
PS   Example 5; Fig 29; 300pp; English.
XX
CC   The present invention describes a method (M1) for designing capture
CC   oligonucleotide probes (I) for use on a support to which complementary
CC   oligonucleotide probes (II) will hybridise with little mismatch, where
CC   (I) have melting temperatures within a narrow range. The method is useful
CC   for detecting infectious diseases caused by bacterial infectious agents
CC   e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC   infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC   Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC   Epstein-Barr virus and polio virus, and parasitic infectious agents
CC   selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC   medinesis. The method is also useful for detecting genetic diseases such
CC   as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC   Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC   involved in DNA amplification, replication, recombination or repair, the
CC   cancer is specifically associated with a gene selected from BRCA1 gene,
CC   p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC   method is also used for environmental monitoring, forensics and the food
CC   and feed industry, detecting comprises scanning (using e.g. a scanning
CC   electron microscope and infrared microscope) the support at the
CC   particular sites and identifying if ligation of the oligonucleotide probe
CC   sets occurred and correlating (using a computer) identified ligation to a
CC   presence or absence of the target nucleotide sequences. ABI82074 to
CC   ABI97546 represent oligonucleotide sequences used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 20 BP; 4 A; 11 C; 2 G; 3 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1053 CAGCCCTGGCCTTCCCATC 1071
              ||||||| |||||||| |
Db          1 CAGCCCTAACCTTCCCAGC 19


RESULT 194
AAD52224
ID   AAD52224 standard; DNA; 20 BP.
XX
AC   AAD52224;
XX
DT   02-MAY-2003  (first entry)
XX
DE   Human IFNGR1 antisense oligonucleotide, ISIS 147640.
XX
KW   Human; interferon gamma receptor 1; IFNGR1; autoimmune disorder; cancer;
KW   diabetes; autoimmune thyroiditis; multiple sclerosis; immunosuppressive;
KW   infection; neuroprotective; inflammation; cytostatic; antisense therapy;
KW   autoimmune arthritis; autoimmune insulinitis; Crohn's disease; tumour;
KW   receptor; antisense; phosphorothioate backbone; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1..20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidine
FT                    residues are 5-methylcytidines"
FT   modified_base    1..5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16..20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO200288162-A1.
XX
PD   07-NOV-2002.
XX
PF   16-APR-2002; 2002WO-US12006.
XX
PR   26-APR-2001; 2001US-0843376.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett FC,  Watt AT;
XX
DR   WPI; 2003-156687/15.
XX
PT   New antisense oligonucleotides targeted to a nucleic acid molecule
PT   encoding interferon gamma receptor 1, useful for treating an autoimmune
PT   disorder, e.g. diabetes, multiple sclerosis or Crohn's disease, or
PT   cancer  -
XX
PS   Example 15; Page 85; 124pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of interferon gamma receptor 1 (IFNGR1).
CC   The compositions comprise antisense compounds, particularly antisense
CC   oligonucleotides, targetted to nucleic acids encoding IFNGR1. The
CC   antisense compound is useful for treating a disease or condition
CC   associated with IFNGR1, such as an autoimmune disorder (e.g. diabetes,
CC   autoimmune thyroiditis, multiple sclerosis, autoimmune arthritis,
CC   autoimmune insulinitis or Crohn's disease), cancer or a disease or
CC   condition caused by aberrant apoptosis. It is also used for inhibiting
CC   the expression of IFNGR1, as research reagents and diagnostics, to
CC   distinguish between functions of various members of a biological
CC   pathway, as prophylactic agents (e.g. to prevent or delay infection,
CC   inflammation or tumour formation), and as probes or primers. It is
CC   also used in antisense therapy. The present sequence is an antisense
CC   oligonucleotide targetted to human IFNGR1 DNA. This sequence is used
CC   in the exemplification of the invention.
XX
SQ   Sequence 20 BP; 9 A; 4 C; 4 G; 3 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1158 GAAGTAAAGCAGCTAAAAC 1176
              | |||||||||||| | |||
Db          1 GTAGTAAAGCAGCAACAAC 19


RESULT 195
AAD52321/c
ID   AAD52321 standard; DNA; 20 BP.
XX
AC   AAD52321;
XX
DT   02-MAY-2003  (first entry)
XX
DE   Human IFNGR2 antisense oligonucleotide, ISIS #142799.
XX
KW   Antisense; interferon gamma receptor 2; autoimmune disorder; cancer;
KW   autoimmune thyroiditis; autoimmune insulinitis; multiple sclerosis;
KW   diabetes; autoimmune arthritis; Crohn's disease; apoptosis; IFNGR2;
KW   gene therapy; prophylaxis; human; phosphorothioate; ss.
XX
OS   Homo sapiens.
```

```
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..20
FT                   /*tag= a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidine
FT                   residues are 5-methylcytidines"
FT   modified_base   1..5
FT                   /*tag= b
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl nucleotides"
FT   modified_base   16..20
FT                   /*tag= c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl nucleotides"
XX
PN   WO200288163-A1.
XX
PD   07-NOV-2002.
XX
PF   16-APR-2002; 2002WO-US12007.
XX
PR   26-APR-2001; 2001US-0843377.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF, Watt AT;
XX
DR   WPI; 2003-156688/15.
XX
PT   New antisense oligonucleotides for modulating Interferon gamma receptor
PT   2, particularly useful for treating autoimmune disorders (e.g. multiple
PT   sclerosis or Crohn's disease), cancers or diseases caused by aberrant
PT   apoptosis -
XX
PS   Claim 3; Page 86; 127pp; English.
XX
CC   The invention relates to antisense compounds, composition and methods for
CC   modulating the expression of human interferon gamma receptor 2 (IFNGR2).
CC   The compositions comprise antisense compounds targetted to nucleic acids
CC   encoding IFNGR2. Antisense compounds of the invention are useful for
CC   treating diseases or conditions associated with IFNGR2, e.g. autoimmune
CC   disorder (e.g. autoimmune thyroiditis, diabetes, multiple sclerosis,
CC   autoimmune arthritis, autoimmune insulinitis or Crohn's disease), cancer,
CC   or a disease/disorder caused by aberrant apoptosis. They are also useful
CC   for diagnostics, therapeutics, prophylaxis or as research reagents or
CC   kits. The invention is useful in gene therapy. The present sequence is
CC   an antisense oligonucleotide targetted to human IFNGR2 DNA.
XX
SQ   Sequence 20 BP; 6 A; 6 C; 5 G; 3 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        654 AGACCTGGTCGGGGACTTG 672
              ||||||||||| | ||||
Db         20 AGACCTGGTCGTCGTCTTG 2


RESULT 196
ABX33984/c
ID   ABX33984 standard; DNA; 20 BP.
XX
AC   ABX33984;
XX
DT   10-FEB-2003  (first entry)
XX
DE   Human interleukin 12 p40 subunit antisense oligonucleotide ISIS #139157.
XX
KW   Human; ss; antisense; interleukin 12 p40 subunit; antibacterial;
KW   antiinflammatory; cytostatic; infection; inflammation; tumour.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..20
FT                   /*tag= a
FT                   /mod_base= OTHER
FT                   /note= "All cytosines are 5-methylcytidines and the
FT                   nucleotides are linked via a phosphorothioate backbone"
FT   modified_base   1..5
FT                   /*tag= b
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base   16..20
FT                   /*tag= c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN   US6448081-B1.
XX
PD   10-SEP-2002.
XX
PF   07-MAY-2001; 2001US-0851062.
XX
PR   07-MAY-2001; 2001US-0851062.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Baker BF, Freier SM;
XX
DR   WPI; 2003-074100/07.
XX
PT   New antisense chimeric oligonucleotide, useful for modulating the
PT   expression of human Interleukin 12 p40 subunit, in treating or
PT   preventing disease states in humans and animals, and as research
PT   reagents and diagnostics -
XX
PS   Example 15; Column 45; 42pp; English.
XX
CC   The invention relates to an antisense compound 20-50 nucleobases in
CC   length targeted to a start codon region, coding region, a stop codon
CC   region or a 3'-untranslated region of a nucleic acid molecule encoding
CC   human Interleukin 12 p40 subunit. The compound specifically hybridises
CC   with one of the regions and inhibits the expression of human Interleukin
CC   12 p40 subunit. The new compound is useful for inhibiting the
CC   expression of human Interleukin 12 p40 subunit in cells or tissues and
CC   comprises contacting the cells or tissues in vitro with the compound,
CC   so that expression of the human Interleukin 12 p40 subunit is inhibited.
CC   The antisense compound may also be used as research reagents
CC   and diagnostics, and as treatment or prevention of disease states, e.g.
CC   to prevent or delay infection, inflammation or tumour formation, in
CC   animals and humans. The present sequence is an antisense oligonucleotide
CC   of the invention.
XX
SQ   Sequence 20 BP; 4 A; 4 C; 9 G; 3 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        227 CTCAGCCTCAGGCATCTGC 245
              ||||||| | | |||||||
Db         20 CTCAGCCACGGTCATCTGC 2


RESULT 197
ABX34251/c
ID   ABX34251 standard; DNA; 20 BP.
XX
AC   ABX34251;
XX
DT   10-FEB-2003  (first entry)
XX
```

```
DE   Antisense oligonucleotide against human SAA4 expression, ISIS 145105.
XX
KW   Human; ss; antisense; serum amyloid A4; SAA4; lipoprotein;
KW   apolipoprotein; high density lipoprotein; HDL; amyloid A; amyloid fibril;
KW   amyloidosis; inhibition; antagonist; diagnosis; antisense therapy;
KW   tumour formation; inflammatory disorder; rheumatoid arthritis;
KW   familial Mediterranean fever.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6455308-B1.
XX
PD   24-SEP-2002.
XX
PF   01-AUG-2001; 2001US-0920672.
XX
PR   01-AUG-2001; 2001US-0920672.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Freier SM;
XX
DR   WPI; 2003-066237/06.
XX
PT   New antisense compounds, useful for inhibiting the expression of serum
PT   amyloid A4, and for diagnosing, preventing or treating diseases
PT   associated with expression of serum amyloid A4, e.g. tumor formation or
PT   inflammatory disorders -
XX
PS   Example 15; Columns 45-46; 42pp; English.
XX
CC   The invention discloses antisense oligonucleotides that specifically
CC   hybridise with a region encoding human serum amyloid A4 (SAA4) and
CC   inhibit its expression. Lipoproteins are globular, micelle-like particles
CC   which have been classified into five categories. The protein components
CC   of lipoproteins are known as apolipoproteins, and one family of these are
CC   the serum amyloid proteins. These apolipoproteins are associated with the
CC   high density lipoprotein (HDL) and act as precursors of the amyloid A
CC   proteins found in amyloid fibril deposits formed during the process of
CC   amyloidosis. The antisense compounds and methods are useful for
CC   modulating, (i.e. inhibiting) the expression of serum amyloid A4
CC   (antagonists). The compounds are also useful for diagnosing, preventing
CC   and treating (using antisense therapy) diseases associated with elevated
CC   expression of serum amyloid A4, e.g. tumour formation or inflammatory
CC   disorders such as rheumatoid arthritis and familial Mediterranean fever.
CC   The antisense compounds can also be used as research reagents and
CC   diagnostics, or as tools in differential and/or combinatorial analyses to
CC   elucidate expression patterns of a portion or the entire complement of
CC   genes expressed within cells or tissues. The sequences presented in
CC   ABX34211-ABX34288 are the antisense oligonucleotides which are directed
CC   against human SAA4 expression. Each antisense oligonucleotide has a
CC   phosphorothioate backbone, all cytidines residues are 5-methylcytidines
CC   and bases 1-5 and 16-20 are 2-methoxyethyl (2'-MOE) nucleotides.
XX
SQ   Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 other;

  Query Match             1.0%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        282 GGAAGCAGCAGCAATGTCT 300
              |||| |||||||| ||| |
Db         20 GGAAACAGCAGCACTGTAT 2


RESULT 198
AAQ20005
ID   AAQ20005 standard; DNA; 17 BP.
XX
AC   AAQ20005;
XX
DT   01-APR-1992  (first entry)
XX
DE   Oligonucleotide #1 able to covalently cross-link to target DNA.
XX
KW   deoxyribonucleic acid; major groove; ethanoamino group;
KW   aziridinylcytosine; cross-linking group; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "N4N4-ethanocytosine"
FT   modified_base   9
FT                   /*tag=  b
FT                   /mod_base= m5c
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= m5c
XX
PN   WO9118997-A.
XX
PD   12-DEC-1991.
XX
PF   24-MAY-1991;   91WO-1003680.
XX
PR   14-JAN-1991;   91US-0640654.
PR   25-MAY-1990;   90US-0529346.
XX
PA   (GILE-) GILEAD SCIE INC.
XX
PI   Matteucci MD,  Krawczyk S;
XX
DR   WPI; 1992-007480/01.
XX
PT   New sequence-specific non-photo-activated crosslinking agents -
PT   bind to the major groove of duplex DNA and are esp. useful for
PT   treating latent infections e.g. HIV
XX
PS   Example 2; Page 20; 42pp; English.
XX
CC   The 3' end of this oligonucleotide carries 1,3-propanediol. The
CC   oligo is one of four oligonucleotides which were designed to
CC   specifically bind and cross-link to the duplex target sequence
CC   AAQ20004. Oligo #1 has the covalent cross-linking group, i.e.
CC   N4N4-ethanocytosine, at its 5' end. An assay for crosslinked triple
CC   helix showed considerable reaction with Oligo #1 and with Oligo #2
CC   (see AAQ20006) which has the crosslinking group at the 3' end.
CC   The most complete reaction was seen with Oligo #3 (see AAQ20007) having
CC   N4N4-ethanocytosine at both the 5' and 3' termini. A control oligo
CC   with no cross-linking group showed no reaction. The half-life of the
CC   cross-linking reaction for Oligo #2 was ca. 1 hr (1 microM);
CC   Oligo #1 showed a rate four times slower. See also AAQ20008.
XX
SQ   Sequence 17 BP; 0 A; 3 C; 0 G; 14 T; 0 other;

  Query Match             1.0%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
              ||||||||||||||
Db          1 CTTTTTTTCTTTTT 14


RESULT 199
AAA21349
ID   AAA21349 standard; RNA; 17 BP.
XX
AC   AAA21349;
XX
DT   19-JUN-2000  (first entry)
XX
```

```
DE   Integrin alpha 6 subunit substrate sequence SEQ ID NO:4575.
XX
KW   Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW   integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW   hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
KW   ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW   dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW   age related macular degeneration; inflammation; neovascular glaucoma;
KW   myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW   tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW   Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS   Homo sapiens.
XX
PN   WO9950403-A2.
XX
PD   07-OCT-1999.
XX
PF   24-MAR-1999;   99WO-US06507.
XX
PR   27-MAR-1998;   98US-0079678.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Pavco PA,  Roberts E,  Jarvis T,  Coeshott C,  McSwiggen JA;
XX
DR   WPI; 1999-591315/50.
XX
PT   Novel ribozymes for modulating the synthesis, expression and/or
PT   stability of an mRNA encoding an angiogenic factors  -
XX
PS   Claim 55; Page 202; 305pp; English.
XX
CC   The present invention describes enzymatic nucleic acid molecules with
CC   RNA cleaving activity, which specifically cleave RNA encoded by an aryl
CC   hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC   gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC   AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC   and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC   corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC   AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC   and AAA19155 to AAA19222 represent their corresponding target sequences;
CC   AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC   sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC   AAA21596 to AAA21688 represent their corresponding target sequences;
CC   AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC   for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC   AAA23422 represent their corresponding target sequences. The ribozymes of
CC   the invention are used for modulating the synthesis, expression and/or
CC   stability of an mRNA encoding angiogenic factor, especially ARNT,
CC   integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC   especially used to treat cancer, diabetic retinopathy, age related
CC   macular degeneration (ARMD), inflammation, and arthritis, as well as
CC   neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC   angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC   syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC   and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC   integrin subunit alpha-6, or integrin subunit beta-3.
XX
SQ   Sequence 17 BP; 0 A; 4 C; 1 G; 12 U; 0 other;

  Query Match             1.0%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   14.3%;  Pred. No. 1.6e+02;
  Matches    2;  Conservative   12;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
              |::::::::|:::::
Db          2 CUUUUUUUCUUUUU 15


RESULT 200
AAA21350
ID   AAA21350 standard; RNA; 17 BP.
XX
AC   AAA21350;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Integrin alpha 6 subunit substrate sequence SEQ ID NO:4576.
XX
KW   Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW   integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW   hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
KW   ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW   dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW   age related macular degeneration; inflammation; neovascular glaucoma;
KW   myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW   tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW   Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS   Homo sapiens.
XX
PN   WO9950403-A2.
XX
PD   07-OCT-1999.
XX
PF   24-MAR-1999;   99WO-US06507.
XX
PR   27-MAR-1998;   98US-0079678.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Pavco PA,  Roberts E,  Jarvis T,  Coeshott C,  McSwiggen JA;
XX
DR   WPI; 1999-591315/50.
XX
PT   Novel ribozymes for modulating the synthesis, expression and/or
PT   stability of an mRNA encoding an angiogenic factors  -
XX
PS   Claim 55; Page 202; 305pp; English.
XX
CC   The present invention describes enzymatic nucleic acid molecules with
CC   RNA cleaving activity, which specifically cleave RNA encoded by an aryl
CC   hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC   gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC   AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC   and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC   corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC   AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC   and AAA19155 to AAA19222 represent their corresponding target sequences;
CC   AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC   sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC   AAA21596 to AAA21688 represent their corresponding target sequences;
CC   AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC   for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC   AAA23422 represent their corresponding target sequences. The ribozymes of
CC   the invention are used for modulating the synthesis, expression and/or
CC   stability of an mRNA encoding angiogenic factor, especially ARNT,
CC   integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC   especially used to treat cancer, diabetic retinopathy, age related
CC   macular degeneration (ARMD), inflammation, and arthritis, as well as
CC   neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC   angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC   syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC   and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC   integrin subunit alpha-6, or integrin subunit beta-3.
XX
SQ   Sequence 17 BP; 0 A; 4 C; 1 G; 12 U; 0 other;

  Query Match             1.0%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   14.3%;  Pred. No. 1.6e+02;
  Matches    2;  Conservative   12;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
              |::::::::|:::::
Db          1 CUUUUUUUCUUUUU 14
```

```
RESULT 201
ACA06319
ID   ACA06319 standard; RNA; 17 BP.
XX
AC   ACA06319;
XX
DT   03-JUN-2003  (first entry)
XX
DE   NFKB sub-unit modulating inozyme substrate #138.
XX
KW   Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
KW   G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
KW   lung cancer; prostate cancer; colorectal cancer; brain cancer;
KW   oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
KW   cervical cancer; head and neck cancer; ovarian cancer; melanoma;
KW   lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
KW   chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
KW   cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
KW   gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
KW   rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW   gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW   transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW   allergic airway inflammation; inflammatory bowel disease; infection;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   US2002177568-A1.
XX
PD   28-NOV-2002.
XX
PF   23-MAY-2001; 2001US-0864785.
XX
PR   15-AUG-1994;   94US-0291932.
PR   07-DEC-1992;   92US-0987132.
PR   18-MAY-1994;   94US-0245466.
PR   23-DEC-1996;   96US-0777916.
XX
PA   (STIN/) STINCHCOMB D T.
PA   (MCSW/) MCSWIGGEN J.
PA   (DRAP/) DRAPER K G.
XX
PI   Stinchcomb DT,  Mcswiggen J,  Draper KG;
XX
DR   WPI; 2003-340953/32.
XX
PT   Novel enzymatic nucleic acid molecules which down regulates expression
PT   of a sequence encoding a subunit of nuclear factor kappa B useful for
PT   treating cancer, inflammatory disorders and autoimmune diseases -
XX
PS   Claim 3; Page 29; 72pp; English.
XX
CC   The invention describes an enzymatic nucleic acid molecule (I) which down
CC   regulates expression of a sequence encoding a subunit of nuclear factor
CC   kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC   configuration. The enzymatic nucleic acid molecule is adapted to treat
CC   cancer and is useful for down-regulating REL-A activity in a cell, for
CC   treating a patient having a condition associated with the level of REL-A.
CC   (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
CC   the presence of a divalent cation, especially Mg^2^+. The enzymatic and
CC   antisense nucleic acid molecules are useful for treating breast, lung,
CC   prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC   cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC   multidrug resistant cancer. The method involves use of other drug
CC   therapies such as monoclonal antibodies, REL-A-specific inhibitors or
CC   chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
CC   cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
CC   gemcitabine or radiation therapy. The enzymatic and antisense nucleic
CC   acid molecules are also useful for treating inflammatory disease such as
CC   rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC   obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
CC   rejection, gene therapy applications, ischaemia/reperfusion injury
CC   (central nervous system (CNS) and myocardial), glomerulonephritis,
CC   sepsis, allergic airway inflammation, inflammatory bowel disease or
CC   infection. This sequence represents the substrate of a novel
CC   enzymatic nucleic acid molecule.
XX
SQ   Sequence 17 BP; 4 A; 7 C; 5 G; 1 U; 0 other;

  Query Match             1.0%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 1.6e+02;
  Matches   13;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1066 CCCATCAGGCAGGC 1079
              ||||:|||||||||
Db          3 CCCAUCAGGCAGGC 16


RESULT 202
AAQ20007
ID   AAQ20007 standard; DNA; 18 BP.
XX
AC   AAQ20007;
XX
DT   01-APR-1992  (first entry)
XX
DE   Oligonucleotide #3 able to covalently cross-link to target DNA.
XX
KW   deoxyribonucleic acid; major groove; ethanoamino group;
KW   aziridinylcytosine; cross-linking group; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "N4N4-ethanocytosine"
FT   modified_base   9
FT                   /*tag=  b
FT                   /mod_base= m5c
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= m5c
FT   modified_base   18
FT                   /*tag=  da
FT                   /mod_base= OTHER
FT                   /note= "N4N4-ethanocytosine"
XX
PN   WO9118997-A.
XX
PD   12-DEC-1991.
XX
PF   24-MAY-1991;   91WO-1003680.
XX
PR   14-JAN-1991;   91US-0640654.
PR   25-MAY-1990;   90US-0529346.
XX
PA   (GILE-) GILEAD SCIE INC.
XX
PI   Matteucci MD,  Krawczyk S;
XX
DR   WPI; 1992-007480/01.
XX
PT   New sequence-specific non-photo-activated crosslinking agents -
PT   bind to the major groove of duplex DNA and are esp. useful for
PT   treating latent infections e.g. HIV
XX
PS   Example 2; Page 21; 42pp; English.
XX
CC   The 3' end of this oligonucleotide carries 1,3-propanediol. The
CC   oligo is one of four oligonucleotides which were designed to
CC   specifically bind and cross-link to the duplex target sequence
CC   AAQ20004. Oligo #3 has a covalent cross-linking group, i.e.
```

```
CC   N4N4-ethanocytosine, at its 5'- and 3'-ends. An assay for
CC   crosslinked triple helix showed the most complete reaction with
CC   Oligo #3. A control oligo with no cross-linking group showed no
CC   reaction while Oligos #1 (see AAQ20005) and #2 (AAQ20006) with the
CC   crosslinking group at the 5' and 3' ends, respectively, showed
CC   considerable reaction. An oligonucleotide with N4N4-ethanocytosine
CC   within its sequence (see AAQ20008) showed less effective binding.
XX
SQ   Sequence 18 BP; 0 A; 4 C; 0 G; 14 T; 0 other;

  Query Match             1.0%;  Score 14;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1143 CTTTTTTTCTTTTT 1156
              ||||||||||||||
Db          1 CTTTTTTTCTTTTT 14


RESULT 203
AAV70248
ID   AAV70248 standard; DNA; 19 BP.
XX
AC   AAV70248;
XX
DT   04-FEB-1999  (first entry)
XX
DE   Human HMGI-C exon 1 and 2 PCR primer.
XX
KW   Human; pygmy locus; YAC; yeast artificial chromosome; HMGI; tumour;
KW   obesity; Saccharomyces cerevisiae; high mobility group; diagnosis;
KW   PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9850536-A1.
XX
PD   12-NOV-1998.
XX
PF   18-NOV-1997;   97WO-US21299.
XX
PR   07-MAY-1997;   97US-0852666.
XX
PA   (UYNE-) UNIV NEW JERSEY.
XX
PI   Ashar H,  Chada K,  Tkachenko A,  Zhou X;
XX
DR   WPI; 1998-610380/51.
XX
PT   Use of HMG-1, high mobility group, genes - for developing products
PT   for treating obesity and tumours by reducing the activity of HMGI
PT   genes and for developing diagnostic and drug screening assays.
XX
PS   Example; Page 48; 97pp; English.
XX
CC   A method has been developed for treating obesity in a mammal. The method
CC   comprises reducing the biological activity of HMGI (high mobility
CC   group-I) genes in the mammal. Reducing the activity of HMGI genes can be
CC   used for treating obesity. The method can also be used for the diagnosis
CC   and treatment of tumours such as uterine leiomyomata, lipomas,
CC   pleomorphic adenomas of the salivary gland, pulmonary chondroid
CC   hamartoma, endometrial polyps, epithelial breast tumours,
CC   hemangiopericytoma or angiomyxoma. The tumours may also be a malignant
CC   tumour of epithelial origin and may be a carcinoma of the lung, colon,
CC   breast, prostate, thyroid gland, or skin. The HMGI genes and proteins
CC   may also be used as a starting point to isolate downstream target genes
CC   regulated by the MHGI genes and proteins. The present sequence
CC   represents a PCR primer for HMGI-C used in an example from the
CC   present invention.
XX
SQ   Sequence 19 BP; 8 A; 5 C; 6 G; 0 U; 0 other;

  Query Match             1.0%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        282 GGAAGCAGCAGCAA 295
              ||||||||||||||
Db          1 GGAAGCAGCAGCAA 14


RESULT 204
AAA82832
ID   AAA82832 standard; DNA; 19 BP.
XX
AC   AAA82832;
XX
DT   04-DEC-2000  (first entry)
XX
DE   cdk4 ribozyme binding site #13.
XX
KW   Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
KW   restenosis; ss.
XX
OS   Mammalia.
XX
PN   WO200032765-A2.
XX
PD   08-JUN-2000.
XX
PF   06-DEC-1999;   99WO-US28772.
XX
PR   04-DEC-1998;   98US-0110954.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Tritz R,  Welch PJ,  Barber JR,  Robbins JM;
XX
DR   WPI; 2000-412314/35.
XX
PT   New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT   RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT   PCNA and Cyclin B1  -
XX
PS   Disclosure; Page 52; 109pp; English.
XX
CC   The present invention relates to a hairpin or hammerhead ribozyme,
CC   designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC   other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC   Representative examples of ribozyme recognition sites are given in
CC   AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC   inhibiting restenosis by introduction of the ribozyme into cells.
CC   The ribozyme is resistant to endonuclease activity and hence is
CC   efficient in restenosis treatment.
XX
SQ   Sequence 19 BP; 4 A; 7 C; 5 G; 3 T; 0 other;

  Query Match             1.0%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1060 GGCCTTCCCATCAG 1073
              ||||||||||||||
Db          5 GGCCTTCCCATCAG 18


RESULT 205
AAA82833
ID   AAA82833 standard; DNA; 19 BP.
XX
AC   AAA82833;
XX
DT   04-DEC-2000  (first entry)
XX
DE   cdk4 ribozyme binding site #14.
```

XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
KW restenosis; ss.
XX
OS Mammalia.
XX
PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US28772.
XX
PR 04-DEC-1998; 98US-0110954.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1 -
XX
PS Disclosure; Page 52; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells.
CC The ribozyme is resistant to endonuclease activity and hence is
CC efficient in restenosis treatment.
XX
SQ Sequence 19 BP; 4 A; 7 C; 5 G; 3 T; 0 other;

Query Match 1.0%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1060 GGCCTTCCCATCAG 1073
||||||||||||||
Db 4 GGCCTTCCCATCAG 17

RESULT 206
AAH57994
ID AAH57994 standard; DNA; 19 BP.
XX
AC AAH57994;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cell-cycle dependent kinase cdk4 ribozyme binding site SEQ ID NO:418.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US29500.
XX
PR 26-OCT-1999; 99US-0161532.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
DR WPI; 2001-300427/31.
XX
PT Treating proliferative skin or eye diseases and scarring, using
PT ribozymes that cleave RNA encoding cytokines involved in inflammation,
PT matrix metalloproteinases, growth factors and cell-cycle dependent
PT kinases -
XX
PS Example 1; Page 102; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnerary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative
CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 7 C; 5 G; 3 T; 0 other;

Query Match 1.0%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1060 GGCCTTCCCATCAG 1073
||||||||||||||
Db 5 GGCCTTCCCATCAG 18

RESULT 207
AAH57995
ID AAH57995 standard; DNA; 19 BP.
XX
AC AAH57995;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cell-cycle dependent kinase cdk4 ribozyme binding site SEQ ID NO:419.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX

PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US29500.
XX
PR 26-OCT-1999; 99US-0161532.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
DR WPI; 2001-300427/31.
XX
PT Treating proliferative skin or eye diseases and scarring, using
PT ribozymes that cleave RNA encoding cytokines involved in inflammation,
PT matrix metalloproteinases, growth factors and cell-cycle dependent
PT kinases -
XX
PS Example 1; Page 102; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnerary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative
CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 7 C; 5 G; 3 T; 0 other;

Query Match 1.0%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1060 GGCCTTCCCATCAG 1073
||||||||||||||
Db 4 GGCCTTCCCATCAG 17

RESULT 208
ABL55323
ID ABL55323 standard; DNA; 19 BP.
XX
AC ABL55323;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human HMGI-C exon 1-2 RACE-PCR primer, SEQ ID NO:6.
XX
KW Human; HMGI-C; high mobility group; DNA binding protein;
KW architectural factor; chromosome 12q15; mesenchyme differentiation;
KW adipogenesis; gene disruption; gene rearrangement; translocation;
KW benign mesenchymal neoplasm; tumour; lipoma; uterine leiomyoma;
KW uterine fibroid; pulmonary hamartoma; salivary gland pleomorphic adenoma;
KW endometrial polyp; epithelial breast tumour; haemangiopericytoma;
KW aggressive myxoma; mammary gland; breast; thyroid; prostate; cancer;
KW malignant tumour; diagnosis; HMGI inhibitor; obesity; RACE-PCR;
KW rapid amplification of cDNA ends; primer; ss.
XX
OS Homo sapiens.

XX
PN US6171779-B1.
XX
PD 09-JAN-2001.
XX
PF 12-JUL-1996; 96US-0679529.
XX
PR 12-JUL-1996; 96US-0679529.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Chada KK, Ashar H, Tkachenko A, Zhou X;
XX
DR WPI; 2001-334467/35.
XX
PT Detection of high mobility group DNA binding proteins HMGI-C or HMG(Y),
PT useful as diagnostic markers for benign mesenchymal or lipoma tumours -
XX
PS Examples; Column 23; 32pp; English.
XX
CC The invention relates to a method for detecting high mobility group DNA
CC binding proteins HMGI-C or HMG(Y) as a diagnostic marker for benign or
CC malignant tumours using a probe specific HMGI-C or HMGI(Y) to detect
CC their presence. HMGI-C and HMGI(Y) are homologous but distinct members of
CC the HMGI family of architectural factors. They are DNA-binding proteins
CC normally expressed in the embryo which mediate mesenchyme differentiation
CC and adipogenesis. In the mouse, lack of HMGI-C function results in the
CC pygmy phenotype, in which the mice are 60% smaller than wild-type
CC animals, are highly resistant to chemically induced skin cancer, and have
CC a disproportionally reduced fat content. In humans, expression of HMGI
CC proteins is highly correlated with the progression and metastasis of
CC malignant tumours of the mammary, thyroid and prostate glands.
CC Rearrangement within the HMGI genes and expression of the resultant
CC chimeric proteins also leads to the development of solid tumours. The
CC human HMGI-C gene, located on chromosome 12q15, has been found to be
CC disrupted by translocations in a wide variety of benign mesenchymal
CC neoplasms such as lipomas, uterine leiomyomata (fibroids), pulmonary
CC hamartoma and pleomorphic adenomas of the salivary gland. Rearrangements
CC of the 12q13-15 region are also involved in endometrial polyps,
CC epithelial breast tumours, haemangiopericytoma and aggressive myxoma.
CC These HMGI-C gene rearrangements result in novel chimeric transcripts
CC which encode fusion proteins comprising the A-T hook DNA binding domains
CC of HMGI-C fused to a portion of a heterologous protein derived from a
CC different chromosome. In lipoma ST90-375, for example, fusion between the
CC 5' end of the HMGI-C gene and a region of chromosome 15 (t(12;15))
CC results in the generation of a protein comprising the HMGI-C A-T hook
CC motifs and a novel acidic serine and threonine-rich domain which
CC resembles the typical activation domains of transcription factors, while
CC in lipoma ST93-724, the fusion protein resulting from the translocation
CC t(3;12) comprises two LIM domains which promote protein-protein
CC interactions. These novel fusion proteins both act to deregulate HMGI-C
CC target genes, thus resulting in cellular transformation. The presence of
CC HMGI proteins, indicating abberant HMGI gene expression, can thus be used
CC as a diagnostic marker of benign or malignant tumours, especially those
CC of mesenchymal origin. Detection of antibodies to HMGI-C or HMGI(Y) may
CC also be used to diagnose such tumours. Inhibitors of HMGI-C or HMGI(Y)
CC activity can be used to treat benign and malignant mesenchymal tumours,
CC and can also be used to treat obesity. Sequences ABL55321-ABL55323
CC represent PCR primers used in 3' RACE (rapid amplification of cDNA ends)
CC to extend human HMGI-C cDNA clones in an exemplification of the
CC invention.
XX
SQ Sequence 19 BP; 8 A; 5 C; 6 G; 0 U; 0 other;

Query Match 1.0%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 282 GGAAGCAGCAGCAA 295
||||||||||||||
Db 1 GGAAGCAGCAGCAA 14

```
RESULT 209
AAQ86242
ID   AAQ86242 standard; DNA; 20 BP.
XX
AC   AAQ86242;
XX
DT   29-NOV-1995  (first entry)
XX
DE   Reverse transcriptionn primer #1.
XX
KW   Polymerase chain reaction; PCR; amplify; primer; target DNA;
KW   restriction site; ss.
XX
OS   Synthetic.
XX
PN   JP07067699-A.
XX
PD   14-MAR-1995.
XX
PF   27-AUG-1993;   93JP-0235681.
XX
PR   27-AUG-1993;   93JP-0235681.
XX
PA   (IATR ) IATRON LAB INC.
XX
DR   WPI; 1995-143879/19.
XX
PT   Determination of mRNA by reverse transcriptase-PCR method -
PT   allows quantitative measurement of very small amounts of mRNA's
XX
PS   Example 1; Page 4; 8pp; Japanese.
XX
CC   The sequences given in AAQ86242-45 are primers which were used to
CC   demonstrate the method of the invention. This method comprises
CC   making a known standard RNA containing an mRNA from a related
CC   organism in formation with DNA fragments from a target DNA to form
CC   hybrid DNA fragments. PCR is carried out using two primers, one
CC   based on the standard DNA and one based on the target DNA. The
CC   standard DNA contains a restriction site which does not appear in
CC   the target DNA The amount of target DNA is determined by comparing
CC   the amount of cut and uncut DNA after treatment with the enzyme
CC   specific for the standard DNA restriction site.
XX
SQ   Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 other;

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        543 TGCCCTGCTGGCAG 556
              ||||||||||||||
Db          3 TGCCCTGCTGGCAG 16


RESULT 210
AAT10191
ID   AAT10191 standard; DNA; 20 BP.
XX
AC   AAT10191;
XX
DT   19-APR-1996  (first entry)
XX
DE   Alkaline endoglucanase Carezyme gene PCR reverse primer.
XX
KW   Alkaline endoglucanase; Carezyme; cellulase; host cell;
KW   Fusarium graminearum; polymerase chain reaction; PCR; primer;
KW   Humicola insolens; ss.
XX
OS   Synthetic.
XX
PN   WO9600787-A1.
XX
PD   11-JAN-1996.
XX
PF   15-JUN-1995;   95WO-US07743.
XX
PR   15-MAR-1995;   95US-0404678.
PR   30-JUN-1994;   94US-0269449.
XX
PA   (NOVO ) NOVO NORDISK BIOTECH INC.
XX
PI   Moyer DL,  Royer JC,  Shuster JR,  Yoder W;
XX
DR   WPI; 1996-077498/08.
XX
PT   Non-toxic, non-toxigenic, non-pathogenic recombinant Fusarium host
PT   cell - used to produce heterologous proteins, pref. enzymes,
PT   hormones, growth factors or receptors
XX
PS   Example 6.6; Page 11; 38pp; English.
XX
CC   A forward primer (AAT10190) is based on the Fusarium oxysporum
CC   trypsin-like protease SP357 gene promoter (AAT10184) and the 5'
CC   end of the Humicola insolens endoglucanase Carezyme gene.  It was
CC   used with a reverse primer (AAT10191) based on the 3' end of the
CC   Carezyme coding region to generate a PCR fragment contg. -18 to -1
CC   of the SP387 promoter directly followed by -1 to +294 of the Carezyme
CC   gene, using vector pCaHj418 as template.  The PCR product was used
CC   to construct vector pDM151, utilised for prodn. of Carezyme (AAR88471)
CC   in Fusarium graminearum ATCC 20334 host cells.
XX
SQ   Sequence 20 BP; 9 A; 3 C; 6 G; 2 T; 0 other;

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        387 AGAGGTGGCAGCAA 400
              ||||||||||||||
Db          5 AGAGGTGGCAGCAA 18


RESULT 211
AAT64842
ID   AAT64842 standard; DNA; 20 BP.
XX
AC   AAT64842;
XX
DT   06-MAR-1998  (first entry)
XX
DE   Fusarium oxysporum gene promoter fragment and "carenzyme" (RTM) primer.
XX
KW   Fusarium oxysporum; trypsin gene promoter; filamentous fungal cell;
KW   carenzyme cellase; restricted colonial phenotype; hyphal branching;
KW   ss.
XX
OS   Synthetic.
OS   Fusarium oxysporum.
XX
PN   WO9726330-A2.
XX
PD   24-JUL-1997.
XX
PF   17-JAN-1997;   97WO-US00829.
XX
PR   04-OCT-1996;   96US-0726114.
PR   19-JAN-1996;   96US-0010238.
XX
PA   (NOVO ) NOVO NORDISK BIOTECH INC.
XX
PI   Royer JC,  Shuster JR;
XX
DR   WPI; 1997-385334/35.
XX
PT   Obtaining mutant filamentous fungal cells with improved polypeptide
PT   production  - by examination for restricted colonial phenotype and
```

PT more extensive hyphal branching than parent fungal cells
XX
PS Example 7; Page 20; 38pp; English.
XX
CC PCR primers AAT64841-2 were used to construct Fusarium expression vector
CC pJRoy30. A PCR fragment containing -18 to -1 of the Fusarium
CC oxysporum trypsin gene promoter directly followed by -1 to +294 of the
CC "carenzyme" (RTM) cellulase gene was generated from the vector pCaHj418
CC using the PCR primers (AAT64841-2). Fusarium wild type and mutant
CC strains were transformed by pJRoy30 and the production of cellulase was
CC monitored. The primers were used to demonstrate a novel method of
CC obtaining a mutant cell from a filamentous fungal parent cell where
CC production of a heterologous polypeptide is improved in the mutant. The
CC method comprises: obtaining mutant cells, identifying a mutant cell
CC exhibiting a more restricted colonial phenotype and/or more extensive
CC hyphal branching than parent cells, and determining that the mutant cell
CC has improved protein production by culturing mutant cells transformed to
CC express a heterologous polypeptide and parent cells under the same
CC conditions. Mutants obtained by the method can be used to express
CC prokaryotic or eukaryotic peptides or polypeptides, e.g. fungal enzymes
CC (native or modified) such as aminopeptidases, amylases and
CC carboxypeptidases or mammalian peptides such as insulin, insulin
CC variants, receptors proteins and antibodies. The mutants may possess
CC improved growth characteristics in fermentation. Mutants may also have
CC better secretion properties.
XX
SQ Sequence 20 BP; 9 A; 3 C; 6 G; 2 T; 0 other;

Query Match 1.0%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 387 AGAGGTGGCAGCAA 400
||||||||||||||
Db 5 AGAGGTGGCAGCAA 18

RESULT 212
AAZ72938/c
ID AAZ72938 standard; DNA; 20 BP.
XX
AC AAZ72938;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:7294.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX
PS Claim 9; Page 1786; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 20 BP; 6 A; 2 C; 9 G; 3 T; 0 other;

Query Match 1.0%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 971 CCCTCACTTGACCA 984
||||||||||||||
Db 14 CCCTCACTTGACCA 1

RESULT 213
AAA53330
ID AAA53330 standard; DNA; 20 BP.
XX
AC AAA53330;
XX
DT 25-SEP-2000 (first entry)
XX
DE Reverse PCR primer used endoglucanase fusion protein construction.
XX
KW Non-toxic; non-pathogenic; recombinant protein production; protease;
KW trypsin-like protease; PCR primer; fungal enzyme; ss.
XX
OS Fusarium oxysporum.
XX
PN US6060305-A.
XX
PD 09-MAY-2000.
XX
PF 13-MAR-1997; 97US-0816915.
XX
PR 30-JUN-1994; 94US-0269449.
PR 15-MAR-1995; 95US-0404678.
PR 04-OCT-1996; 96US-0726105.
XX
PA (NOVO) NOVO NORDISK BIOTECH INC.
XX
PI Wendy YT, Shuster JR, Moyer DL, Royer JC;
XX
DR WPI; 2000-349678/30.
XX
PT New non-pathogenic recombinant fusarium host cell, useful for
PT expressing heterologous proteins especially fungal enzymes such as
PT alkaline endoglucanase or alkaline protease -
XX
PS Example 6; Column 9; 32pp; English.
XX
CC The invention relates to a non-toxic, non-pathogenic recombinant Fusarium
CC host cell of the section Discolor, with ATCC accession number 20334. The
CC cell is used in the recombinant production of proteins. The present
CC sequence represents a PCR primer used to construct a trypsin-like
CC protease gene SP387 promoter and endoglucanase fusion nucleotide
CC sequence. The fragment is used in the production of the cells of the

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CC   invention. The cells are useful for expressing heterologous proteins
CC   especially fungal enzymes such as alkaline endoglucanase or alkaline
CC   proteases, e.g. F. oxysporum pre-pro trypsin gene, and also hormones,
CC   growth factors and receptors. The cells are non-toxic and are efficient
CC   in the recombinant production of fungal enzymes.
XX
SQ   Sequence 20 BP; 9 A; 3 C; 6 G; 2 T; 0 other;

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        387 AGAGGTGGCAGCAA 400
              ||||||||||||||
Db          5 AGAGGTGGCAGCAA 18


RESULT 214
AAF83877/c
ID   AAF83877 standard; DNA; 20 BP.
XX
AC   AAF83877;
XX
DT   06-AUG-2001  (first entry)
XX
DE   Human NOVINTRA C DNA specific forward primer of primer-probe set Ag903.
XX
KW   NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;
KW   gonadotropin-like protein; NOVGON; interleukin-1; NOVINTRA; human;
KW   cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;
KW   antibacterial; cerebroprotective; antidiabetic; antiarthritic;
KW   antiasthmatic; antiallergic; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200140291-A2.
XX
PD   07-JUN-2001.
XX
PF   06-DEC-2000; 2000WO-US33029.
XX
PR   06-DEC-1999;   99US-0169056.
PR   09-DEC-1999;   99US-0169866.
PR   09-DEC-1999;   99US-0169886.
PR   10-DEC-1999;   99US-0170252.
PR   12-JAN-2000; 2000US-0175740.
PR   05-DEC-2000; 2000US-0170252.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Burgess CE,  Prayaga SK,  Shimkets RA,  Rastelli L,  Zerhusen BD;
PI   Mezes PS;
XX
DR   WPI; 2001-374790/39.
XX
PT   Novel isolated human transmembrane, neuromedin peptide
PT   gonadotropin-like protein and interleukin-1 receptor antagonist
PT   proteins, useful for treating cancer, immune response disorder,
PT   metabolic function disorders  -
XX
PS   Examples; Page 86; 138pp; English.
XX
CC   The invention provides novel polypeptides (NOVX) selected from human
CC   transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),
CC   gonadotropin-like protein (NOVGON) and two interleukin-1 receptor
CC   antagonist proteins (NOVINTRA A and B). The invention also provides
CC   methods in which a NOVX polypeptide, polynucleotide  and antibody are
CC   used in the detection, prevention and treatment of a broad range of
CC   pathological states. NOVTRAN can be used to treat is a cell signaling
CC   disorder such as cancer, immune  response disorder, hematopoietic
CC   disorder, neurodegenerative disorder. NOVNEUR can be used to treat
CC   endocrine disorder, muscle disorder, neurologic disorder, cancers of
CC   central nervous system, breast, colon, ovary, kidney, prostate and
CC   thyroid. NOVGON can be used to treat reproductive development disorder,
CC   metabolic function disorder and melanoma. NOVINTRA A and B can be used
CC   to treat bone metabolism or structure disorder, inflammatory response
CC   disorder, immune regulation disorder, septic shock, stroke, diabetes,
CC   arthritis and cancer. Sequences AAF83877-79 represent a primer-probe set
CC   Ag903 specific for the NOVINTRA C nucleic acid sequence.
XX
SQ   Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 other;

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        827 TGCAGCTGAAGCTT 840
              ||||||||||||||
Db         16 TGCAGCTGAAGCTT 3


RESULT 215
AAC83988/c
ID   AAC83988 standard; DNA; 20 BP.
XX
AC   AAC83988;
XX
DT   05-MAR-2001  (first entry)
XX
DE   PrP gene PrnD PCR primer ORFP-R2.
XX
KW   Dpl; doppel protein; prion protein; PrP; PCR primer;
KW   neurodegenerative disorder; Purkinje cell degeneration;
KW   hereditary cerebellar cortical atrophy; ss.
XX
OS   Mus sp.
XX
PN   WO200068382-A1.
XX
PD   16-NOV-2000.
XX
PF   11-MAY-2000; 2000WO-US13099.
XX
PR   11-MAY-1999;   99US-0309317.
XX
PA   (REGC ) UNIV CALIFORNIA.
PA   (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Prusiner SB,  Tremblay P,  Moore R,  Westaway D,  Hood LE,  Lee I;
XX
DR   WPI; 2001-007396/01.
XX
PT   New nucleic acids encoding the Doppel protein and assays involving the
PT   use of the nucleic acids/peptides for understanding the mechanisms
PT   involved in the progression of neurodegenerative diseases involving
PT   prions -
XX
PS   Example 2; Page 39; 70pp; English.
XX
CC   The present invention relates to doppel (Dpl) proteins (see AAB49404-
CC   AAB49406). Dpl protein has similarity to all known prion proteins (PrP)
CC   and is used to help determine the function of PrP. The identification
CC   and study of prion-related genes may give insight into the general
CC   biology and progression of neurodegenerative disorders, and the
CC   mechanistic alterations that result in prion-mediated disorders and
CC   plaque formation. Detection of Dpl levels and/or presence of different
CC   conformations of Dpl can provide a means for diagnosing neurodegenerative
CC   disorders associated with Dpl particularly those involving Purkinje cell
CC   degeneration, such as hereditary cerebellar cortical atrophy. The present
CC   sequence is a PCR primer for PrP gene.
XX
SQ   Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 other;

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
```

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        269 GGCTGATCAAAGAG 282
              ||||||||||||||
Db         20 GGCTGATCAAAGAG 7
```

RESULT 216
ABQ82751
ID ABQ82751 standard; DNA; 20 BP.
XX
AC ABQ82751;
XX
DT 09-JAN-2003 (first entry)
XX
DE AttacinD AMP gene promoter PCR primer SEQ ID NO:30.
XX
KW Human; potassium channel beta subunit; K+betaM3; cytostatic; anti-HIV;
KW antiaddictive; antiarthritic; antiasthmatic; antirheumatic; antianaemic;
KW antibacterial; immunosuppressive; antipsoriatic; dermatological;
KW nootropic; neuroprotective; anticonvulsant; neuroleptic; antimanic;
KW antidepressant; antiulcer; antiinflammatory; antidiarrheic; antipyretic;
KW nephrotropic; hypotensive; antianginal; uropathic; tocolytic; vulnerary;
KW antiallergic; gene therapy; neural disorder; immune disorder; cancer;
KW proliferative disorder; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200268587-A2.
XX
PD 06-SEP-2002.
XX
PF 07-FEB-2002; 2002WO-US03986.
XX
PR 07-FEB-2001; 2001US-267039P.
PR 03-APR-2001; 2001US-281224P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Feder J, Lee L, Chen J, Jackson DG, Ramanathan C, Siemers N;
PI Chang H, Ryseck R, Watson AJ, Carroll P;
XX
DR WPI; 2002-682813/73.
XX
PT Novel human potassium channel beta-subunit, K+betaM3 polypeptide and
PT polynucleotide for diagnosing, preventing and treating immune,
PT metabolic, gastrointestinal, renal, neural and proliferative diseases
PT or disorders -
XX
PS Example 7; Page 245; 367pp; English.
XX
CC The present invention describes the human potassium channel beta-subunit
CC K+betaM3 protein (I). (I) has cytostatic, antiaddictive, antiarthritic,
CC antiasthmatic, anti-HIV, antirheumatic, antibacterial, immunosuppressive,
CC antipsoriatic, dermatological, antianaemic, nootropic, neuroprotective,
CC anticonvulsant, neuroleptic, antimanic, antidepressant, antiulcer,
CC antiinflammatory, antidiarrheic, antipyretic, nephrotropic, hypotensive,
CC antianginal, uropathic, tocolytic, antiallergic and vulnerary activities,
CC and can be used in gene therapy. (I) can be used for diagnosing a
CC pathological condition (or susceptibility) in a subject, and for
CC preventing and treating a medical condition, e.g. neural disorders
CC related to aberrant neurotransmitter release or drug addiction, a
CC disorder related to hyper potassium channel activity, an immune disorder
CC related to aberrant nuclear factor-KappaB (NF-kB) activity, immune
CC disorder related to transplant rejection, immune disorder in which
CC immunosuppression is desirable, a proliferative disorder, especially
CC cancer, or a proliferative disorder related to aberrant cell cycle
CC regulation, a proliferative disorder related to an aberration(s) in the
CC G1 or G2 cell cycle checkpoint, or aberrant DNA damage repair. (I) can
CC also be used for diagnosing, treating, prognosing, and/or preventing
CC immune, haematopoietic, metabolic, gastrointestinal, renal, neural and/or
CC proliferative diseases or disorders. The present sequence represents a
CC PCR primer for attacinD AMP gene promoter region, which is used in an
CC example from the present invention.
XX
SQ Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 other;

Query Match 1.0%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        603 CCTGAAGCCTGACA 616
              ||||||||||||||
Db          1 CCTGAAGCCTGACA 14
```

RESULT 217
AAD46116
ID AAD46116 standard; DNA; 20 BP.
XX
AC AAD46116;
XX
DT 27-DEC-2002 (first entry)
XX
DE Drosophila melanogaster attacinD AMP gene amplifying reverse PCR primer.
XX
KW Potassium channel beta-subunit; K+betaM2 protein; neural disorder;
KW reproductive disorder; metabolic disorder; premature puberty; nephritis;
KW endocrine disorder; memory disorder; neuroendocrine condition; asthma;
KW spermatogenesis; renal disease; learning deficiency; Alzheimer's disease;
KW neurodegenerative disease; proliferative disorder; autoimmune disease;
KW carcinoid tumour; blood coagulation disease; blood platelet disease;
KW rheumatoid arthritis; allergy; hyperproliferative disease; gene therapy;
KW graft-versus-host disease; organ rejection; antisterility; thrombolytic;
KW antiinflammatory; neuroprotective; anti-Parkinsonian; immunosuppressive;
KW nephrotropic; cytostatic; nootropic; hypotensive; vulnerary; PCR; primer;
KW fruit fly; antimicrobial peptide; AMP; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200266601-A2.
XX
PD 29-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US02332.
XX
PR 24-JAN-2001; 2001US-263872P.
PR 14-FEB-2001; 2001US-269794P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Feder J, Lee L, Chen J, Jackson D, Ramanathan C, Siemers N;
PI Chang H, Carroll P;
XX
DR WPI; 2002-691617/74.
XX
PT New potassium channel beta-subunit, K+betaM2, proteins and nucleic
PT acids, useful for diagnosing, treating and/or preventing e.g.
PT reproductive, neural, metabolic, endocrine, memory, neurodegenerative
PT disorders or diseases -
XX
PS Example 56; Page 365; 366pp; English.
XX
CC The present invention relates to human potassium channel beta-subunit
CC (K+betaM2) proteins and polynucleotides encoding such proteins. The
CC K+betaM2 sequences are useful for diagnosing, treating and/or preventing
CC reproductive disorders, neural disorders, disorders related to aberrant
CC potassium regulation or hyper potassium channel activity, metabolic
CC disorders (e.g. premature puberty), endocrine disorders (e.g. aberrant
CC growth hormone synthesis and/or secretion), memory disorder, disorders
CC of the testis (e.g. spermatogenesis), neuroendocrine condition related
CC to aberrant thyroid hormone release, renal disease or disorders (e.g.
CC nephritis), disorders related to aberrant higher brain function (e.g.
CC learning deficiencies), neurodegenerative diseases (e.g. Alzheimer's
CC disease), proliferative disorders (e.g. carcinoid tumour) and disorders
CC involving excessive smooth muscle tone or excitability (e.g. asthma).

```
CC   They may be used to modulate haemostatic or thrombolytic activity, to
CC   treat or prevent blood coagulation diseases or disorders, blood platelet
CC   diseases, wounds, autoimmune diseases, disorders or conditions (e.g.
CC   rheumatoid arthritis), allergic reactions (e.g. asthma), organ rejection
CC   or graft-versus-host disease, and hyperproliferative diseases. K+betaM2
CC   sequences are also used in gene therapy. The present DNA sequence is
CC   a PCR primer which is used for amplifying Drosophila melanogaster
CC   attacinD antimicrobial peptide (AMP) gene. This sequence is used in
CC   the exemplification of the invention.
XX
SQ   Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 other;

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        603 CCTGAAGCCTGACA 616
              ||||||||||||||
Db          1 CCTGAAGCCTGACA 14


RESULT 218
ABT09862
ID   ABT09862 standard; DNA; 20 BP.
XX
AC   ABT09862;
XX
DT   05-DEC-2002  (first entry)
XX
DE   K+beta M6 related PCR primer SEQ ID No 70.
XX
KW   Cytostatic; cardiant; neuroprotective; immunomodulator; antimigraine;
KW   sedative; gynaecological;; potassium channel beta subunit; K+betaM6;
KW   gastrointestinal; reproductive; neural; sleep; low DNA repair capacity;
KW   hyperpotassium channel activity; cardiovascular; melatonin synthesis;
KW   mammary cancer tumourigenesis; pineal gland associated disorder;
KW   pulmonary disorder; immune disorder; NF-kB activity; migraine headache;
KW   low free-radical buffering capacity; delayed sleep phase syndrome;
KW   circadian cycle; melatonin secretion; cancer; PCR; primer; ss.
XX
OS   Drosophila melanogaster.
XX
PN   WO200270727-A2.
XX
PD   12-SEP-2002.
XX
PF   21-FEB-2002; 2002WO-US05674.
XX
PR   21-FEB-2001; 2001US-270132P.
PR   27-MAR-2001; 2001US-278953P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Feder J,  Lee L,  Chen J,  Jackson DG,  Ramanathan C,  Siemers N;
PI   Chang H;
XX
DR   WPI; 2002-713455/77.
XX
PT   New polynucleotide encoding human potassium channel beta subunit
PT   polypeptide, useful for diagnosing, preventing, treating or
PT   ameliorating e.g. cancer  -
XX
PS   Example 6; Page 217; 332pp; English.
XX
CC   The invention relates to an isolated polynucleotide encoding a potassium
CC   channel beta subunit (K+betaM6) polypeptide or its variants. The human
CC   potassium beta subunit polynucleotide or polypeptide is useful for
CC   diagnosing, preventing, treating or ameliorating a pathological condition
CC   such as gastrointestinal, reproductive, neural, sleep, cardiovascular or
CC   pulmonary disorders, a disorder related to hyperpotassium channel
CC   activity, an immune disorder related to aberrant NF-kB activity, pineal
CC   gland associated disorders, migraine headaches, disorders associated with
CC   aberrant melatonin synthesis and/or release or with low DNA repair
CC   capacities or low free-radical buffering capacity, delayed sleep phase
CC   syndrome, aberrations in circadian cycle, mammary cancer tumourigenesis,
CC   age related disorders associated with decreased melatonin secretion, or
CC   cancer. This polynucleotide sequence represents a PCR primer relating to
CC   the potassium channel beta subunit (K+betaM6) of the invention.
XX
SQ   Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 other;

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        603 CCTGAAGCCTGACA 616
              ||||||||||||||
Db          1 CCTGAAGCCTGACA 14


RESULT 219
ABL59377/c
ID   ABL59377 standard; DNA; 20 BP.
XX
AC   ABL59377;
XX
DT   22-OCT-2002  (first entry)
XX
DE   Primer based on a protein producing (S)-4-bromo-3-hydroxybutanoate.
XX
KW   (S)-4-bromo-3-hydroxybutanoate; 4-bromo-3-oxobutanoate; pharmaceutical;
KW   agrochemical; 4-cyano-3-hydroxybutanoic acid; PCR; primer; ss.
XX
OS   Penicillium citrinum.
XX
PN   EP1213354-A2.
XX
PD   12-JUN-2002.
XX
PF   07-DEC-2001; 2001EP-0310251.
XX
PR   07-DEC-2000; 2000JP-0372704.
PR   15-JAN-2001; 2001JP-0006144.
PR   02-FEB-2001; 2001JP-0026594.
PR   11-JUN-2001; 2001JP-0175175.
XX
PA   (SUMO ) SUMITOMO CHEM CO LTD.
XX
PI   Asako H,  Matsumura K,  Shimizu M,  Ito N,  Wakita R;
XX
DR   WPI; 2002-550350/59.
XX
PT   New protein preferentially producing (S)-4-bromo-3-hydroxybutanoate by
PT   asymmetrically reducing 4-bromo-3-oxobutanoate, useful in
PT   pharmaceuticals and agrochemicals  -
XX
PS   Example 1; Page 34; 56pp; English.
XX
CC   PCR primers ABL59377-83 are based on a peptide (ABB77966) which is
CC   derived from a Penicillium citrinum protein. This protein is is capable
CC   of producing (S)-4-bromo-3-hydroxybutanoate by asymmetrically reducing
CC   4-bromo-3-oxobutanoate. The protein and polynucleotides are useful
CC   for producing optically active (S)-4-bromo-3-hydroxybutanoate,
CC   which is useful as an intermediate in the production of pharmaceuticals
CC   and agrochemicals. The (S)-4-bromo-3-hydroxybutanoate produced can
CC   also be used to produce 4-cyano-3-hydroxybutanoic acid.
XX
SQ   Sequence 20 BP; 3 A; 3 C; 5 G; 4 T; 5 other;

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   70.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        867 GGTCCCCACAGCCAAGTTCC 886
              ||| :||| | :||:|||||
Db         20 GGTWSCCARAAYCARGTTCC 1
```

```
RESULT 220
ABQ74025/c
ID   ABQ74025 standard; DNA; 20 BP.
XX
AC   ABQ74025;
XX
DT   10-OCT-2002  (first entry)
XX
DE   Human NOVINTRA C forward PCR primer SEQ ID NO:98.
XX
KW   Human; transmembrane protein; neuromedin protein; gonadotropin protein;
KW   interleukin-1 receptor antagonist; interleukin-1 epsilon; NOVX; probe;
KW   IL-1 epsilon; IL-1 receptor antagonist; lung disease; nootropic;
KW   cytostatic; neuroprotective; antiinflammatory; antibacterial; PCR primer;
KW   immunosuppressive; cerebroprotective; antidiabetic; antiarthritic;
KW   antiasthmatic; antiallergic; gene therapy; antibody-based therapy;
KW   cell signalling disorder; haematopoietic disorder; endocrine; muscle;
KW   neurodegenerative disorder; neurological disorder; cancer; melanoma;
KW   central nervous system cancer; reproductive development disorder; asthma;
KW   metabolic function disorder; bone metabolism; structure disorder; stroke;
KW   inflammatory response disorder; immune regulation disorder; septic shock;
KW   diabetes; arthritis; lung cancer; emphysema; allergic lung irritation;
KW   lung inflammation; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US2002068279-A1.
XX
PD   06-JUN-2002.
XX
PF   05-DEC-2000; 2000US-0730617.
XX
PR   06-DEC-1999;   99US-169056P.
PR   09-DEC-1999;   99US-169866P.
PR   09-DEC-1999;   99US-169886P.
PR   10-DEC-1999;   99US-170252P.
PR   12-JAN-2000; 2000US-175740P.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Burgess C,  Prayaga SK,  Shimkets RA,  Rastelli L,  Zerhusen B;
PI   Mezes P;
XX
DR   WPI; 2002-582472/62.
XX
PT   New NOVX proteins for diagnosing or treating cell signaling, immune
PT   response, hematopoietic, neurodegenerative, muscle, endocrine, bone,
PT   and reproductive development disorders  -
XX
PS   Example 1; Page 37; 110pp; English.
XX
CC   The present invention describes an isolated NOVX polypeptide, chosen from
CC   human transmembrane (NOVTRAN), neuromedin (NOVNEUR), gonadotropin
CC   (NOVGON), interleukin-1 (IL-1) receptor antagonist (NOVINTRA A and B),
CC   and IL-1 epsilon proteins. NOVX polypeptides have nootropic, cytostatic,
CC   neuroprotective, antiinflammatory, antibacterial, immunosuppressive,
CC   cerebroprotective, antidiabetic, antiarthritic, antiasthmatic and
CC   antiallergic activities, and can be used in gene therapy and antibody-
CC   based therapy. NOVX polypeptides, nucleic acid (I) encoding them and an
CC   antibody (III) that binds the polypeptide, are useful for treating or
CC   preventing a NOVX protein-associated disorder in humans. NOVTRAN can be
CC   used in the treatment of a cell signalling disorder, such as, a
CC   haematopoietic disorder or a neurodegenerative disorder. NOVNEUR can be
CC   used in the treatment of an endocrine, muscle, neurological disorder,
CC   central nervous system cancer, breast, colon, ovarian, kidney, prostate
CC   or thyroid cancer. NOVGON can be used in the treatment of a reproductive
CC   development disorder, metabolic function disorder or melanoma. NOVINTRA
CC   proteins can be used in the treatment of and a bone metabolism or
CC   structure disorder, an inflammatory response disorder, an immune
CC   regulation disorder, septic shock, stroke, diabetes, arthritis or
CC   cancer. An agent which modulates the expression or activity of a human
CC   IL-1 epsilon protein is useful for treating a lung disease such as lung
CC   cancer, asthma, emphysema, allergic lung irritation and lung inflammation
CC   in a mammal. ABQ73996 to ABQ74027 and ABP51981 to ABP52048 represent
CC   sequences used in the exemplification of the present invention.
XX
SQ   Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 other;

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        827 TGCAGCTGAAGCTT 840
              ||||||||||||||
Db         16 TGCAGCTGAAGCTT 3


RESULT 221
AAD39371
ID   AAD39371 standard; DNA; 20 BP.
XX
AC   AAD39371;
XX
DT   04-OCT-2002  (first entry)
XX
DE   S2 gene amplifying reverse PCR primer.
XX
KW   Ubiquitin conjugating enzyme; UBC; RATL1d6; immune disorder;
KW   regulated in activated T-lymphocyte 1d6; neuronal disorder; cancer;
KW   tumour; lymphoproliferative; cancer; adenocarcinoma; leukaemia; myeloma;
KW   sarcoma; neurodegenerative; inflammatory; rheumatoid arthritis; asthma;
KW   multiple sclerosis; psoriasis; neuronal; Alzheimer's disease; dementia;
KW   depression; epilepsy; acquired immuno deficiency syndrome; allergy;
KW   AIDS; anaemia; atopic dermatitis; diabetes mellitus; dermatological;
KW   myocardial infarction; renal tubular acidosis; gonadal dysgenesis;
KW   dysplasia; cataract; cytostatic; neuroprotective; nootropic; anti-HIV;
KW   anticonvulsant; antiinflammatory; Cushing's syndrome; cardiant;
KW   ophthalmological; S2 gene; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200236741-A2.
XX
PD   10-MAY-2002.
XX
PF   29-OCT-2001; 2001WO-US46559.
XX
PR   30-OCT-2000; 2000US-244688P.
PR   30-JUL-2001; 2001US-308706P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Bowen MA,  Wu Y,  Yang W,  Finger JN;
XX
DR   WPI; 2002-479758/51.
XX
PT   Novel ubiquitin conjugating enzyme polypeptide isolated from activated
PT   human T cell, for screening modulators useful for treating cancer,
PT   immune disorder, lymphoproliferative disorder, neurodegenerative
PT   disorder  -
XX
PS   Example 14; Page 121; 169pp; English.
XX
CC   The invention relates to a novel ubiquitin conjugating enzyme (UBC)
CC   homologue, RATL1d6 (regulated in activated T-lymphocytes 1d6) and its
CC   corresponding nucleic acid. The invention also relates to methods for
CC   treating, diagnosing, preventing and screening for disorders related
CC   to the expression of RATL1d6. UBC is useful for screening for candidate
CC   compounds capable of binding to and/or modulating its activity. UBC is
CC   useful for treating an immune or neuronal disorder in a mammal. The
CC   method is useful for treating a cancer or tumour. It is useful for
CC   suppressing the immune response in a subject requiring the suppression.
CC   It is also useful for treating lymphoproliferative disorder, cancer e.g.
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CC   adenocarcinoma, leukaemia, myeloma, sarcoma, etc, neurodegenerative
CC   disorder, inflammatory disorders e.g. rheumatoid arthritis, asthma,
CC   multiple sclerosis, psoriasis, etc, neuronal disorders e.g. Alzheimer's
CC   disease, dementia, depression, epilepsy, etc, immune disorder or immune
CC   related disorders such as acquired immuno deficiency syndrome (AIDS),
CC   allergy, anaemia, atopic dermatitis, diabetes mellitus, myocardial
CC   infarction, etc, developmental disorders e.g. Cushing's syndrome, renal
CC   tubular acidosis, gonadal dysgenesis, dysplasia, cataract, etc. The
CC   present sequence is a PCR primer used for amplifying S2 gene. This
CC   sequence is used in the exemplification of the invention.
XX
SQ   Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 other;

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        603 CCTGAAGCCTGACA 616
              ||||||||||||||
Db          1 CCTGAAGCCTGACA 14


RESULT 222
ABI93616/c
ID   ABI93616 standard; DNA; 20 BP.
XX
AC   ABI93616;
XX
DT   15-FEB-2002  (first entry)
XX
DE   Capture oligonucleptide Zip ID#703 oligo #9.
XX
KW   Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW   ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW   infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW   cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW   environmental monitoring; food industry; feed industry; ss.
XX
OS   Synthetic.
XX
PN   WO200179548-A2.
XX
PD   25-OCT-2001.
XX
PF   04-APR-2001; 2001WO-US10958.
XX
PR   14-APR-2000; 2000US-197271P.
XX
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Barany F,  Zirvi M,  Gerry NP,  Favis R,  Kliman R;
XX
DR   WPI; 2002-034366/04.
XX
PT   Designing capture oligonucleotide probes for use on a support to which
PT   complementary oligonucleotides hybridize with little mismatch -
XX
PS   Example 5; Fig 29; 300pp; English.
XX
CC   The present invention describes a method (M1) for designing capture
CC   oligonucleotide probes (I) for use on a support to which complementary
CC   oligonucleotide probes (II) will hybridise with little mismatch, where
CC   (I) have melting temperatures within a narrow range. The method is useful
CC   for detecting infectious diseases caused by bacterial infectious agents
CC   e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC   infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC   Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC   Epstein-Barr virus and polio virus, and parasitic infectious agents
CC   selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC   medinesis. The method is also useful for detecting genetic diseases such
CC   as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC   Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC   involved in DNA amplification, replication, recombination or repair, the
CC   cancer is specifically associated with a gene selected from BRCA1 gene,
CC   p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC   method is also used for environmental monitoring, forensics and the food
CC   and feed industry, detecting comprises scanning (using e.g. a scanning
CC   electron microscope and infrared microscope) the support at the
CC   particular sites and identifying if ligation of the oligonucleotide probe
CC   sets occurred and correlating (using a computer) identified ligation to a
CC   presence or absence of the target nucleotide sequences. ABI82074 to
CC   ABI97546 represent oligonucleotide sequences used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 20 BP; 5 A; 10 C; 3 G; 2 T; 0 other;

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        262 CTGGGCTGGCTGAT 275
              ||||||||||||||
Db         15 CTGGGCTGGCTGAT 2


RESULT 223
ABI95663
ID   ABI95663 standard; DNA; 20 BP.
XX
AC   ABI95663;
XX
DT   16-FEB-2002  (first entry)
XX
DE   Capture oligonucleptide Zip ID#2750 oligo #9.
XX
KW   Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW   ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW   infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW   cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW   environmental monitoring; food industry; feed industry; ss.
XX
OS   Synthetic.
XX
PN   WO200179548-A2.
XX
PD   25-OCT-2001.
XX
PF   04-APR-2001; 2001WO-US10958.
XX
PR   14-APR-2000; 2000US-197271P.
XX
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Barany F,  Zirvi M,  Gerry NP,  Favis R,  Kliman R;
XX
DR   WPI; 2002-034366/04.
XX
PT   Designing capture oligonucleotide probes for use on a support to which
PT   complementary oligonucleotides hybridize with little mismatch -
XX
PS   Example 5; Fig 29; 300pp; English.
XX
CC   The present invention describes a method (M1) for designing capture
CC   oligonucleotide probes (I) for use on a support to which complementary
CC   oligonucleotide probes (II) will hybridise with little mismatch, where
CC   (I) have melting temperatures within a narrow range. The method is useful
CC   for detecting infectious diseases caused by bacterial infectious agents
CC   e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC   infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC   Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC   Epstein-Barr virus and polio virus, and parasitic infectious agents
CC   selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC   medinesis. The method is also useful for detecting genetic diseases such
CC   as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC   Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC   involved in DNA amplification, replication, recombination or repair, the
```

```
CC   cancer is specifically associated with a gene selected from BRCA1 gene,
CC   p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC   method is also used for environmental monitoring, forensics and the food
CC   and feed industry, detecting comprises scanning (using e.g. a scanning
CC   electron microscope and infrared microscope) the support at the
CC   particular sites and identifying if ligation of the oligonucleotide probe
CC   sets occurred and correlating (using a computer) identified ligation to a
CC   presence or absence of the target nucleotide sequences. ABI82074 to
CC   ABI97546 represent oligonucleotide sequences used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 other;

  Query Match             1.0%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         40 GCAAAATCTTAGCA 53
              ||||||||||||||
Db          5 GCAAAATCTTAGCA 18


RESULT 224
AAT88942/c
ID   AAT88942 standard; DNA; 17 BP.
XX
AC   AAT88942;
XX
DT   22-JAN-1998  (first entry)
XX
DE   Bumper primer 2 for the gag gene of HIV.
XX
KW   HIV; gag; HLA-DQ-alpha; human acute myelogenous leukaemia; AML; PCR;
KW   primer; thermophilic strand displacement amplification; tSDA;
KW   in situ amplification; ss.
XX
OS   Synthetic.
OS   Human immunodeficiency virus.
XX
PN   WO9711196-A2.
XX
PD   27-MAR-1997.
XX
PF   12-SEP-1996;   96WO-US14648.
XX
PR   21-SEP-1995;   95US-0531749.
PR   21-SEP-1995;   95US-0531747.
XX
PA   (BECT ) BECTON DICKINSON CO.
XX
PI   Cleve MV,  Lohman KL,  Ostrerova NV,  Reid RA,  Van Cleve M;
XX
DR   WPI; 1997-202902/18.
XX
PT   Detection of nucleic acids in cells - by in situ amplification of
PT   target sequences by thermophilic strand displacement amplification
XX
PS   Disclosure; Page 16; 37pp; English.
XX
CC   This primer is an example of a "bumper" primer, for the gag gene of HIV
CC   It is used in a modified version of thermophilic strand displacement
CC   amplification (tSDA) to amplify double stranded DNA in situ.
CC   Amplification primers (see AAT88932-3) are hybridised to both strands of
CC   the gene, and are extended. Both primers have a restriction endonuclease
CC   (RE) recognition site, and the products will also contain these sites.
CC   The products are displaced from the target sequence, by extension of the
CC   bumper primers, which anneal upstream of the amplification primers, and
CC   made double stranded by synthesising complementary strands. Making the
CC   products double stranded causes "nicks" to be created (via the RE
CC   recognition sites). Furthur extension occurs from the nicks, thereby
CC   displacing a copy of the target sequence from the double stranded
CC   amplification primer extension products. The nicking, extending and
CC   displacing steps are repeated, and the target sequence amplified in
CC   situ. The method can be used for the amplification of DNA in situ in
CC   cells in suspension, on slides or in tissues, with speed, sensitivity
CC   and specificity. In situ tSDA also remains compatible with
CC   immunochemical techniques in spite of the increased reaction temparature
CC   so both amplification of DNA and immunological staining (see AAT88934 for
CC   an example of a detector probe) can be performed on the same specimen.
XX
SQ   Sequence 17 BP; 3 A; 5 C; 3 G; 6 T; 0 other;

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGC 290
              ||||| |||||||| ||
Db         17 ATCAATGAGGAAGCTGC 1


RESULT 225
AAV97865/c
ID   AAV97865 standard; RNA; 17 BP.
XX
AC   AAV97865;
XX
DT   17-MAR-1999  (first entry)
XX
DE   Human EGF-R target sequence nucleotide position 4842.
XX
KW   Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
KW   hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
KW   cancer; genetic drift; detection; mutation; ss.
XX
OS   Homo sapiens.
XX
PN   WO9833893-A2.
XX
PD   06-AUG-1998.
XX
PF   14-JAN-1998;   98WO-US00730.
XX
PR   04-DEC-1997;   97US-0985162.
PR   31-JAN-1997;   97US-0036476.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (UYAS-) UNIV ASTON.
XX
PI   Akhtar S,  Fell P,  McSwiggen JA;
XX
DR   WPI; 1998-437449/37.
XX
PT   Enzymatic nucleic acids - which cleave RNA derived from an epidermal
PT   growth factor receptor, useful for inhibiting cell proliferation and
PT   for treating cancers
XX
PS   Claim 5; Page 81; 109pp; English.
XX
CC   The present invention describes enzymatic nucleic acid molecules (NAMs)
CC   which specifically cleave RNA derived from an epidermal growth factor
CC   receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
CC   represent specifically claimed target sequence from human EGF-R. AAV98044
CC   to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
CC   hairpin ribozymes respectively for human EGF-R. The NAMs are useful for
CC   cleaving EGF-R RNA in the treatment of a condition associated with EGFR
CC   expression levels e.g. to inhibit cell proliferation in the prevention or
CC   treatment of cancers. The NAMs can also be used as diagnostic tools to
CC   examine genetic drift and mutations within diseased cells or to detect
CC   the presence of EGF-R RNA in a cell.
XX
SQ   Sequence 17 BP; 4 A; 4 C; 2 G; 7 U; 0 other;

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy        916 CTAAAGGAGATGGCAGA 932
              ||||||||||  ||||
Db         17 CTAAAGGAGATTTCAGA 1


RESULT 226
AAV97237/c
ID   AAV97237 standard; RNA; 17 BP.
XX
AC   AAV97237;
XX
DT   17-MAR-1999  (first entry)
XX
DE   Human EGF-R target sequence nucleotide position 219.
XX
KW   Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
KW   hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
KW   cancer; genetic drift; detection; mutation; ss.
XX
OS   Homo sapiens.
XX
PN   WO9833893-A2.
XX
PD   06-AUG-1998.
XX
PF   14-JAN-1998;   98WO-US00730.
XX
PR   04-DEC-1997;   97US-0985162.
PR   31-JAN-1997;   97US-0036476.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (UYAS-) UNIV ASTON.
XX
PI   Akhtar S,  Fell P,  McSwiggen JA;
XX
DR   WPI; 1998-437449/37.
XX
PT   Enzymatic nucleic acids - which cleave RNA derived from an epidermal
PT   growth factor receptor, useful for inhibiting cell proliferation and
PT   for treating cancers
XX
PS   Claim 5; Page 68; 109pp; English.
XX
CC   The present invention describes enzymatic nucleic acid molecules (NAMs)
CC   which specifically cleave RNA derived from an epidermal growth factor
CC   receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
CC   represent specifically claimed target sequence from human EGF-R. AAV98044
CC   to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
CC   hairpin ribozymes respectively for human EGF-R. The NAMs are useful for
CC   cleaving EGF-R RNA in the treatment of a condition associated with EGFR
CC   expression levels e.g. to inhibit cell proliferation in the prevention or
CC   treatment of cancers. The NAMs can also be used as diagnostic tools to
CC   examine genetic drift and mutations within diseased cells or to detect
CC   the presence of EGF-R RNA in a cell.
XX
SQ   Sequence 17 BP; 1 A; 7 C; 6 G; 3 U; 0 other;

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        629 AGCTCCAGGAGCTCTGC 645
              ||| |||||||| ||||
Db         17 AGCGCCAGGAGCGCTGC 1


RESULT 227
AAX30261/c
ID   AAX30261 standard; DNA; 17 BP.
XX
AC   AAX30261;
XX
DT   21-JUN-1999  (first entry)
XX
DE   HIV gag bumper primer B2.
XX
KW   HIV; gag; bumper primer; amplification primer; probe; detection;
KW   fluorescence quenching; Chlamydia trachomatis; Neisseria gonorrheae;
KW   human; placental DNA; pathogen; ss.
XX
OS   Synthetic.
XX
PN   EP915173-A2.
XX
PD   12-MAY-1999.
XX
PF   03-NOV-1998;   98EP-0120832.
XX
PR   04-NOV-1997;   97US-0964020.
XX
PA   (BECT ) BECTON DICKINSON & CO.
XX
PI   Little MC,  Vonk GP;
XX
DR   WPI; 1999-265943/23.
XX
PT   New method for real-time fluorescence-detection assays useful for
PT   detecting nucleic acids from pathogens in samples from patients
XX
PS   Example 1; Page 8; 16pp; English.
XX
CC   The present invention describes a kit for conducting a fluorescence
CC   detection assay to determine the presence, absence or amount of a target
CC   analyte in a sample. The method and kit may be used to detect
CC   amplification of nucleic acid molecules in real time using fluorescence
CC   quenching for example. The assays may be used to detect the presence of
CC   nucleic acids from pathogens in samples of body fluid from patients.
CC   The kit allows a homogeneous nucleic acid amplification and real time
CC   nucleic acid probe detection assay to be carried out with minimal
CC   complexity which yields a consistent reliable fluorescent detection
CC   signal. The present sequence represents a primer used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 17 BP; 3 A; 5 C; 3 G; 6 T; 0 other;

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        274 ATCAAAGAGGAAGCAGC 290
              ||||| |||||||| ||
Db         17 ATCAATGAGGAAGCTGC 1


RESULT 228
AAF02208
ID   AAF02208 standard; DNA; 17 BP.
XX
AC   AAF02208;
XX
DT   16-FEB-2001  (first entry)
XX
DE   Hammerhead ribozyme substrate #503.
XX
KW   Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW   interferon alpha; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061729-A2.
XX
PD   19-OCT-2000.
XX
PF   11-APR-2000; 2000WO-US09721.
XX
```

PR 12-APR-1999; 99US-0129390.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor
PT protein, interferon alpha and erythropoietin -
XX
PS Claim 37; Page 67; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
CC transcription factor gene, IRF-2 and/or the CAATT Displacement
CC Protein (CDP). Inhibition of the repressors removes prevents
CC inhibition (and consequently increases expression of) genes involved in
CC the production of erythropoietin, granulocyte colony stimulating factor
CC protein and interferon alpha.
XX
SQ Sequence 17 BP; 1 A; 11 C; 1 G; 4 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 581 CCCTCCGTCTGCCCCCC 597
| |||||||| ||||||
Db 1 CTCTCCGTCTACCCCCC 17

RESULT 229
AAF02788
ID AAF02788 standard; DNA; 17 BP.
XX
AC AAF02788;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #1083.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US09721.
XX
PR 12-APR-1999; 99US-0129390.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor
PT protein, interferon alpha and erythropoietin -
XX
PS Claim 37; Page 80; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
CC transcription factor gene, IRF-2 and/or the CAATT Displacement
CC Protein (CDP). Inhibition of the repressors removes prevents
CC inhibition (and consequently increases expression of) genes involved in
CC the production of erythropoietin, granulocyte colony stimulating factor
CC protein and interferon alpha.
XX
SQ Sequence 17 BP; 0 A; 8 C; 4 G; 5 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 145 CTCGGCTCCGCTCCGCG 161
||||||| | |||||||
Db 1 CTCGGCTTCTCTCCGCG 17

RESULT 230
AAF05406/c
ID AAF05406 standard; DNA; 17 BP.
XX
AC AAF05406;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #2625.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US09721.
XX
PR 12-APR-1999; 99US-0129390.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor
PT protein, interferon alpha and erythropoietin -
XX
PS Claim 18; Page 116; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
CC transcription factor gene, IRF-2 and/or the CAATT Displacement
CC Protein (CDP). Inhibition of the repressors removes prevents
CC inhibition (and consequently increases expression of) genes involved in
CC the production of erythropoietin, granulocyte colony stimulating factor
CC protein and interferon alpha.
XX
SQ Sequence 17 BP; 3 A; 6 C; 3 G; 5 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1247 TGGCCATGTGAGGCCAG 1263
||| ||||| |||||||
Db 17 TGGACATGTAAGGCCAG 1

RESULT 231
AAZ45525

ID AAZ45525 standard; DNA; 17 BP.
XX
AC AAZ45525;
XX
DT 06-APR-2000 (first entry)
XX
DE Primer used to screen for the presence of the pelB or g3 leader sequence.
XX
KW Virus selection; phage display system; p3 coat protein; proteolysis;
KW interacting protein element; pelB; g3; PCR primer; ss.
XX
OS Unidentified.
XX
PN WO9958655-A2.
XX
PD 18-NOV-1999.
XX
PF 13-MAY-1999; 99WO-GB01526.
XX
PR 13-MAY-1998; 98GB-0010223.
PR 13-MAY-1998; 98GB-0010228.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Riechmann L, Kristensen P, Jestin J, Winter GP;
XX
DR WPI; 2000-116289/10.
XX
PT Selection system used for the selection of polypeptides displayed in a
PT phage display system -
XX
PS Example 6; Page 30; 64pp; English.
XX
CC The specification describes a method for the selection of viruses
CC displaying polypeptides in a phage display system. The method
CC comprises insertion of a polypeptide sequence in the p3 coat protein,
CC followed by proteolysis. The method reduces background in phage
CC display techniques. The method is used to select for viruses displaying
CC desired polypeptides. The methods may also be used for the
CC identification of interacting protein elements, and for the selection of
CC a repertoire of polypeptides which interact with a selected polypeptide
CC and/or repertoire. PCR primers AAZ45524-25 were used to screen for the
CC presence of the pelB or g3 leader sequences. The leader sequences were
CC used to generate libraries, which are used to generate cleavable phage
CC vectors in which poorly displayed proteins such as DNA polymerases are
CC better displayed.
XX
SQ Sequence 17 BP; 3 A; 8 C; 3 G; 3 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 983 CAGTCCCATTCAGATCC 999
|| |||||||||||||
Db 1 CGGCCCCATTCAGATCC 17

RESULT 232
ABA79028/c
ID ABA79028 standard; DNA; 17 BP.
XX
AC ABA79028;
XX
DT 24-JAN-2002 (first entry)
XX
DE Factor VIII mutation correcting oligonucleotide SEQ ID NO: 1874.
XX
KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
KW Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
KW antilipemic; ss.
XX
OS Homo sapiens.
XX
PN WO200173002-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US09761.
XX
PR 27-MAR-2000; 2000US-192176P.
PR 27-MAR-2000; 2000US-192179P.
PR 01-JUN-2000; 2000US-208538P.
PR 30-OCT-2000; 2000US-244989P.
XX
PA (UYDE) UNIV DELAWARE.
XX
PI Kmiec EB, Gamper HB, Rice MC;
XX
DR WPI; 2001-639230/73.
XX
PT Oligonucleotide for targeted alterations of genetic sequences and for
PT treating cystic fibrosis, comprises at least one mismatch and chemical
PT modification -
XX
PS Claim 7; Page 154; 294pp; English.
XX
CC The present invention provides single-stranded oligonucleotides which can
CC be used for the targeted alteration of genomic sequences, where the
CC oligonucleotide has at least one mismatch compared with the genomic
CC sequence to be altered. In particular, these sequences are directed at
CC the following genes: adenosine deaminase, p53, beta-globin,
CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
CC various syndromes. The present sequence is one of the gene correcting
CC oligonucleotides of the invention.
XX
SQ Sequence 17 BP; 2 A; 4 C; 4 G; 7 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 600 CAGCCTGAAGCCTGACA 616
|||| ||||| ||||||
Db 17 CAGCATGAAGACTGACA 1

RESULT 233
ABA79029
ID ABA79029 standard; DNA; 17 BP.
XX
AC ABA79029;
XX
DT 24-JAN-2002 (first entry)
XX
DE Factor VIII mutation correcting oligonucleotide SEQ ID NO: 1875.
XX
KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;

KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
KW Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
KW antilipemic; ss.
XX
OS Homo sapiens.
XX
PN WO200173002-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US09761.
XX
PR 27-MAR-2000; 2000US-192176P.
PR 27-MAR-2000; 2000US-192179P.
PR 01-JUN-2000; 2000US-208538P.
PR 30-OCT-2000; 2000US-244989P.
XX
PA (UYDE) UNIV DELAWARE.
XX
PI Kmiec EB, Gamper HB, Rice MC;
XX
DR WPI; 2001-639230/73.
XX
PT Oligonucleotide for targeted alterations of genetic sequences and for
PT treating cystic fibrosis, comprises at least one mismatch and chemical
PT modification -
XX
PS Claim 7; Page 154; 294pp; English.
XX
CC The present invention provides single-stranded oligonucleotides which can
CC be used for the targeted alteration of genomic sequences, where the
CC oligonucleotide has at least one mismatch compared with the genomic
CC sequence to be altered. In particular, these sequences are directed at
CC the following genes: adenosine deaminase, p53, beta-globin,
CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
CC various syndromes. The present sequence is one of the gene correcting
CC oligonucleotides of the invention.
XX
SQ Sequence 17 BP; 7 A; 4 C; 4 G; 2 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 600 CAGCCTGAAGCCTGACA 616
|||| ||||| ||||||
Db 1 CAGCATGAAGACTGACA 17

RESULT 234
AAF92872
ID AAF92872 standard; DNA; 17 BP.
XX
AC AAF92872;
XX
DT 17-MAY-2001 (first entry)
XX
DE Human ABC1 transcription factor binding site #33.
XX
KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
XX
OS Homo sapiens.
XX
PN WO200115676-A2.
XX
PD 08-MAR-2001.
XX
PF 01-SEP-2000; 2000WO-IB01492.
XX
PR 01-SEP-1999; 99US-0151977.
PR 15-MAR-2000; 2000US-0526193.
PR 23-JUN-2000; 2000US-0213958.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (XENO-) XENON GENETICS INC.
XX
PI Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;
XX
DR WPI; 2001-244356/25.
XX
PT Treating a lower than normal high density lipoprotein-cholesterol
PT (HDL-C) level, a higher than normal triglyceride level, or a
PT cardiovascular disease, by administering a compound that modulates LXR-
PT or RXR-mediated transcriptional activity -
XX
PS Disclosure; Fig 3; 317pp; English.
XX
CC The present invention relates to a method for treating a patient
CC diagnosed as having a lower than normal high density
CC lipoprotein-cholesterol (HDL-C) level, a higher than normal
CC triglyceride level, or a cardiovascular disease, involving
CC administering a compound that modulates LXR- or RXR-mediated
CC transcriptional activity or ABC1 expression or activity.
CC The LXR gene product may be used in an assay to identify
CC compounds useful for the treatment of a disease or condition selected a
CC lower than normal HDL cholesterol level, a higher than normal
CC triglyceride level, and a cardiovascular disease.
XX
SQ Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 498 GCAGCGTCTTGGGGTCA 514
|||| ||| ||||||||
Db 1 GCAGAGTCCTGGGGTCA 17

RESULT 235
ABK03156/c
ID ABK03156 standard; RNA; 17 BP.
XX
AC ABK03156;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human CD20 Inozyme #107.
XX
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
OS Synthetic.
XX

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PN   WO200159103-A2.
XX
PD   16-AUG-2001.
XX
PF   09-FEB-2001; 2001WO-US04273.
XX
PR   11-FEB-2000; 2000US-181797P.
PR   28-FEB-2000; 2000US-185516P.
PR   06-MAR-2000; 2000US-187128P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MCSW/) MCSWIGGEN J.
PA   (CHOW/) CHOWRIRA B M.
XX
PI   Blatt L,  McSwiggen J,  Chowrira BM;
XX
DR   WPI; 2001-607195/69.
XX
PT   Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT   constructs, which down regulate expression of a CD20 gene or neurite
PT   growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
PT   and central nervous system injury  -
XX
PS   Claim 30; Page 147; 200pp; English.
XX
CC   The invention relates to a nucleic acid molecule which down regulates
CC   expression of a CD20 gene and a nucleic acid molecule which down
CC   regulates expression of a neurite growth inhibitor gene (NOGO).
CC   The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC   DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
CC   possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN
CC   motif) pr an amberzyme (cleaving RNA with an NGN triplet), a zinzyme
CC   (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used
CC   to cleave RNA of CD20 in the presence of a divalent cation that is
CC   preferably Mg^2^+. Furthermore, it may be contacted with a cell to reduce
CC   CD20 activity of the cell and treat a patient having a condition
CC   associated with the level of CD20. The treatment may further comprise the
CC   use of one or more therapies. In particular, the CD20 targetting
CC   nucleic acid may be used to treat lymphoma, leukaemia, B-cell
CC   lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
CC   low-grade or follicular NHL, lymphocytic leukaemia, HIV (human
CC   immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
CC   immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
CC   thrombocytopaenia, and inflammatory arthropathy. The NOGO-targetting
CC   nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
CC   divalent cation that is preferably Mg^2^+. Furthermore, the nucleic acid
CC   may be contacted with a cell to reduce NOGO activity of the cell and
CC   treat a patient having a condition associated with the level of NOGO. The
CC   treatment may further comprise the use of one or more therapies.
CC   In particular, the NOGO-targetting nucleic acid may be used to treat
CC   central nervous system (CNS) injury and cerebrovascular accident (CVA,
CC   stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC   chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC   Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC   disease, muscular dystrophy, and/or other neurodegenerative disease
CC   states which respond to the modulation of NOGO expression. The
CC   present sequence is an inozyme of the invention.
XX
SQ   Sequence 17 BP; 2 A; 4 C; 4 G; 7 U; 0 other;

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        384 TCCAGAGGTGGCAGCAA 400
              ||||||  |||||||||
Db         17 TCCAGAAATGGCAGCAA 1


RESULT 236
ABV90547/c
ID   ABV90547 standard; DNA; 17 BP.
XX
AC   ABV90547;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Human POSHL1 scanning oligonucleotide SEQ ID NO 1260.
XX
KW   Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW   Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW   gene therapy; transgenic; ss.
XX
OS   Homo sapiens.
XX
PN   EP1239051-A2.
XX
PD   11-SEP-2002.
XX
PF   28-JAN-2002; 2002EP-0001165.
XX
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00666.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   30-JAN-2001; 2001WO-US00670.
PR   23-MAY-2001; 2001US-0864761.
PR   10-OCT-2001; 2001US-0328205.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M;
XX
DR   WPI; 2002-684061/74.
XX
PT   Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,
PT   POSHL-1, useful for treating disorders associated with decreased
PT   expression or activity of human POSHL1 -
XX
PS   Example 2; SEQ ID NO 1260; 60pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated SH3 domain (POSH)-like signalling
CC   protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC   acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC   (S1) having 95% deviations, especially conservative substitutions or a
CC   fragment of the sequences comprising at least 8 contiguous amino acids.
CC   Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC   adaptor protein that interacts with Rho family small GTPases as well as
CC   downstream components of the signal transduction pathway. (I) is useful
CC   for identifying a specific binding partner. (I) and nucleic acids (II)
CC   encoding (I) are useful for diagnosing, monitoring disease and treating
CC   caused by altered expression of human POSHL1 including diagnosing and
CC   treating cancer, they useful in the development of vaccines and (II) is
CC   useful in gene therapy. (II) is useful for constructing microarrays which
CC   are useful for measuring and for surveying gene expression and creating
CC   transgenic non-human animals capable of producing the proteins. The
CC   present sequence is that of a scanning oligonucleotide useful in examples
CC   of the invention.
CC   Note: The present sequence did not form part of the printed
CC   specification, but is based on sequence information supplied to Derwent
CC   by the European Patent Office.
XX
SQ   Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 other;

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        267 CTGGCTGATCAAAGAGG 283
              |||| |||||| |||||
Db         17 CTGGGTGATCACAGAGG 1
```

```
RESULT 237
ABV90548/c
ID   ABV90548 standard; DNA; 17 BP.
XX
AC   ABV90548;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Human POSHL1 scanning oligonucleotide SEQ ID NO 1261.
XX
KW   Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW   Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW   gene therapy; transgenic; ss.
XX
OS   Homo sapiens.
XX
PN   EP1239051-A2.
XX
PD   11-SEP-2002.
XX
PF   28-JAN-2002; 2002EP-0001165.
XX
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00666.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   30-JAN-2001; 2001WO-US00670.
PR   23-MAY-2001; 2001US-0864761.
PR   10-OCT-2001; 2001US-0328205.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M;
XX
DR   WPI; 2002-684061/74.
XX
PT   Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,
PT   POSHL-1, useful for treating disorders associated with decreased
PT   expression or activity of human POSHL1 -
XX
PS   Example 2; SEQ ID NO 1261; 60pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated SH3 domain (POSH)-like signalling
CC   protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC   acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC   (S1) having 95% deviations, especially conservative substitutions or a
CC   fragment of the sequences comprising at least 8 contiguous amino acids.
CC   Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC   adaptor protein that interacts with Rho family small GTPases as well as
CC   downstream components of the signal transduction pathway. (I) is useful
CC   for identifying a specific binding partner. (I) and nucleic acids (II)
CC   encoding (I) are useful for diagnosing, monitoring disease and treating
CC   caused by altered expression of human POSHL1 including diagnosing and
CC   treating cancer, they useful in the development of vaccines and (II) is
CC   useful in gene therapy. (II) is useful for constructing microarrays which
CC   are useful for measuring and for surveying gene expression and creating
CC   transgenic non-human animals capable of producing the proteins. The
CC   present sequence is that of a scanning oligonucleotide useful in examples
CC   of the invention.
CC   Note: The present sequence did not form part of the printed
CC   specification, but is based on sequence information supplied to Derwent
CC   by the European Patent Office.
XX
SQ   Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 other;

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        266 GCTGGCTGATCAAAGAG 282
              ||||| |||||| ||||
Db         17 GCTGGGTGATCACAGAG 1


RESULT 238
ABV90549/c
ID   ABV90549 standard; DNA; 17 BP.
XX
AC   ABV90549;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Human POSHL1 scanning oligonucleotide SEQ ID NO 1262.
XX
KW   Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW   Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW   gene therapy; transgenic; ss.
XX
OS   Homo sapiens.
XX
PN   EP1239051-A2.
XX
PD   11-SEP-2002.
XX
PF   28-JAN-2002; 2002EP-0001165.
XX
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00666.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   30-JAN-2001; 2001WO-US00670.
PR   23-MAY-2001; 2001US-0864761.
PR   10-OCT-2001; 2001US-0328205.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M;
XX
DR   WPI; 2002-684061/74.
XX
PT   Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,
PT   POSHL-1, useful for treating disorders associated with decreased
PT   expression or activity of human POSHL1 -
XX
PS   Example 2; SEQ ID NO 1262; 60pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated SH3 domain (POSH)-like signalling
CC   protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC   acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC   (S1) having 95% deviations, especially conservative substitutions or a
CC   fragment of the sequences comprising at least 8 contiguous amino acids.
CC   Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC   adaptor protein that interacts with Rho family small GTPases as well as
CC   downstream components of the signal transduction pathway. (I) is useful
CC   for identifying a specific binding partner. (I) and nucleic acids (II)
CC   encoding (I) are useful for diagnosing, monitoring disease and treating
CC   caused by altered expression of human POSHL1 including diagnosing and
CC   treating cancer, they useful in the development of vaccines and (II) is
CC   useful in gene therapy. (II) is useful for constructing microarrays which
CC   are useful for measuring and for surveying gene expression and creating
CC   transgenic non-human animals capable of producing the proteins. The
CC   present sequence is that of a scanning oligonucleotide useful in examples
CC   of the invention.
CC   Note: The present sequence did not form part of the printed
CC   specification, but is based on sequence information supplied to Derwent
CC   by the European Patent Office.
XX
SQ   Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 other;
```

```
  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        265 GGCTGGCTGATCAAAGA 281
              |||||| |||||| |||
Db         17 GGCTGGGTGATCACAGA 1


RESULT 239
ABV90550/c
ID   ABV90550 standard; DNA; 17 BP.
XX
AC   ABV90550;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Human POSHL1 scanning oligonucleotide SEQ ID NO 1263.
XX
KW   Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW   Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW   gene therapy; transgenic; ss.
XX
OS   Homo sapiens.
XX
PN   EP1239051-A2.
XX
PD   11-SEP-2002.
XX
PF   28-JAN-2002; 2002EP-0001165.
XX
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00666.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   30-JAN-2001; 2001WO-US00670.
PR   23-MAY-2001; 2001US-0864761.
PR   10-OCT-2001; 2001US-0328205.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M;
XX
DR   WPI; 2002-684061/74.
XX
PT   Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,
PT   POSHL-1, useful for treating disorders associated with decreased
PT   expression or activity of human POSHL1 -
XX
PS   Example 2; SEQ ID NO 1263; 60pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated SH3 domain (POSH)-like signalling
CC   protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC   acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC   (S1) having 95% deviations, especially conservative substitutions or a
CC   fragment of the sequences comprising at least 8 contiguous amino acids.
CC   Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC   adaptor protein that interacts with Rho family small GTPases as well as
CC   downstream components of the signal transduction pathway. (I) is useful
CC   for identifying a specific binding partner. (I) and nucleic acids (II)
CC   encoding (I) are useful for diagnosing, monitoring disease and treating
CC   caused by altered expression of human POSHL1 including diagnosing and
CC   treating cancer, they useful in the development of vaccines and (II) is
CC   useful in gene therapy. (II) is useful for constructing microarrays which
CC   are useful for measuring and for surveying gene expression and creating
CC   transgenic non-human animals capable of producing the proteins. The
CC   present sequence is that of a scanning oligonucleotide useful in examples
CC   of the invention.
CC   Note: The present sequence did not form part of the printed
CC   specification, but is based on sequence information supplied to Derwent
CC   by the European Patent Office.
XX
SQ   Sequence 17 BP; 3 A; 8 C; 3 G; 3 T; 0 other;

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        264 GGGCTGGCTGATCAAAG 280
              ||||||| |||||| ||
Db         17 GGGCTGGGTGATCACAG 1


RESULT 240
ABV90551/c
ID   ABV90551 standard; DNA; 17 BP.
XX
AC   ABV90551;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Human POSHL1 scanning oligonucleotide SEQ ID NO 1264.
XX
KW   Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW   Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW   gene therapy; transgenic; ss.
XX
OS   Homo sapiens.
XX
PN   EP1239051-A2.
XX
PD   11-SEP-2002.
XX
PF   28-JAN-2002; 2002EP-0001165.
XX
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00666.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   30-JAN-2001; 2001WO-US00670.
PR   23-MAY-2001; 2001US-0864761.
PR   10-OCT-2001; 2001US-0328205.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M;
XX
DR   WPI; 2002-684061/74.
XX
PT   Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,
PT   POSHL-1, useful for treating disorders associated with decreased
PT   expression or activity of human POSHL1 -
XX
PS   Example 2; SEQ ID NO 1264; 60pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated SH3 domain (POSH)-like signalling
CC   protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC   acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC   (S1) having 95% deviations, especially conservative substitutions or a
CC   fragment of the sequences comprising at least 8 contiguous amino acids.
CC   Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC   adaptor protein that interacts with Rho family small GTPases as well as
CC   downstream components of the signal transduction pathway. (I) is useful
CC   for identifying a specific binding partner. (I) and nucleic acids (II)
CC   encoding (I) are useful for diagnosing, monitoring disease and treating
CC   caused by altered expression of human POSHL1 including diagnosing and
CC   treating cancer, they useful in the development of vaccines and (II) is
CC   useful in gene therapy. (II) is useful for constructing microarrays which
CC   are useful for measuring and for surveying gene expression and creating
CC   transgenic non-human animals capable of producing the proteins. The
```

CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention.
CC Note: The present sequence did not form part of the printed
CC specification, but is based on sequence information supplied to Derwent
CC by the European Patent Office.
XX
SQ Sequence 17 BP; 4 A; 7 C; 3 G; 3 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 263 TGGGCTGGCTGATCAAA 279
||||||||| |||||| |
Db 17 TGGGCTGGGTGATCACA 1

RESULT 241
ABV90553/c
ID ABV90553 standard; DNA; 17 BP.
XX
AC ABV90553;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1266.
XX
KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX
OS Homo sapiens.
XX
PN EP1239051-A2.
XX
PD 11-SEP-2002.
XX
PF 28-JAN-2002; 2002EP-0001165.
XX
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 23-MAY-2001; 2001US-0864761.
PR 10-OCT-2001; 2001US-0328205.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M;
XX
DR WPI; 2002-684061/74.
XX
PT Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,
PT POSHL-1, useful for treating disorders associated with decreased
PT expression or activity of human POSHL1 -
XX
PS Example 2; SEQ ID NO 1266; 60pp + Sequence Listing; English.
XX
CC The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention.
CC Note: The present sequence did not form part of the printed
CC specification, but is based on sequence information supplied to Derwent
CC by the European Patent Office.
XX
SQ Sequence 17 BP; 4 A; 7 C; 3 G; 3 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 261 CCTGGGCTGGCTGATCA 277
| ||||||||| ||||||
Db 17 CATGGGCTGGGTGATCA 1

RESULT 242
ABQ63635/c
ID ABQ63635 standard; DNA; 17 BP.
XX
AC ABQ63635;
XX
DT 20-AUG-2002 (first entry)
XX
DE Human KTOM1a portion (ABQ63232) probe # 348.
XX
KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200224750-A2.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-US29656.
XX
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US00661.
PR 30-JAN-2001; 2001WO-US00662.
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 23-MAY-2001; 2001US-0864761.
PR 28-AUG-2001; 2001US-315676P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhang J;
XX
DR WPI; 2002-479509/51.
XX
PT New human kidney tumor overexpressed membrane (KTOM1) protein and
PT nucleic acids encoding the protein, useful for treating subjects having
PT defects in KTOM1 which can manifest as cancer of the kidney, or as a
PT disorder of e.g., liver or bone -
XX
PS Example 2; Page 203; 418pp; English.
XX
CC The invention relates to a novel isolated nucleic acid encoding human

CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC invention has cytostatic activity. The nucleotide may have a use in gene
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC monitor a disease caused by altered expression of human KTOM1.
CC Compositions comprising the nucleic acids, proteins or antibodies may be
CC used to treat subjects having defects in KTOM1 which can manifest as
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC function. The sequence represents a probe used in the invention to
CC scan the nt 1-1001 portion of human KTOM1a (ABQ63232).
XX
SQ Sequence 17 BP; 2 A; 9 C; 5 G; 1 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1248 GGCCATGTGAGGCCAGG 1264
|||| |||| |||||||
Db 17 GGCCCTGTGGGGCCAGG 1

RESULT 243
ABK56690
ID ABK56690 standard; RNA; 17 BP.
XX
AC ABK56690;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human CLCA1 gene enzymatic nucleic acid #1061.
XX
KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcysteine.
XX
OS Homo sapiens.
XX
PN WO200211674-A2.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US24970.
XX
PR 09-AUG-2000; 2000US-224383P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (SYNT) SYNTEX USA LLC.
PA (THOM/) THOMPSON J.
XX
PI Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
PI Grupe A;
XX
DR WPI; 2002-217145/27.
XX
PT Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma -
XX
PS Claim 4; Page 78; 152pp; English.
XX
CC The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention.
XX
SQ Sequence 17 BP; 6 A; 6 C; 3 G; 2 U; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.8e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 644 GCATCCCCCAAGACCTG 660
| |:|| |||||||:|
Db 1 GAAUCCACCAAGACCUG 17

RESULT 244
ABK57443/c
ID ABK57443 standard; RNA; 17 BP.
XX
AC ABK57443;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human CLCA1 gene enzymatic nucleic acid #1814.
XX
KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcysteine.
XX
OS Homo sapiens.
XX
PN WO200211674-A2.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US24970.
XX
PR 09-AUG-2000; 2000US-224383P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (SYNT) SYNTEX USA LLC.
PA (THOM/) THOMPSON J.
XX
PI Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
PI Grupe A;
XX
DR WPI; 2002-217145/27.
XX
PT Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma -
XX
PS Claim 4; Page 113; 152pp; English.
XX
CC The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The

CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention.
XX
SQ Sequence 17 BP; 5 A; 7 C; 3 G; 2 U; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 661 GTCGGGGACTTGGCCAG 677
||||| || ||||||||
Db 17 GTCGGTGATTTGGCCAG 1

RESULT 245
ABN01791/c
ID ABN01791 standard; DNA; 17 BP.
XX
AC ABN01791;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1783.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US16981.
XX
PR 26-MAY-2000; 2000US-207456P.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US00661.
PR 30-JAN-2001; 2001WO-US00662.
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 05-FEB-2001; 2001US-266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption ionization, comprises human
PT myosin-like protein hGDMLP-1 -
XX
PS Disclosure; SEQ ID 1783; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of
CC hGDMLP-1 can be used in gene therapy and vaccine production. The
CC hGDMLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMLP-1, in
CC particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX
SQ Sequence 17 BP; 4 A; 6 C; 6 G; 1 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 546 CCTGCTGGCAGGCATGC 562
||||||||||| |||
Db 17 CCTGCTGGCAGGTCTGC 1

RESULT 246
ABN06165
ID ABN06165 standard; DNA; 17 BP.
XX
AC ABN06165;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6157.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US16981.
XX
PR 26-MAY-2000; 2000US-207456P.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US00661.
PR 30-JAN-2001; 2001WO-US00662.
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 05-FEB-2001; 2001US-266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX

PT New polypeptide, for raising antibodies that recognize hGDMLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption ionization, comprises human
PT myosin-like protein hGDMLP-1 -
XX
PS Disclosure; SEQ ID 6157; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of
CC hGDMLP-1 can be used in gene therapy and vaccine production. The
CC hGDMLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMLP-1, in
CC particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX
SQ Sequence 17 BP; 2 A; 7 C; 6 G; 2 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 255 CGACCTCCTGGGCTGGC 271
||||||| ||||||||
Db 1 CGACCTCACGGGCTGGC 17

RESULT 247
ABN06166
ID ABN06166 standard; DNA; 17 BP.
XX
AC ABN06166;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6158.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US16981.
XX
PR 26-MAY-2000; 2000US-207456P.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
PR 30-JAN-2001; 2001WO-US00661.
PR 30-JAN-2001; 2001WO-US00662.
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00666.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 30-JAN-2001; 2001WO-US00670.
PR 05-FEB-2001; 2001US-266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1
PT proteins, or as specific biomolecule capture probes for
PT surface-enhanced laser desorption ionization, comprises human
PT myosin-like protein hGDMLP-1 -
XX
PS Disclosure; SEQ ID 6158; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of
CC hGDMLP-1 can be used in gene therapy and vaccine production. The
CC hGDMLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMLP-1, in
CC particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX
SQ Sequence 17 BP; 2 A; 6 C; 6 G; 3 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 256 GACCTCCTGGGCTGGCT 272
|||||| |||||||||
Db 1 GACCTCACGGGCTGGCT 17

RESULT 248
ABN08390/c
ID ABN08390 standard; DNA; 17 BP.
XX
AC ABN08390;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8382.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX

```
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US16981.
XX
PR   26-MAY-2000; 2000US-207456P.
PR   21-SEP-2000; 2000US-234687P.
PR   27-SEP-2000; 2000US-236359P.
PR   04-OCT-2000; 2000GB-0024263.
PR   30-JAN-2001; 2001WO-US00661.
PR   30-JAN-2001; 2001WO-US00662.
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00666.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   30-JAN-2001; 2001WO-US00670.
PR   05-FEB-2001; 2001US-266860P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Gu Y,  Ji Y,  Penn SG,  Hanzel DK,  Rank DR,  Chen W,  Shannon ME;
XX
DR   WPI; 2002-179446/23.
XX
PT   New polypeptide, for raising antibodies that recognize hGDMLP-1
PT   proteins, or as specific biomolecule capture probes for
PT   surface-enhanced laser desorption ionization, comprises human
PT   myosin-like protein hGDMLP-1 -
XX
PS   Disclosure; SEQ ID 8382; 214pp; English.
XX
CC   The present invention describes a human genome-derived myosin-like
CC   protein 1 (hGDMLP-1). The protein and polynucleotide sequences of
CC   hGDMLP-1 can be used in gene therapy and vaccine production. The
CC   hGDMLP-1 nucleic acids can be used as probes to detect, characterise
CC   and quantify hGDMLP-1 nucleic acids in samples, as amplification
CC   substrates, to provide initial substrates for the recombinant engineering
CC   of hGDMLP-1 protein variants having desired phenotypic improvements, and
CC   for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
CC   be used as immunogens to raise antibodies that specifically recognise
CC   hGDMLP-1 proteins, as standards in assays used to determine the
CC   concentration and/or amount specifically of hGDMLP proteins, as specific
CC   biomolecule capture probes for surface-enhanced laser desorption
CC   ionisation, as therapeutic supplement in patients having specific
CC   deficiency in hGDMLP-1 production, and in vaccines or for replacement
CC   therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
CC   diagnosing a disorder associated with the expression of hGDMLP-1, in
CC   particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
CC   chromosome 22. The present sequence represents an oligomer used in the
CC   screening of the hGDMLP-1 sequence in the exemplification of the present
CC   invention.
CC   N.B. The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequence.
XX
SQ   Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 other;

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        565 ACACTGCTCCAGCAGGC 581
              || |||||||||| |||
Db         17 ACTCTGCTCCAGCTGGC 1


RESULT 249
ABN08391/c
ID   ABN08391 standard; DNA; 17 BP.
XX
AC   ABN08391;
XX
DT   29-MAY-2002  (first entry)
XX
DE   Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8383.
XX
KW   Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW   muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW   skeletal muscle disorder; amplicon; screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192524-A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US16981.
XX
PR   26-MAY-2000; 2000US-207456P..
PR   21-SEP-2000; 2000US-234687P.
PR   27-SEP-2000; 2000US-236359P.
PR   04-OCT-2000; 2000GB-0024263.
PR   30-JAN-2001; 2001WO-US00661.
PR   30-JAN-2001; 2001WO-US00662.
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00666.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   30-JAN-2001; 2001WO-US00670.
PR   05-FEB-2001; 2001US-266860P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Gu Y,  Ji Y,  Penn SG,  Hanzel DK,  Rank DR,  Chen W,  Shannon ME;
XX
DR   WPI; 2002-179446/23.
XX
PT   New polypeptide, for raising antibodies that recognize hGDMLP-1
PT   proteins, or as specific biomolecule capture probes for
PT   surface-enhanced laser desorption ionization, comprises human
PT   myosin-like protein hGDMLP-1 -
XX
PS   Disclosure; SEQ ID 8383; 214pp; English.
XX
CC   The present invention describes a human genome-derived myosin-like
CC   protein 1 (hGDMLP-1). The protein and polynucleotide sequences of
CC   hGDMLP-1 can be used in gene therapy and vaccine production. The
CC   hGDMLP-1 nucleic acids can be used as probes to detect, characterise
CC   and quantify hGDMLP-1 nucleic acids in samples, as amplification
CC   substrates, to provide initial substrates for the recombinant engineering
CC   of hGDMLP-1 protein variants having desired phenotypic improvements, and
CC   for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
CC   be used as immunogens to raise antibodies that specifically recognise
CC   hGDMLP-1 proteins, as standards in assays used to determine the
CC   concentration and/or amount specifically of hGDMLP proteins, as specific
CC   biomolecule capture probes for surface-enhanced laser desorption
CC   ionisation, as therapeutic supplement in patients having specific
CC   deficiency in hGDMLP-1 production, and in vaccines or for replacement
CC   therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
CC   diagnosing a disorder associated with the expression of hGDMLP-1, in
CC   particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
CC   chromosome 22. The present sequence represents an oligomer used in the
CC   screening of the hGDMLP-1 sequence in the exemplification of the present
CC   invention.
CC   N.B. The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequence.
XX
SQ   Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 other;

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
```

```
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        564 CACACTGCTCCAGCAGG 580
              ||| |||||||||| ||
Db         17 CACTCTGCTCCAGCTGG 1


RESULT 250
ABN10236
ID   ABN10236 standard; DNA; 17 BP.
XX
AC   ABN10236;
XX
DT   29-MAY-2002  (first entry)
XX
DE   Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10228.
XX
KW   Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW   muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW   skeletal muscle disorder; amplicon; screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192524-A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US16981.
XX
PR   26-MAY-2000; 2000US-207456P.
PR   21-SEP-2000; 2000US-234687P.
PR   27-SEP-2000; 2000US-236359P.
PR   04-OCT-2000; 2000GB-0024263.
PR   30-JAN-2001; 2001WO-US00661.
PR   30-JAN-2001; 2001WO-US00662.
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00666.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   30-JAN-2001; 2001WO-US00670.
PR   05-FEB-2001; 2001US-266860P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Gu Y,  Ji Y,  Penn SG,  Hanzel DK,  Rank DR,  Chen W,  Shannon ME;
XX
DR   WPI; 2002-179446/23.
XX
PT   New polypeptide, for raising antibodies that recognize hGDMLP-1
PT   proteins, or as specific biomolecule capture probes for
PT   surface-enhanced laser desorption ionization, comprises human
PT   myosin-like protein hGDMLP-1 -
XX
PS   Disclosure; SEQ ID 10228; 214pp; English.
XX
CC   The present invention describes a human genome-derived myosin-like
CC   protein 1 (hGDMLP-1). The protein and polynucleotide sequences of
CC   hGDMLP-1 can be used in gene therapy and vaccine production. The
CC   hGDMLP-1 nucleic acids can be used as probes to detect, characterise
CC   and quantify hGDMLP-1 nucleic acids in samples, as amplification
CC   substrates, to provide initial substrates for the recombinant engineering
CC   of hGDMLP-1 protein variants having desired phenotypic improvements, and
CC   for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
CC   be used as immunogens to raise antibodies that specifically recognise
CC   hGDMLP-1 proteins, as standards in assays used to determine the
CC   concentration and/or amount specifically of hGDMLP proteins, as specific
CC   biomolecule capture probes for surface-enhanced laser desorption
CC   ionisation, as therapeutic supplement in patients having specific
CC   deficiency in hGDMLP-1 production, and in vaccines or for replacement
CC   therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
CC   diagnosing a disorder associated with the expression of hGDMLP-1, in
CC   particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
CC   chromosome 22. The present sequence represents an oligomer used in the
CC   screening of the hGDMLP-1 sequence in the exemplification of the present
CC   invention.
CC   N.B. The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequence.
XX
SQ   Sequence 17 BP; 2 A; 7 C; 3 G; 5 T; 0 other;

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.8e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        253 ACCGACCTCCTGGGCTG 269
              ||| ||||||| |||||
Db          1 ACCTACCTCCTTGGCTG 17


RESULT 251
ABN10237
ID   ABN10237 standard; DNA; 17 BP.
XX
AC   ABN10237;
XX
DT   29-MAY-2002  (first entry)
XX
DE   Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10229.
XX
KW   Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW   muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW   skeletal muscle disorder; amplicon; screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192524-A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US16981.
XX
PR   26-MAY-2000; 2000US-207456P.
PR   21-SEP-2000; 2000US-234687P.
PR   27-SEP-2000; 2000US-236359P.
PR   04-OCT-2000; 2000GB-0024263.
PR   30-JAN-2001; 2001WO-US00661.
PR   30-JAN-2001; 2001WO-US00662.
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00666.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   30-JAN-2001; 2001WO-US00670.
PR   05-FEB-2001; 2001US-266860P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Gu Y,  Ji Y,  Penn SG,  Hanzel DK,  Rank DR,  Chen W,  Shannon ME;
XX
DR   WPI; 2002-179446/23.
XX
PT   New polypeptide, for raising antibodies that recognize hGDMLP-1
PT   proteins, or as specific biomolecule capture probes for
PT   surface-enhanced laser desorption ionization, comprises human
PT   myosin-like protein hGDMLP-1 -
XX
PS   Disclosure; SEQ ID 10229; 214pp; English.
XX
CC   The present invention describes a human genome-derived myosin-like
```

CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of
CC hGDMLP-1 can be used in gene therapy and vaccine production. The
CC hGDMLP-1 nucleic acids can be used as probes to detect, characterise
CC and quantify hGDMLP-1 nucleic acids in samples, as amplification
CC substrates, to provide initial substrates for the recombinant engineering
CC of hGDMLP-1 protein variants having desired phenotypic improvements, and
CC for expressing the proteins. The hGDMLP-1 proteins or polypeptides may
CC be used as immunogens to raise antibodies that specifically recognise
CC hGDMLP-1 proteins, as standards in assays used to determine the
CC concentration and/or amount specifically of hGDMLP proteins, as specific
CC biomolecule capture probes for surface-enhanced laser desorption
CC ionisation, as therapeutic supplement in patients having specific
CC deficiency in hGDMLP-1 production, and in vaccines or for replacement
CC therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for
CC diagnosing a disorder associated with the expression of hGDMLP-1, in
CC particular heart and skeletal muscle disorders. hGDMLP-1 is localised to
CC chromosome 22. The present sequence represents an oligomer used in the
CC screening of the hGDMLP-1 sequence in the exemplification of the present
CC invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.
XX
SQ Sequence 17 BP; 1 A; 7 C; 4 G; 5 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 254 CCGACCTCCTGGGCTGG 270
|| ||||||| ||||||
Db 1 CCTACCTCCTTGGCTGG 17

RESULT 252
ABK18358
ID ABK18358 standard; RNA; 17 BP.
XX
AC ABK18358;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG hammerhead ribozyme target sequence, Seq ID No 1005.
XX
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.
XX
OS Homo sapiens.
XX
PN WO200188124-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US15866.
XX
PR 16-MAY-2000; 2000US-0572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Jarvis T, Von Carlowitz I, McSwiggen JA, Mclaughlin F, Randi AM;
XX
DR WPI; 2002-082995/11.
XX
PT Novel polynucleotide which down regulates expression of Ets-related
PT gene, useful for treating cancer, diabetic retinopathy, macular
PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
PT syndrome -
XX
PS Claim 4; Page 77; 149pp; English.
XX
CC The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention.
XX
SQ Sequence 17 BP; 4 A; 6 C; 4 G; 3 U; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.8e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 713 CTGTGGCCCAGCAGCAG 729
|:|:|||||| || |||
Db 1 CUGUGGCCCAUCAACAG 17

RESULT 253
ABK19019/c
ID ABK19019 standard; RNA; 17 BP.
XX
AC ABK19019;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG DNAzyme target sequence Seq ID No 1666.
XX
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.
XX
OS Homo sapiens.
XX
PN WO200188124-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US15866.
XX
PR 16-MAY-2000; 2000US-0572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.

PA (GLAX) GLAXO GROUP LTD.
XX
PI Jarvis T, Von Carlowitz I, McSwiggen JA, Mclaughlin F, Randi AM;
XX
DR WPI; 2002-082995/11.
XX
PT Novel polynucleotide which down regulates expression of Ets-related
PT gene, useful for treating cancer, diabetic retinopathy, macular
PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
PT syndrome -
XX
PS Claim 4; Page 107; 149pp; English.
XX
CC The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention.
XX
SQ Sequence 17 BP; 7 A; 1 C; 6 G; 3 U; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 46 TCTTAGCATACTCCTCA 62
|||||||| |||||||
Db 17 TTTTAGCATCCTCCTCA 1

RESULT 254
ABK19334/c
ID ABK19334 standard; RNA; 17 BP.
XX
AC ABK19334;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG Amberzyme target sequence Seq ID No 1981.
XX
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.
XX
OS Homo sapiens.
XX
PN WO200188124-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US15866.
XX
PR 16-MAY-2000; 2000US-0572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Jarvis T, Von Carlowitz I, McSwiggen JA, Mclaughlin F, Randi AM;
XX
DR WPI; 2002-082995/11.
XX
PT Novel polynucleotide which down regulates expression of Ets-related
PT gene, useful for treating cancer, diabetic retinopathy, macular
PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
PT syndrome -
XX
PS Claim 4; Page 126; 149pp; English.
XX
CC The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention.
XX
SQ Sequence 17 BP; 7 A; 1 C; 6 G; 3 U; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 48 TTAGCATACTCCTCAAT 64
||||||| ||||||| |
Db 17 TTAGCATCCTCCTCATT 1

RESULT 255
ABT35326
ID ABT35326 standard; DNA; 17 BP.
XX
AC ABT35326;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 963.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX

OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB04208.
XX
PR 17-SEP-2001; 2001FR-0011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases
PT associated with tumors and cell degeneration, also related
PT polypeptides, antibodies and transfected cells -
XX
PS Disclosure; Page 145; 720pp; French.
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15
CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
CC sequence that hybridizes to them under highly stringent conditions, or
CC the complement of any of them, or the corresponding RNA. The novel
CC isolated nucleic acids of the invention are useful as probes and primers
CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
CC and for production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention.
XX
SQ Sequence 17 BP; 2 A; 10 C; 1 G; 4 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1199 GACCTTCACACCTCCCC 1215
|| |||| |||||||||
Db 1 GATCTTCCCACCTCCCC 17

RESULT 256
ABT35714
ID ABT35714 standard; DNA; 17 BP.
XX
AC ABT35714;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 1351.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB04208.
XX
PR 17-SEP-2001; 2001FR-0011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases
PT associated with tumors and cell degeneration, also related
PT polypeptides, antibodies and transfected cells -
XX
PS Disclosure; Page 191; 720pp; French.
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15
CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
CC sequence that hybridizes to them under highly stringent conditions, or
CC the complement of any of them, or the corresponding RNA. The novel
CC isolated nucleic acids of the invention are useful as probes and primers
CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
CC and for production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention.
XX
SQ Sequence 17 BP; 9 A; 3 C; 4 G; 1 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 273 GATCAAAGAGGAAGCAG 289
||||||| || ||||||
Db 1 GATCAAAAAGCAAGCAG 17

RESULT 257
ACA06320
ID ACA06320 standard; RNA; 17 BP.
XX
AC ACA06320;
XX
DT 03-JUN-2003 (first entry)
XX
DE NFKB sub-unit modulating inozyme substrate #139.
XX
KW Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;

KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW allergic airway inflammation; inflammatory bowel disease; infection;
KW ss.
XX
OS Homo sapiens.
XX
PN US2002177568-A1.
XX
PD 28-NOV-2002.
XX
PF 23-MAY-2001; 2001US-0864785.
XX
PR 15-AUG-1994; 94US-0291932.
PR 07-DEC-1992; 92US-0987132.
PR 18-MAY-1994; 94US-0245466.
PR 23-DEC-1996; 96US-0777916.
XX
PA (STIN/) STINCHCOMB D T.
PA (MCSW/) MCSWIGGEN J.
PA (DRAP/) DRAPER K G.
XX
PI Stinchcomb DT, Mcswiggen J, Draper KG;
XX
DR WPI; 2003-340953/32.
XX
PT Novel enzymatic nucleic acid molecules which down regulates expression
PT of a sequence encoding a subunit of nuclear factor kappa B useful for
PT treating cancer, inflammatory disorders and autoimmune diseases -
XX
PS Claim 3; Page 29; 72pp; English.
XX
CC The invention describes an enzymatic nucleic acid molecule (I) which down
CC regulates expression of a sequence encoding a subunit of nuclear factor
CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC configuration. The enzymatic nucleic acid molecule is adapted to treat
CC cancer and is useful for down-regulating REL-A activity in a cell, for
CC treating a patient having a condition associated with the level of REL-A.
CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
CC the presence of a divalent cation, especially Mg^2^+. The enzymatic and
CC antisense nucleic acid molecules are useful for treating breast, lung,
CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC multidrug resistant cancer. The method involves use of other drug
CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
CC acid molecules are also useful for treating inflammatory disease such as
CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
CC rejection, gene therapy applications, ischaemia/reperfusion injury
CC (central nervous system (CNS) and myocardial), glomerulonephritis,
CC sepsis, allergic airway inflammation, inflammatory bowel disease or
CC infection. This sequence represents the substrate of a novel
CC enzymatic nucleic acid molecule.
XX
SQ Sequence 17 BP; 3 A; 8 C; 4 G; 2 U; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.8e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1068 CATCAGGCAGGCTCTTC 1084
||:||||||||| | :|
Db 1 CAUCAGGCAGGCCCCUC 17

RESULT 258
ABZ61741
ID ABZ61741 standard; RNA; 17 BP.
XX
AC ABZ61741;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human H-Ras DNAzyme target #532.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US16840.
XX
PR 29-MAY-2001; 2001US-294140P.
PR 06-JUN-2001; 2001US-296249P.
PR 10-SEP-2001; 2001US-318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J;
XX
DR WPI; 2003-140484/13.
XX
PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
PS Claim 58; Page 121; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,
CC ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
CC sequences for the human ribozymes of the invention.
XX
SQ Sequence 17 BP; 2 A; 7 C; 5 G; 3 U; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 1.8e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 456 TGTGGTCAGCAGCCTGC 472
:| ||:||||||||: |
Db 1 UGCGGUCAGCAGCCUCC 17

RESULT 259
ABZ64935
ID ABZ64935 standard; RNA; 17 BP.
XX
AC ABZ64935;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human HER2 DNAzyme substrate #392.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.

XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US16840.
XX
PR 29-MAY-2001; 2001US-294140P.
PR 06-JUN-2001; 2001US-296249P.
PR 10-SEP-2001; 2001US-318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J;
XX
DR WPI; 2003-140484/13.
XX
PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
PS Claim 4; Page 140; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,
CC ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
CC sequences for the human ribozymes of the invention.
XX
SQ Sequence 17 BP; 5 A; 6 C; 6 G; 0 U; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 517 GCCAACCTGCCGGAGGA 533
||||||| ||| |||||
Db 1 GCCAACCGGCCAGAGGA 17

RESULT 260
ABZ65512
ID ABZ65512 standard; RNA; 17 BP.
XX
AC ABZ65512;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human HER2 DNAzyme substrate #969.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US16840.
XX
PR 29-MAY-2001; 2001US-294140P.
PR 06-JUN-2001; 2001US-296249P.
PR 10-SEP-2001; 2001US-318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J;
XX
DR WPI; 2003-140484/13.
XX
PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX
PS Claim 4; Page 151; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for
CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
CC acids are also useful for treating breast, ovarian, colorectal, lung,
CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
CC The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,
CC ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
CC sequences for the human ribozymes of the invention.
XX
SQ Sequence 17 BP; 8 A; 2 C; 6 G; 1 U; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 281 AGGAAGCAGCAGCAATG 297
|||||| | ||||||:|
Db 1 AGGAAGGAACAGCAAUG 17

RESULT 261
AAQ10847
ID AAQ10847 standard; DNA; 18 BP.
XX
AC AAQ10847;
XX
DT 08-MAY-1991 (first entry)
XX
DE Probe to N-terminal region of MAb T84.66 gamma heavy chain.
XX
KW MAb T84.66; gamma heavy chain; carcinoembryonic antigen; CEA;
KW human adenocarcinoma; mouse-human chimaeric antibody; ss.
XX
OS Mus musculus.
XX
PN WO9101990-A.
XX
PD 21-FEB-1991.
XX
PF 19-JUL-1990; 90WO-US04049.
XX
PR 26-JUL-1989; 89US-0385102.
XX
PA (CITY) CITY OF HOPE.
XX
PI Shively JE, Riggs AD, Neumaier M;
XX
DR WPI; 1991-073486/10.
XX
PT Novel anti-CEA antibody - comparable to ATCC Accession No. BH
PT 8747, produced by recombinant DNA, used in diagnosis of tumours
XX
PS Disclosure; Page 6; 24pp; English.
XX
CC The heavy chain variable region of murine MAb 84.66 was cloned as
CC follows: Hybridoma DNA was extracted, completely restricted with
CC EcoRI and run on a gel. Fragments were extracted and ligated in the

CC EcoRI site of Lambda-ZAP.Phage were packaged and plated. Plaque
CC screening was with a 991bp XbaI fragment from the mouse
CC enhancer region, a 1.5kb cDNA fragment from the heavy chain
CC constant region gene of hybridoma CEA.66-E3 and a 5.4kb EcoRI
CC fragment containing an aberrantly rearranged heavy chain from
CC Sp2/0. Positive clones were further characterised by hybridisation
CC to J-region oligonucleotides and a probe specific to the N-terminal
CC region. This probe was used to allow upstream characterisation of
CC the promoter region.
CC See also AAQ10834-Q10846, AAQ10848 and AAQ11098.
XX
SQ Sequence 18 BP; 3 A; 7 C; 4 G; 4 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 823 CTGATGCAGCTGAAGCT 839
||| |||||||||| ||
Db 1 CTGCTGCAGCTGAACCT 17

RESULT 262
AAQ78449
ID AAQ78449 standard; DNA; 18 BP.
XX
AC AAQ78449;
XX
DT 25-MAR-2003 (updated)
DT 27-JUN-1995 (first entry)
XX
DE TGF-beta gene phosphorothioate antisense oligonucleotide.
XX
KW Transforming growth factor beta; TGF-beta; antisense; treatment;
KW tumour; angiogenesis; breast tumour; neurofibroma; glioma;
KW glioblastoma; carcinogenesis; carcinoma; oesophagus; oesophageal;
KW gastric; gut; immunosuppression; oligonucleotide; ss.
XX
OS Synthetic.
XX
PN WO9425588-A2.
XX
PD 10-NOV-1994.
XX
PF 29-APR-1994; 94WO-EP01362.
XX
PR 30-APR-1993; 93EP-0107089.
PR 13-MAY-1993; 93EP-0107849.
XX
PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI Bogdahn U, Brysch W, Schlingensiepen G, Schlingensiepen K;
PI Schlingensiepen R;
XX
DR WPI; 1994-358266/44.
XX
PT New transforming growth factor beta anti:sense
PT oligo:nucleotide(s) - for treating immunosuppression, tumours,
PT etc.
XX
PS Claim 6; Page 52; 74pp; English.
XX
CC The antisense oligonucleotides are useful in the treatment of
CC tumours in which expression of TGF-beta is of relevance for
CC pathogenicity and/or inhibition of pathological angiogenesis. They
CC are used especially for the treatment of the immunosuppressive
CC effect of TGF-beta, augmentation of the proliferation of cytotoxic
CC lymphocytes, treatment of endogenous hyperexpression of TGF-beta,
CC treatment of breast tumours, neurofibromas and malignant gliomas,
CC including glioblastomas, treatment and prophylaxis of skin
CC carcinogenesis, and treatment of oesophageal and gastric carcinomas.
CC See AAQ78352-Q78488. The sequences given in GENESEQ files
CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of
CC TGF-beta 1. The sequences given in GENESEQ files AAQ78408-78487 are
CC antisense oligodeoxynucleotides of TGF-beta 2 in the form of
CC phosphorothioate analogues.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 18 BP; 7 A; 2 C; 5 G; 4 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1018 AGATGGTGCCAAAGTGC 1034
||||||| | |||||||
Db 2 AGATGGTACAAAAGTGC 18

RESULT 263
AAX67046/c
ID AAX67046 standard; RNA; 18 BP.
XX
AC AAX67046;
XX
DT 20-JUL-1999 (first entry)
XX
DE Mouse B7 hairpin ribozyme target SEQ ID NO:3678.
XX
KW Arthritic condition; graft tolerance; immune response; target; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
KW diagnosis; ss.
XX
OS Mus sp.
XX
PN WO9618736-A2.
XX
PD 20-JUN-1996.
XX
PF 22-NOV-1995; 95WO-US15516.
XX
PR 05-OCT-1995; 95US-0541365.
PR 13-DEC-1994; 94US-0354920.
PR 23-DEC-1994; 94US-0363253.
PR 23-DEC-1994; 94US-0363254.
PR 17-FEB-1995; 95US-0390850.
PR 20-APR-1995; 95US-0426124.
PR 02-MAY-1995; 95US-0432874.
PR 04-MAY-1995; 95US-0434509.
PR 07-JUL-1995; 95US-0000951.
PR 07-JUL-1995; 95US-0000974.
PR 07-AUG-1995; 95US-0512861.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Draper K, Gustofson J, McSwiggen J, Pavco P, Stinchcomb DT;
PI Beigelman L, Karpeisky A, Modak A, Usman N, Burgin A;
PI Matulic-Adamic J, Jarvis T, Thompson JD, Wincott F;
XX
DR WPI; 1996-300653/30.
XX
PT Enzymatic nucleic acid molecules having a hammer-head motif - used
PT for the treatment of arthritis, induction of graft tolerance or
PT treatment of auto-immune diseases
XX
PS Claim 10; Page 215; 307pp; English.
XX
CC The present invention describes a novel enzymatic nucleic acid (ENA)
CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose
CC residues; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii)
CC at least ten 2'-O-methyl modifications; and (iv) a 3'-end modification.
CC The ENA's can inhibit collagenase and stromelysin production in the
CC synovial membrane of joints for the treatment or prevention of arthritis,
CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also

CC be used to treat antigen presenting cells of a donor to induce tolerance
CC in a recipient to an alloantigen of a donor. They can also be used for
CC enhancing graft tolerance or for treating autoimmune disease, and for
CC treating allergies and other inflammatory conditions. The ENA's can also
CC be used in diagnosis. Ribozyme therapy impacts on the expression of
CC stromelysin without introducing the non-specific effects upon gene
CC expression which accompany treatment with retinoids and dexamethasone.
CC The concentration of ribozyme required to affect a therapeutic treatment
CC is lower than that required of antisense molecules, and is highly
CC specific. The present sequence is used in the exemplification of the
CC present invention.
XX
SQ Sequence 18 BP; 2 A; 6 C; 2 G; 8 U; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1157 GGAAGTAAAGCAGCTAA 1173
||||| ||||||| |||
Db 18 GGAAGCAAAGCAGGTAA 2

RESULT 264
AAX62708
ID AAX62708 standard; RNA; 18 BP.
XX
AC AAX62708;
XX
DT 16-JUL-1999 (first entry)
XX
DE Granule bound starch synthase hairpin substrate SEQ ID NO:583.
XX
KW Maize; corn; Zea mays; delta-9 desaturase; GBSS; target; substrate;
KW granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
KW modulation; gene expression; transgenic plant; cleavage; canola plant;
KW caffeine synthesis; coffee plant; nicotine production; tobacco;
KW fruit ripening; flower pigmentation; lignin production; ss.
XX
OS Zea mays.
XX
PN WO9710328-A2.
XX
PD 20-MAR-1997.
XX
PF 12-JUL-1996; 96WO-US11689.
XX
PR 13-JUL-1995; 95US-0001135.
XX
PA (DOWC) DOWELANCO.
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Edington BE, Folkerts O, Guo L, McSwiggen JA, Merlo DJ;
PI Merlo PAO, Skokut TA, Young SA, Zwick MG;
XX
DR WPI; 1997-202224/18.
XX
PT Ribozyme which modulates plant gene expression - preferably
PT modulates expression of DELTA-9 desaturase or granule bound starch
PT synthase in maize or canola
XX
PS Claim 42; Page 83; 155pp; English.
XX
CC The present invention describes an enzymatic nucleic acid molecule (I)
CC with RNA cleaving activity, which modulates the expression of a plant
CC gene. Also described is a gene comprising a cDNA sequence encoding maize
CC Delta-9 desaturase. (I) can be used to modulate expression of a gene,
CC preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)
CC gene, in a plant (preferably a maize or canola plant). (I) can be used
CC to modulate caffeine synthesis in a coffee plant, nicotine production in
CC a tobacco plant, fruit ripening processes in an apple, tomato, pear,
CC plum or peach plant, flower pigmentation in a rose, petunia,
CC chrysanthemum or marigold plant or lignin production in a tobacco,
CC aspen, poplar or pine plant.
XX
SQ Sequence 18 BP; 2 A; 6 C; 6 G; 4 U; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 18;
Best Local Similarity 70.6%; Pred. No. 1.9e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 890 AGCTGCGGTACAGCGTG 906
|||:||||: |||| :|
Db 1 AGCUGCGGUUCAGCCUG 17

RESULT 265
AAT87896/c
ID AAT87896 standard; DNA; 18 BP.
XX
AC AAT87896;
XX
DT 12-JAN-1998 (first entry)
XX
DE Lower primer for exon 1 of human interleukin 9 gene.
XX
KW Human; interleukin 9; asthma associated factor 1; IL-9; primer;
KW atopic allergy; asthma; bronchial hyperesponsiveness; BHR; eczema;
KW rhinitis; urticaria; allergic inflammation; bowel; amplification;
KW polymorphism; polymerase chain reaction; PCR; exon 1; ss.
XX
OS Synthetic.
XX
PN WO9708321-A1.
XX
PD 06-MAR-1997.
XX
PF 23-AUG-1996; 96WO-US12757.
XX
PR 06-AUG-1996; 96US-0023800.
PR 24-AUG-1995; 95US-0002765.
XX
PA (MAGA-) MAGAININ PHARM INC.
XX
PI Lee MW, Levitt RC, Nicholas N, Prasad KU;
XX
DR WPI; 1997-179278/16.
XX
PT Human interleukin-9 variant with Met at position 117 - useful for
PT treating atopic allergy, esp. asthma
XX
PS Disclosure; Page 42; 142pp; English.
XX
CC The present sequence is a primer for the PCR amplification of
CC exon 1 from the human interleukin 9 (hIL-9), also known as asthma
CC associated factor 1, gene. hIL-9 plays a role in atopic allergy,
CC asthma and related disorders, e.g. bronchial hyperesponsiveness
CC (BHR), rhinitis, urticaria, allergic inflammatory disorders of the
CC bowel and various forms of eczema. A naturally occurring
CC polymorphism has been identified at position 117 of hIL-9,
CC individuals homozygous for Met at position 117 demonstrate, e.g. a
CC lack of asthma and low serum immunoglobulin E (IgE) levels, while
CC Thr/Thr homozygotes and Thr/Met heterozygotes are susceptible to
CC asthma.
XX
SQ Sequence 18 BP; 2 A; 11 C; 2 G; 3 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 464 GCAGCCTGCAGGGGGAG 480
| || ||||||||||||
Db 17 GTAGGCTGCAGGGGGAG 1

```
RESULT 266
AAV57794
ID   AAV57794 standard; DNA; 18 BP.
XX
AC   AAV57794;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Human chromosome 18 PCR mapping primer clone 47r.
XX
KW   Manic-depressive illness; susceptibility; genotype; diagnosis;
KW   chromosomal marker; polymorphic marker; chromosome 18; human;
KW   myo-inositol monophosphatase protein; IMP-18p; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9818963-A1.
XX
PD   07-MAY-1998.
XX
PF   28-OCT-1997;   97WO-US19381.
XX
PR   28-OCT-1996;   96US-0029278.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Badner JA,  Berrettini WH,  Detera-Wadleigh SD,  Esterling LE;
PI   Gershon ES,  Goldin LR,  Sanders AR,  Yoshikawa T;
XX
DR   WPI; 1998-272247/24.
XX
PT   New isolated IMP.18p myo-inositol monophosphatase - used to develop
PT   products for determining susceptibility to manic depressive illness
PT   and as targets for preventive and therapeutic treatments
XX
PS   Example 5; Page 71; 118pp; English.
XX
CC   A method has been developed for determining a genotype associated with
CC   increased susceptibility to manic-depressive (MD) illness. The method
CC   comprises determining the genotype of an affected individual with at
CC   least one polymorphic marker localised within the chromosomal region
CC   defined by and including markers D18S843 and D18S869 and determining the
CC   genotype associated with increased susceptibility to MD disorder. The
CC   method can be used for determining susceptibility to MD illness
CC   including bipolar disorder, genetic counselling of individuals from
CC   families affected with MD illness, and aid in the differential diagnosis
CC   of MD illness from other psychiatric pathologies. Products from the
CC   present invention can also be used to obtain modulators of IMP.18p myo-
CC   inositol monophosphatase protein activity and as targets for preventive
CC   and therapeutic treatments. The present sequence represents a PCR primer
CC   used in the mapping of human chromosome 18 for determining the genotype
CC   of MD illness susceptibility, used in an example from the present
CC   invention.
XX
SQ   Sequence 18 BP; 2 A; 4 C; 4 G; 8 T; 0 other;

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1319 GTGCTTTTGTAGATCTT 1335
              ||||||  |||||  ||||
Db          2 GTGCTTCTGTAGCTCTT 18


RESULT 267
AAV41332/c
ID   AAV41332 standard; DNA; 18 BP.
XX
AC   AAV41332;
XX
DT   06-OCT-1998  (first entry)
XX
DE   Interleukin-9 (IL-9) gene exon 1 specific lower primer.
XX
KW   Interleukin; IL-9; AAF1; asthma associated factor; human; IBD;
KW   inflammatory bowel disease; Th2 mediated immune response; lupus;
KW   Crohn's disease; chronic non-specific ulcerative colitis; diabetes;
KW   multiple sclerosis; arthritis; autoimmune disease; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9827997-A1.
XX
PD   02-JUL-1998.
XX
PF   22-DEC-1997;   97WO-US23527.
XX
PR   19-DEC-1997;   97US-0994986.
PR   20-DEC-1996;   96US-0034331.
XX
PA   (MAGA-) MAGAININ PHARM INC.
XX
PI   Levitt RC,  Nicolaides NC;
XX
DR   WPI; 1998-377404/32.
XX
PT   Treating inflammatory bowel diseases, e.g. Crohn's disease - and
PT   chronic non-specific ulcerative colitis by administering compounds
PT   up-regulating function of interleukin-9 or its receptor
XX
PS   Disclosure; Page 23; 61pp; English.
XX
CC   Sequences shown in AAV41331 to AAV41340 represent exon specific primers
CC   of human interleukin (IL-9) gene. The invention provides a method
CC   for the treatment of inflammatory bowel disease (IBD) or related
CC   disorders that comprises administering a compound that up-regulates the
CC   function of IL-9 or the IL-9 receptor. A method for monitoring humans
CC   undergoing IBD treatment with polypeptides with human IL-9 sequence
CC   (or fragments), by evaluating IL-9 levels in samples taken at different
CC   times, and a method for screening for cells expressing the IL-9 receptor
CC   by detecting binding of a specific ligand are also provided. Compounds
CC   up-regulating the function of IL-9 or the IL-9 receptor can be used
CC   therapeutically (in pharmaceutical compositions, optionally with
CC   acceptable carriers) to treat IBD and other related inflammatory
CC   disorders. IBDs (which include Crohn's diseases and chronic non-specific
CC   ulcerative colitis) are diseases characterised by an inappropriate
CC   inflammatory response to environmental stimuli. Immune responses to
CC   antigens are classified as Th1 or Th2 responses, and evidence suggests
CC   that IBDs are dominated by a Th1 mediated, antigen induced, inflammatory
CC   response. Other related Th1 mediated diseases include multiple
CC   sclerosis, diabetes, arthritis, lupus and autoimmune diseases. The method
CC   is based on the observation that the Th2 response is up-regulated by
CC   IL-9.
XX
SQ   Sequence 18 BP; 2 A; 11 C; 2 G; 3 T; 0 other;

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        464 GCAGCCTGCAGGGGGAG 480
              | || ||||||||||||
Db         17 GTAGGCTGCAGGGGGAG 1


RESULT 268
AAZ70371
ID   AAZ70371 standard; DNA; 18 BP.
XX
AC   AAZ70371;
XX
DT   10-SEP-2001  (first entry)
XX
```

DE Human biallelic marker upstream amplification primer SEQ ID NO:4727.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX
PS Claim 8; Page 1239; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 18 BP; 4 A; 0 C; 8 G; 6 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy        935 TGGAGAAGAGGTGTGAG 951
              ||||||||||| || |
Db          2 TGGAGAAGAGGTTTGTG 18
```

RESULT 269
AAA09267
ID AAA09267 standard; cDNA; 18 BP.
XX
AC AAA09267;
XX
DT 10-AUG-2000 (first entry)
XX
DE 3' primer for rat alpha-2-delta-C DNA amplification.
XX
KW alpha-2-delta-C; calcium channel subunit; gabapentin; cytostatic;
KW anticonvulsant; antimigrane; antiparkinsonian; antidepressant;
KW primer; ss.
XX
OS Rattus sp.
XX
PN WO200020450-A2.
XX
PD 13-APR-2000.
XX
PF 07-OCT-1999; 99WO-US23519.
XX
PR 07-OCT-1998; 98US-0103322.
PR 30-OCT-1998; 98US-0106473.
PR 29-DEC-1998; 98US-0114088.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Johns MA, Moldover B, Offord JD;
XX
DR WPI; 2000-303744/26.
XX
PT New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
PT proteins, useful in the treatment of epilepsy, migraine, chronic pain,
PT anxiety, multiple sclerosis or cancer
XX
PS Example 2; Page 82; 88pp; English.
XX
CC The alpha-2-delta-C gene encodes a calcium channel subunit polypeptide.
CC The human gene has been mapped to chromosome 3p21.1. This gene and the
CC alpha-2-delta-D and -B genes are useful for protecting mammalian cells
CC from abnormal calcium flux by introducing expression vectors containing
CC the respective gene into mammalian cells. The antisense genes are also
CC useful for treating or preventing epilepsy. The alpha-delta-2-A protein
CC is a high-affinity binding target of the anti-convulsant drug gabapentin.
CC Therefore, alpha-delta-2 proteins may also be targeted to treat
CC seizure-related syndromes, migraine, ataxia, vestibular defects, chronic
CC pain, sleep interference, anxiety, amyotropic lateral sclerosis (ALS),
CC multiple sclerosis, mania, tremor, parkinsonism, substance abuse or
CC addiction syndromes, mood, depression or cancer.
XX
SQ Sequence 18 BP; 6 A; 4 C; 8 G; 0 U; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy        279 AGAGGAAGCAGCAGCAA 295
              || || ||||||||||
Db          1 AGGGGCAGCAGCAGCAA 17
```

RESULT 270
AAD19799/c
ID AAD19799 standard; DNA; 18 BP.
XX
AC AAD19799;
XX
DT 18-DEC-2001 (first entry)
XX
DE CmYLCV viral genomic DNA amplifying S1 forward PCR primer.
XX
KW Cestrum yellow leaf curling virus; CmYLCV; transcription; PCR primer;
KW transgenic plant; ss.
XX
OS Cestrum yellow leaf curling virus.
XX
PN WO200173087-A1.
XX
PD 04-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-EP03408.
XX
PR 27-MAR-2000; 2000GB-0007427.
PR 28-APR-2000; 2000GB-0010486.
PR 26-JAN-2001; 2001EP-0101802.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX
PI Hohn T, Stavolone L, De Haan PT, Ligon HT, Kononova M;
XX
DR WPI; 2001-616524/71.
XX
PT Novel DNA sequence obtained from genome of Cestrum yellow leaf curling
PT virus for conferring constitutive expression of an associated desired
PT polynucleotide -
XX
PS Example 1; Page 21; 100pp; English.
XX
CC The invention relates to Cestrum yellow leaf curling virus (CmYLCV) novel
CC DNA sequences which functions as transcription promoters of an associated
CC polynucleotide sequence. These CmYLCV DNA molecules confers constitutive
CC expression of associated polynucleotide sequences. The invention also
CC relates to recombinant DNA sequences containing promoter sequences which
CC are used for creating transgenic plants expressing DNA of interest at all
CC times and in most tissues and organs. The present DNA sequence is a PCR
CC primer which is used for amplifying Cestrum yellow leaf curling virus
CC genomic DNA related to the invention.
XX
SQ Sequence 18 BP; 9 A; 5 C; 3 G; 1 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 446 TGCTGAAGTTTGTGGTC 462
|| |||| ||||||||||
Db 17 TTCTGATGTTTGTGGTC 1

RESULT 271
AAS45542/c
ID AAS45542 standard; DNA; 18 BP.
XX
AC AAS45542;
XX
DT 18-DEC-2001 (first entry)
XX
DE Tumour-specific IgV region gene, PCR primer Cgamma3.
XX
KW Human; B cell lymphoma; cytostatic; immunostimulator; self-antigen;
KW tumour-specific vaccine; tumour; polyclonal immune response;
KW idiotype-specific anti-lymphoma immune response; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200168682-A1.
XX
PD 20-SEP-2001.
XX
PF 13-OCT-2000; 2000WO-US28362.
XX
PR 10-MAR-2000; 2000US-0522900.
XX
PA (LARG-) LARGE SCALE BIOLOGY CORP.
PA (MCCO/) MCCORMICK A A.
PA (TUSE/) TUSE D.
XX
PI Reinl SJ, Turpen TH;
XX
DR WPI; 2001-596903/67.
XX
PT Novel polypeptide vaccine produced in plants, useful for inducing an
PT immune response to a self-antigen on the surface of certain tumour cells
PT -
XX
PS Disclosure; Page 26; 89pp; English.
XX
CC The invention relates to a novel polypeptide self-antigen (I) useful as a
CC tumour-specific vaccine in a subject with a tumour or at risk of
CC developing a tumour. (I) includes an epitope or epitopes unique to,
CC or over expressed by, cells of the tumour, thereby distinguishing the
CC tumour from all other tumours of the same or different histological type,
CC or in the subject or in another member of the subject's species. (I) is
CC epitopes in their native form. (I) is capable of inducing an immune
CC response in a mammal, when used as an individual-specific immunogenic
CC product comprising (I); and as a vaccine composition useful for inducing
CC a tumour-specific immune response, idiotype-specific anti-lymphoma immune
CC response, a polyclonal immune response to at least one idiotype of a
CC surface immunoglobulin or a polyclonal immune response to an idiotype.
CC The vaccine composition is useful for inducing a tumour-specific immune
CC antibody response in a tumour-bearing subject or a subject who had a
CC tumour e.g. B-cell lymphoma, and was treated so that no tumour is
CC clinically or radiographically evident. (I) is useful for inducing a
CC protective antitumour immune response. (I) can be produced at high
CC levels, is easy to purify and can be appropriately folded to mimic the
CC conformation of the native epitopes displayed at the tumour cell surface.
CC AAS45529-AAS45579 represent B cell lymphoma self antigen vaccine
CC linker sequences and PCR primers of the invention.
XX
SQ Sequence 18 BP; 4 A; 7 C; 5 G; 2 T; 0 other;

Query Match 1.0%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 262 CTGGGCTGGCTGATCAA 278
|||||||| ||| ||||
Db 18 CTGGGCTGCCTGGTCAA 2

RESULT 272
AAF62371/c
ID AAF62371 standard; DNA; 18 BP.
XX
AC AAF62371;
XX
DT 06-JUN-2001 (first entry)
XX
DE Zinc finger coding sequence related oligo SEQ ID NO: 96.
XX
KW Leptin; human; LSR; lipolysis stimulated receptor; obesity;
KW hypertension; anorexia; cachexia; stroke; atherosclerosis; ds.
XX
OS Synthetic.
XX
PN WO200121647-A2.
XX
PD 29-MAR-2001.
XX
PF 22-SEP-2000; 2000WO-IB01470.
XX
PR 22-SEP-1999; 99US-0155506.
XX
PA (GEST) GENSET.
XX
PI Yen F, Erickson MR, Fruebis J, Bihain B;
XX
DR WPI; 2001-218642/22.
XX
PT New leptin polypeptide fragment and related polynucleotides, useful for
PT the prevention and treatment of obesity and obesity-related diseases
PT such as hypertension and diabetes -
XX
PS Example 12; Page 245; 247pp; English.
XX
CC The present invention provides the protein and coding sequences of leptin
CC fragments which modulate the activity of lipolysis stimulated factor
CC (LSR). These sequences are useful in the treatment of obesity related
CC diseases, including obesity, anorexia, cachexia, cardiac and coronary
CC insufficiency, stroke, hypertension, atheromatous disease,
CC atherosclerosis, non-insulin dependent diabetes, hyperlipidaemia,
CC hyperuricaemia and syndrome X.
XX

```
SQ   Sequence 18 BP; 1 A; 4 C; 12 G; 1 T; 0 other;

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        192 CGCCCACCCGGACGCCG 208
              | ||||||||| |||||
Db         18 CTCCCACCCGGCCGCCG 2


RESULT 273
AAF92873
ID   AAF92873 standard; DNA; 18 BP.
XX
AC   AAF92873;
XX
DT   17-MAY-2001  (first entry)
XX
DE   Human ABC1 transcription factor binding site #34.
XX
KW   High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
XX
OS   Homo sapiens.
XX
PN   WO200115676-A2.
XX
PD   08-MAR-2001.
XX
PF   01-SEP-2000; 2000WO-IB01492.
XX
PR   01-SEP-1999;   99US-0151977.
PR   15-MAR-2000; 2000US-0526193.
PR   23-JUN-2000; 2000US-0213958.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
PA   (XENO-) XENON GENETICS INC.
XX
PI   Hayden MR,  Brooks-Wilson AR,  Pimstone SN,  Clee SM;
XX
DR   WPI; 2001-244356/25.
XX
PT   Treating a lower than normal high density lipoprotein-cholesterol
PT   (HDL-C) level, a higher than normal triglyceride level, or a
PT   cardiovascular disease, by administering a compound that modulates LXR-
PT   or RXR-mediated transcriptional activity -
XX
PS   Disclosure; Fig 3; 317pp; English.
XX
CC   The present invention relates to a method for treating a patient
CC   diagnosed as having a lower than normal high density
CC   lipoprotein-cholesterol (HDL-C) level, a higher than normal
CC   triglyceride level, or a cardiovascular disease, involving
CC   administering a compound that modulates LXR- or RXR-mediated
CC   transcriptional activity or ABC1 expression or activity.
CC   The LXR gene product may be used in an assay to identify
CC   compounds useful for the treatment of a disease or condition selected a
CC   lower than normal HDL cholesterol level, a higher than normal
CC   triglyceride level, and a cardiovascular disease.
XX
SQ   Sequence 18 BP; 3 A; 5 C; 7 G; 3 T; 0 other;

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        498 GCAGCGTCTTGGGGTCA 514
              |||| ||| ||||||||
Db          2 GCAGAGTCCTGGGGTCA 18


RESULT 274
AAH47607/c
ID   AAH47607 standard; DNA; 18 BP.
XX
AC   AAH47607;
XX
DT   30-NOV-2001  (first entry)
XX
DE   Human Her-3 mRNA inhibiting antisense oligo ISIS # 19622.
XX
KW   Her-3; epidermal growth factor; EGF; receptor/tyrosine kinase; human;
KW   antiinflammatory; cytostatic; antibacterial; antisense; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US6277640-B1.
XX
PD   21-AUG-2001.
XX
PF   31-JUL-2000; 2000US-0630706.
XX
PR   31-JUL-2000; 2000US-0630706.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Cowsert LM;
XX
DR   WPI; 2001-535134/59.
XX
PT   Antisense compounds capable of modulating expression of human Her-3,
PT   member of epidermal growth factor family of receptor/tyrosine kinases,
PT   useful for preventing or delaying infection, inflammation or tumor
PT   formation -
XX
PS   Example 15; Column 43-44; 49pp; English.
XX
CC   The invention provides antisense compounds capable of inhibiting the
CC   expression of human Her-3, a member of epidermal growth factor (EGF)
CC   family of receptor/tyrosine kinases. The antisense oligonucleotides are
CC   useful for inhibiting the expression of Her-3 in cells or tissues. They
CC   are commonly used as research reagents and in diagnostics for example, to
CC   elucidate the function of particular genes. The antisense compounds are
CC   also useful for distinguishing between functions of various members of a
CC   biological pathway and for research use. They are also utilized for
CC   diagnostics, therapeutics, prophylaxis and in kits. They are useful
CC   prophylactically, e.g. to prevent or delay infection, inflammation or
CC   tumor formation. Sequences AAH47532-47615 represent chimeric antisense
CC   phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap,
CC   used for the inhibition of Her-3 mRNA expression.
XX
SQ   Sequence 18 BP; 6 A; 1 C; 9 G; 2 T; 0 other;

  Query Match             1.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 1.9e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        977 CTTGACCAGTCCCATTC 993
              |||  ||||||||||||
Db         18 CTTTCCCAGTCCCATTC 2


RESULT 275
ABX03799
ID   ABX03799 standard; cDNA; 18 BP.
XX
AC   ABX03799;
XX
DT   09-JAN-2003  (first entry)
XX
DE   DNA encoding secreted protein signal peptide sequence #8.
XX
KW   Differential display method; leucine-rich motif; transmembrane protein;
KW   secreted protein; secreted protein signal peptide; ss.
XX
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